

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2007, 19:53:50 ; Search time 7245 seconds
(without alignments)
21790.305 Million cell updates/sec

Title: US-09-944-929-82
 Perfect score: 2284
 Sequence: 1 gggagagcatccggtgcgggc.....ataaatcttttggttactcaa 2284

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters:	15137082
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Database : GenEmbl.*
1: gb env.*
2: gb pat.*
3: gb ph.*
4: gb pl.*
5: gb pr.*
6: gb ro.*
7: gb sts.*
8: gb sy.*
9: gb un.*
10: gb vi.*
11: gb ov.*
12: gb hcg.*
13: gb ln.*
14: gb om.*
15: gb ba.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2284	100.0	2284	2	BD140585	BD140585 Polypeptide
2	2284	100.0	2284	2	BD378361	BD378361 SECRETED
3	2284	100.0	2284	2	AR252736	AR252736 Sequence
4	2284	100.0	2284	2	DD028540	DD028540 Secreted
5	2284	100.0	2284	2	DD031661	DD031661 COMPOSITI
6	2284	100.0	2284	2	DD039442	DD039442 Secreted
7	2284	100.0	2284	2	DD249590	DD249590 Secreted
8	2284	100.0	2284	2	AR429104	AR429104 Sequence
9	2284	100.0	2284	2	AR534995	AR534995 Sequence
10	2284	100.0	2284	2	AR691142	AR691142 Sequence
11	2284	100.0	2284	2	AR693626	AR693626 Sequence
12	2284	100.0	2284	2	AR705580	AR705580 Sequence
13	2284	100.0	2284	2	AR706178	AR706178 Sequence
14	2284	100.0	2284	2	AR708652	AR708652 Sequence
15	2284	100.0	2284	2	AR757551	AR757551 Sequence
16	2284	100.0	2284	2	AR759051	AR759051 Sequence
17	2284	100.0	2284	2	AR776365	AR776365 Sequence
18	2284	100.0	2284	2	AR809069	AR809069 Sequence

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C 93	242.6	10.6	115136	5	AL390994 Human DNA
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C 95	242.4	10.6	120224	5	BA000041_09
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C 97	242.2	10.6	102564	5	AC015916 Homo sapi
C 98	242.2	10.6	77027	5	AL161792 Human DNA
C 99	242.2	10.6	170864	12	AL187719 Pan trogl
C 100	242.2	10.6	205167	12	AP002891 Homo sapi
C 101	242.2	10.6	208038	12	AC187740 Pan trogl
C 102	241.8	10.6	223844	5	AC183380 Pan trogl
C 103	241.6	10.6	157879	5	AC149230 Pan trogl
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C 112	241.4	10.6	150285	5	AL109936 Human DNA
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C 115	241.2	10.6	155769	5	AC026164 Homo sapi
C 116	241.2	10.6	180915	5	HS495L19
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C 166	239.2	10.5	70448	5	CR388372 Human DNA
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C 178	239.2	10.5	184469	12	AL365447 Homo sapi
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243	237.4	10.4	113241	5	HUAC002425	HUAC002425 Homo sapi	c 316	236.2	10.3	130381	5	AC002402	AC002402 Human Chr
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245	237.4	10.4	137371	5	AC026411	AC026411 Homo sapi	c 318	236.2	10.3	157393	12	AC036212	AC036212 Homo sapi
246	237.4	10.4	148290	5	AL359199	AL359199 Human DNA	c 319	236.2	10.3	162696	12	AC090417	AC090417 Homo sapi
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250	237.4	10.4	167390	5	AC007263	AC007263 Homo sapi	c 323	236.2	10.3	180766	5	AC090691	AC090691 Homo sapi
251	237.4	10.4	170039	12	AC138814	AC138814 Homo sapi	c 324	236.2	10.3	182303	5	AL356750	AL356750 Human DNA
252	237.4	10.4	182289	5	AC138894	AC138894 Homo sapi	c 325	236.2	10.3	188712	5	AC016582	AC016582 Homo sapi
253	237.4	10.4	184125	12	AC145283	AC145283 Homo sapi	326	236.2	10.3	189357	12	AC160025	AC160025 Pan trogl
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255	237.4	10.4	200542	5	CNS01R63	AL157736 Human chr	328	236.2	10.3	208185	12	AC009105	AC009105 Homo sapi
256	237.4	10.4	202478	5	AC006560	AC006560 Homo sapi	c 329	236	10.3	57084	5	AL158813	AL158813 Human DNA
257	237.4	10.4	208932	12	AC137487	AC137487 Homo sapi	c 330	236	10.3	97114	5	AL356389	AL356389 Human DNA
258	237.4	10.4	239008	12	AC022460	AC022460 Homo sapi	c 331	236	10.3	103146	5	HS187N21	HS187N21 Human DNA
259	237.2	10.4	45746	5	AC005619	AC005619 Homo sapi	c 332	236	10.3	121068	5	AC015876	AC015876 Homo sapi
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261	237.2	10.4	120883	12	CT009524	CT009524 Homo sapi	c 334	236	10.3	146500	5	AC004453	AC004453 Homo sapi
262	237.2	10.4	151834	5	AC005399	AC005399 Homo sapi	c 335	236	10.3	151828	5	AL354740	AL354740 Human DNA
263	237.2	10.4	156507	12	AC036184	AC036184 Homo sapi	336	236	10.3	167512	12	AC015708	AC015708 Homo sapi
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266	237.2	10.4	260409	5	AC004019	AC004019 Homo sapi	c 339	236	10.3	168898	12	AC026974	AC026974 Homo sapi
267	237	10.4	601	2	AR660594	AR660594 Sequence	c 340	236	10.3	170790	12	AC068238	AC068238 Homo sapi
268	237	10.4	601	2	AR664602	AR664602 Sequence	c 341	236	10.3	173341	12	AC068238	AC068238 Homo sapi
269	237	10.4	41087	5	HSJ659F15	AL096791 Human DNA	c 342	236	10.3	175382	5	AC112135	AC112135 Homo sapi
270	237	10.4	45670	5	AL391094	AL391094 Human DNA	c 343	236	10.3	178026	12	AC146438	AC146438 Pan trogl
271	237	10.4	96376	12	AC007626	AC007626 Homo sapi	c 344	236	10.3	187795	12	AC025405	AC025405 Homo sapi
272	237	10.4	100000	5	AP000065	AP000065 Homo sapi	c 345	236	10.3	188296	5	AC022324	AC022324 Homo sapi
273	237	10.4	103699	5	AC034305	AC034305 Homo sapi	c 346	236	10.3	188470	12	AC093305	AC093305 Homo sapi
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277	237	10.4	173452	5	AC003013	AC003013 Human PAC	c 350	235.8	10.3	127334	5	AC109579	AC109579 Homo sapi
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280	236.8	10.4	152037	5	CS350835	CS350835 Sequence	c 353	235.8	10.3	152355	5	AC005668	AC005668 Homo sapi
281	236.8	10.4	152037	5	HS167A19	AL031427 Human DNA	c 354	235.8	10.3	168606	5	AC109133	AC109133 Homo sapi
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283	236.8	10.4	167099	5	AC110079	AC110079 Homo sapi	c 356	235.8	10.3	174021	5	AL358612	AL358612 Human DNA
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286	236.6	10.4	79319	5	AL512274	AL512274 Human DNA	c 359	235.8	10.3	194730	5	AC136967	AC136967 Papio anu
287	236.6	10.4	158591	5	AC010188	AC010188 Homo sapi	c 360	235.6	10.3	42265	5	AC007136	AC007136 Homo sapi
288	236.6	10.4	170388	12	AC027750	AC027750 Homo sapi	361	235.6	10.3	75224	5	AC134510	AC134510 Homo sapi
289	236.6	10.4	171193	5	AC183807	AC183807 Pan trogl	c 362	235.6	10.3	88848	5	AC107377	AC107377 Homo sapi
290	236.6	10.4	175833	5	AC046135	AC046135 Homo sapi	363	235.6	10.3	124949	5	AL358794	AL358794 Human DNA
291	236.6	10.4	177623	12	AC067825	AC067825 Homo sapi	364	235.6	10.3	128871	5	AL157838	AL157838 Human DNA
292	236.6	10.4	182632	5	AC007282	AC007282 Homo sapi	c 365	235.6	10.3	142707	5	HSJ279A18	HSJ279A18 Human DNA
293	236.6	10.4	182956	12	AC068297	AC068297 Homo sapi	c 366	235.6	10.3	150136	5	AC187992	AC187992 Pan trogl
294	236.6	10.4	208237	5	AC182586	AC182586 Pan trogl	367	235.6	10.3	159875	5	AC148692	AC148692 Macaca mu
295	236.4	10.4	579	2	AX871164	AX871164 Sequence	c 368	235.6	10.3	163417	5	AP002518	AP002518 Homo sapi
296	236.4	10.4	579	2	BD151226	BD151226 Primer fo	c 369	235.6	10.3	164795	5	AC148660	AC148660 Macaca mu
297	236.4	10.4	1555	2	AX878552	AX878552 Sequence	370	235.6	10.3	176267	5	AC132868	AC132868 Homo sapi
298	236.4	10.4	1555	2	BD157296	BD157296 Primer fo	c 371	235.6	10.3	179759	12	AP001149	AP001149 Homo sapi
299	236.4	10.4	1555	5	AK021652	AK021652 Homo sapi	c 372	235.6	10.3	181938	12	AC143326	AC143326 Homo sapi
300	236.4	10.4	30826	5	AL807743	AL807743 Human DNA	373	235.6	10.3	183032	12	AC143326	AC143326 Homo sapi
301	236.4	10.4	41257	5	AC005330	AC005330 Homo sapi	374	235.6	10.3	186687	5	AC134943	AC134943 Homo sapi
302	236.4	10.4	56935	5	AL591802	AL591802 Human DNA	375	235.6	10.3	189143	12	AC142077	AC142077 Homo sapi
303	236.4	10.4	110000	12	AC146444	AC146444 Pan trogl	c 376	235.6	10.3	191280	12	AC087389	AC087389 Homo sapi
304	236.4	10.4	110000	12	AC146444	Continuation (2 of	c 377	235.6	10.3	206192	5	AL133173	AL133173 Human DNA
305	236.4	10.4	118695	5	HSJ672M15	HSJ672M15	378	235.4	10.3	18968	2	CQ413230	CQ413230 Sequence
306	236.4	10.4	154902	5	AC005799	AC005799 Homo sapi	379	235.4	10.3	83557	2	AL138735	AL138735 Human DNA
307	236.4	10.4	172476	5	AC007736	AC007736 Homo sapi	c 380	235.4	10.3	100608	2	CQ869961	CQ869961 Sequence
308	236.4	10.4	191681	5	AC079210	AC079210 Homo sapi	c 381	235.4	10.3	106585	5	AL160392	AL160392 Human DNA
309	236.4	10.4	215960	12	AC144881	AC144881 Gorilla g	382	235.4	10.3	122903	5	AC005833	AC005833 Homo sapi
310	236.4	10.4	218733	5	AC091809	AC091809 Homo sapi	c 383	235.4	10.3	135404	5	AC084024	AC084024 Homo sapi

384	235.4	10.3	153640	5	AL445669	AL445669 Human DNA	C 457	234.6	10.3	45120	5	AC090156 Homo sapi
385	235.4	10.3	187275	5	AL445669	AL445669 Human DNA	C 458	234.6	10.3	82921	5	AL356747 Homo sapi
386	235.4	10.3	187960	5	AP000866	AP000866 Homo sapi	C 459	234.6	10.3	85975	5	AC110011 Homo sapi
387	235.4	10.3	202889	5	AC010552	AC010552 Homo sapi	C 460	234.6	10.3	102818	12	AP000621 Homo sapi
388	235.4	10.3	205715	12	AC007604	AC007604 Homo sapi	C 461	234.6	10.3	117166	5	AP000436 Homo sapi
389	235.4	10.3	214426	5	DO431198	DO431198 Homo sapi	C 462	234.6	10.3	133615	5	AC092326 Homo sapi
390	235.4	10.3	214776	12	AC165191	AC165191 Colobus g	C 463	234.6	10.3	153645	5	AC025426 Homo sapi
C 391	235.2	10.3	757	7	BV662034	BV662034 S217P6184	C 464	234.6	10.3	157733	12	AC055810 Homo sapi
392	235.2	10.3	916	7	BV572142	BV572142 GS91P6326	C 465	234.6	10.3	165110	5	AL450311 Human DNA
393	235.2	10.3	37680	12	AL359985	AL359985 Homo sapi	C 466	234.6	10.3	168721	5	AC136431 Homo sapi
394	235.2	10.3	43452	5	AC007901	AC007901 Homo sapi	C 467	234.6	10.3	169541	5	AL136178 Human DNA
395	235.2	10.3	55034	5	AC021072	AC021072 Homo sapi	C 468	234.6	10.3	170572	12	AC140894 Homo sapi
C 396	235.2	10.3	110000	12	AC092950	AC092950 Homo sapi	C 469	234.6	10.3	171860	5	AC010373 Homo sapi
397	235.2	10.3	117711	5	AP000662	AP000662 Homo sapi	C 470	234.6	10.3	173113	12	AC138962 Homo sapi
398	235.2	10.3	144578	5	AC092948	AC092948 Homo sapi	C 471	234.6	10.3	173271	12	AC141623 Homo sapi
C 399	235.2	10.3	156842	12	AC026284	AC026284 Homo sapi	C 472	234.6	10.3	173912	12	AC141075 Homo sapi
C 400	235.2	10.3	162996	5	AC006441	AC006441 Homo sapi	C 473	234.6	10.3	174428	12	AC136441 Homo sapi
401	235.2	10.3	164297	12	AC012138	AC012138 Homo sapi	C 474	234.6	10.3	175069	12	AC140895 Homo sapi
C 402	235.2	10.3	176206	5	AC009967	AC009967 Homo sapi	C 475	234.6	10.3	175785	12	AC138897 Homo sapi
C 403	235.2	10.3	178059	5	AC144411	AC144411 Homo sapi	C 476	234.6	10.3	180664	12	AC140896 Homo sapi
404	235.2	10.3	178980	12	AC188380	AC188380 Pan trogl	C 477	234.6	10.3	187063	12	AC146081 Pan trogl
405	235.2	10.3	182341	12	AC073337	AC073337 Homo sapi	C 478	234.6	10.3	189646	12	AC140909 Homo sapi
C 406	235.2	10.3	184841	12	AC129486	AC129486 Homo sapi	C 479	234.6	10.3	189911	12	AC136434 Homo sapi
C 407	235.2	10.3	185980	5	AC090610	AC090610 Homo sapi	C 480	234.6	10.3	195740	12	AC141269 Homo sapi
C 408	235.2	10.3	195913	12	AC022988	AC022988 Homo sapi	C 481	234.6	10.3	197086	12	AC140875 Homo sapi
C 409	235.2	10.3	197782	5	AC012377	AC012377 Homo sapi	C 482	234.6	10.3	211419	5	AC126760 Homo sapi
C 410	235.2	10.3	199992	12	AC021522	AC021522 Homo sapi	C 483	234.6	10.3	213025	12	AC021159 Homo sapi
C 411	235.2	10.3	217921	5	AC019163	AC019163 Homo sapi	C 484	234.6	10.3	235330	12	AC140522 Homo sapi
C 412	235.2	10.3	238417	2	Q0870127	Q0870127 Sequence	C 485	234.6	10.3	24019	5	AL359184 Human DNA
C 413	235.2	10.3	38173	5	AC093235	AC093235 Homo sapi	C 486	234.6	10.3	40103	5	AC160860 Homo sapi
C 414	235.2	10.3	39967	5	AL136983	AL136983 Human DNA	C 487	234.6	10.3	40524	5	AC154091 Homo sapi
C 415	235.2	10.3	62825	5	AL136960	AL136960 Human DNA	C 488	234.6	10.3	57434	5	AC005808 Homo sapi
C 416	235.2	10.3	66144	12	AC031191	AC031191 Homo sapi	C 489	234.6	10.3	64476	12	AC124232 Homo sapi
C 417	235.2	10.3	82806	5	AC007111	AC007111 Homo sapi	C 490	234.6	10.3	74577	5	AL391415 Human DNA
C 418	235.2	10.3	114631	5	AC084876	AC084876 Homo sapi	C 491	234.6	10.3	100462	5	AP007216 Homo sapi
C 419	235.2	10.3	117899	5	AC016590	AC016590 Homo sapi	C 492	234.6	10.3	101458	12	AP000680 Homo sapi
C 420	235.2	10.3	135173	5	AC008806	AC008806 Homo sapi	C 493	234.6	10.3	122048	12	AC170757 Macaca mu
421	235.2	10.3	152103	12	AC012130	AC012130 Homo sapi	C 494	234.6	10.3	128450	5	AC108861 Homo sapi
422	235.2	10.3	158456	5	AC092198	AC092198 Homo sapi	C 495	234.6	10.3	153026	5	AL391280 Human DNA
423	235.2	10.3	163924	12	AL162592	AL162592 Homo sapi	C 496	234.6	10.3	158702	5	AC104472 Homo sapi
424	235.2	10.3	168113	5	BX664608	BX664608 Human DNA	C 497	234.6	10.3	159707	5	AC013403 Homo sapi
425	235.2	10.3	168117	12	BX664620	BX664620 Homo sapi	C 498	234.6	10.3	170956	12	AC024973 Homo sapi
426	235.2	10.3	171267	12	AC040979	AC040979 Homo sapi	C 499	234.6	10.3	172069	5	AC171635 Rhesus Ma
C 427	235.2	10.3	175067	12	AC040898	AC040898 Homo sapi	C 500	234.6	10.3	179604	5	AC112128 Homo sapi
428	235.2	10.3	179350	5	AC026351	AC026351 Homo sapi	C 501	234.6	10.3	180333	12	AC021695 Homo sapi
429	235.2	10.3	180388	5	HUMETBLAS	LI1910 Human retin	C 502	234.6	10.3	196911	5	AC126773 Homo sapi
C 430	235.2	10.3	180782	5	AF551763	AF551763 Homo sapi	C 503	234.6	10.3	341560	12	AL596304 Homo sapi
C 431	235.2	10.3	186609	5	AC083872	AC083872 Homo sapi	C 504	234.6	10.3	349980	2	AX590980 Sequence
C 432	235.2	10.3	191935	5	AL356128	AL356128 Human DNA	C 505	234.6	10.3	746	7	BV590452 GS91P6414
C 433	235.2	10.3	199759	5	AC009065	AC009065 Homo sapi	C 506	234.6	10.3	6200	2	CS373942 Sequence
C 434	235.2	10.3	200822	5	AL591806	AL591806 Human DNA	C 507	234.6	10.3	17505	5	AC012333 Homo sapi
C 435	235.2	10.3	206361	5	AC159216	AC159216 Pan trogl	C 508	234.6	10.3	72383	12	AC027746 Homo sapi
C 436	235.2	10.3	216785	12	AC169000	AC169000 Colobus g	C 509	234.6	10.3	83111	5	HS12513 Human DNA
C 437	235.2	10.3	220353	12	AC168999	AC168999 Colobus g	C 510	234.6	10.3	83840	5	HSJ148HL7 Human DNA
C 438	235.2	10.3	239434	12	AC012171	AC012171 Homo sapi	C 511	234.6	10.3	99187	5	HS35M08 Homo sapi
C 439	234.8	10.3	765	7	BV676217	BV676217 S217P6055	C 512	234.6	10.3	100590	5	BX470102 Human DNA
C 440	234.8	10.3	20890	5	HSU29895	U29895 Human 4-hyd	C 513	234.6	10.3	128978	2	Q0861712 Sequence
C 441	234.8	10.3	39233	5	AC005626	AC005626 Homo sapi	C 514	234.6	10.3	128978	2	Q0861712 Sequence
C 442	234.8	10.3	39801	5	AC005955	AC005955 Homo sapi	C 515	234.6	10.3	128978	2	Q0861712 Sequence
C 443	234.8	10.3	82732	5	AL512347	AL512347 Human DNA	C 516	234.6	10.3	152033	5	AC020773 Human PAC
C 444	234.8	10.3	97065	12	AP000768	AP000768 Homo sapi	C 517	234.6	10.3	158424	5	AC027319 Human chr
C 445	234.8	10.3	117297	5	AL672040	AL672040 Human DNA	C 518	234.6	10.3	159539	5	CNS01R13 Homo sapi
C 446	234.8	10.3	131906	12	AC083983	AC083983 Homo sapi	C 519	234.6	10.3	160302	12	AC096632 Homo sapi
447	234.8	10.3	137411	5	AC092066	AC092066 Homo sapi	C 520	234.6	10.3	164282	12	AC068818 Homo sapi
448	234.8	10.3	146181	5	AP001269	AP001269 Homo sapi	C 521	234.6	10.3	164764	12	AC015734 Homo sapi
C 449	234.8	10.3	151828	5	AL354740	AL354740 Human DNA	C 522	234.6	10.3	167217	5	AC02350 Homo sapi
450	234.8	10.3	162413	5	AC091530	AC091530 Papio anu	C 523	234.6	10.3	170943	12	AC166591 Homo sapi
451	234.8	10.3	163144	12	AL365339	AL365339 Homo sapi	C 524	234.6	10.3	172905	12	AC097640 Homo sapi
C 452	234.8	10.3	173126	5	AC005988	AC005988 Homo sapi	C 525	234.6	10.3	173910	5	BX855602 Human DNA
C 453	234.8	10.3	179993	12	AC015879	AC015879 Homo sapi	C 526	234.6	10.3	184535	12	AL355100 Homo sapi
C 454	234.8	10.3	181102	5	AC090058	AC090058 Homo sapi	C 527	234.6	10.3	188340	5	AC135178 Homo sapi
C 455	234.8	10.3	220120	5	AC145906	AC145906 Pan trogl	C 528	234.6	10.3	193117	5	AC163767 Pan trogl
C 456	234.8	10.3	262483	5	CT005239	CT005239 Pan trogl	C 529	234.6	10.3	195923	5	AC022489 Homo sapi

C 530	234.2	10.3	196380	5	AC188102	AC188102 Pongo pyg
C 531	234.2	10.3	197605	5	AC096770	AC096770 Homo sapi
C 532	234.2	10.3	200452	5	AC015804	AC015804 Homo sapi
C 533	234.2	10.3	227737	5	AC160055	AC160055 Pan trogl
C 534	234	10.2	679	7	BV556693	BV556693 S222P6127
C 535	234	10.2	778	7	BV528567	BV528567 G591P6142
C 536	234	10.2	885	7	BV524987	BV524987 G591P6077
C 537	234	10.2	30098	12	BX294170	BX294170 Homo sapi
C 538	234	10.2	40847	5	AL731696	AL731696 Human DNA
C 539	234	10.2	42107	5	AC004409	AC004409 Homo sapi
C 540	234	10.2	54146	5	BX248244	BX248244 Human DNA
C 541	234	10.2	91025	5	AL359270	AL359270 Human DNA
C 542	234	10.2	99109	5	AL805934	AL805934 Human DNA
C 543	234	10.2	107226	5	AC010618	AC010618 Homo sapi
C 544	234	10.2	110773	12	BX005259	BX005259 Homo sapi
C 545	234	10.2	110820	5	AC015020	AC015020 Homo sapi
C 546	234	10.2	126347	5	HS58A9	HS58A9
C 547	234	10.2	126625	5	AY028079	AY028079 Homo sapi
C 548	234	10.2	135173	5	AC008806	AC008806 Homo sapi
C 549	234	10.2	143389	2	CS200149	CS200149 Sequence
C 550	234	10.2	150314	2	CS200143	CS200143 Sequence
C 551	234	10.2	152714	5	BS000156	BS000156 Pan trogl
C 552	234	10.2	152825	5	BS000164	BS000164 Pan trogl
C 553	234	10.2	158676	12	AC133821	AC133821 Homo sapi
C 554	234	10.2	158755	5	AP004291	AP004291 Homo sapi
C 555	234	10.2	163893	12	AC137497	AC137497 Homo sapi
C 556	234	10.2	176051	12	AC156747	AC156747 Macaca mu
C 557	234	10.2	181689	12	AC146129	AC146129 Pan trogl
C 558	234	10.2	191827	5	AC093904	AC093904 Homo sapi
C 559	234	10.2	194602	5	AC113188	AC113188 Homo sapi
C 560	234	10.2	200899	12	AC141291	AC141291 Homo sapi
C 561	234	10.2	204622	5	AC157524	AC157524 Pan trogl
C 562	234	10.2	220895	2	CS0861455	CS0861455 Sequence
C 563	234	10.2	220895	5	HS250D10	Z99716 Human DNA s
C 564	234	10.2	230038	12	AC187615	AC187615 Pan trogl
C 565	234	10.2	298345	7	AL616156	AL616156 Pan trogl
C 566	233.8	10.2	751	7	BV487437	BV487437 S216P6520
C 567	233.8	10.2	9552	5	AY764184	AY764184 Homo sapi
C 568	233.8	10.2	71903	5	AL607035	AL607035 Human DNA
C 569	233.8	10.2	74054	5	AC064824	AC064824 Homo sapi
C 570	233.8	10.2	77192	12	AL713858_3	Continuation (4 of
C 571	233.8	10.2	90550	12	AL592166	AL592166 Human DNA
C 572	233.8	10.2	90940	5	AC104052	AC104052 Homo sapi
C 573	233.8	10.2	94651	12	AL389882	AL389882 Homo sapi
C 574	233.8	10.2	107603	5	HS934G17	AL021155 Human DNA
C 575	233.8	10.2	110000	12	AL831785_0	AL831785 Homo sapi
C 576	233.8	10.2	110837	5	AC092455	AC092455 Homo sapi
C 577	233.8	10.2	118616	5	AL157706	AL157706 Human DNA
C 578	233.8	10.2	140915	12	AC022361	AC022361 Homo sapi
C 579	233.8	10.2	143697	12	AL358572	AL358572 Homo sapi
C 580	233.8	10.2	151382	5	AC112221	AC112221 Homo sapi
C 581	233.8	10.2	154080	12	AC024416	AC024416 Homo sapi
C 582	233.8	10.2	156826	12	AC055767	AC055767 Homo sapi
C 583	233.8	10.2	159273	12	AC025001	AC025001 Homo sapi
C 584	233.8	10.2	160410	5	AC092334	AC092334 Homo sapi
C 585	233.8	10.2	161946	5	AC094014	AC094014 Papio anu
C 586	233.8	10.2	163384	5	AC009180	AC009180 Homo sapi
C 587	233.8	10.2	170787	5	AC121247	AC121247 Homo sapi
C 588	233.8	10.2	172238	5	AC090942	AC090942 Homo sapi
C 589	233.8	10.2	179938	5	AC185347	AC185347 Pan trogl
C 590	233.8	10.2	182171	5	AC066589	AC066589 Homo sapi
C 591	233.8	10.2	185146	12	AC104311	AC104311 Homo sapi
C 592	233.8	10.2	185232	12	AL611948	AL611948 Homo sapi
C 593	233.8	10.2	192465	5	AC187989	AC187989 Pan trogl
C 594	233.8	10.2	194844	5	AC160656	AC160656 Pan trogl
C 595	233.8	10.2	205130	12	AC105425	AC105425 Homo sapi
C 596	233.8	10.2	208989	5	AC027124	AC027124 Homo sapi
C 597	233.6	10.2	796	7	BV589028	BV589028 HS91P6377
C 598	233.6	10.2	809	7	BV646799	BV646799 S217P6025
C 599	233.6	10.2	39470	5	AC005390	AC005390 Homo sapi
C 600	233.6	10.2	69663	12	AC090747	AC090747 Homo sapi
C 601	233.6	10.2	76326	5	AC105762	AC105762 Homo sapi
C 602	233.6	10.2	87758	5	AC068768	AC068768 Homo sapi
C 603	233.6	10.2	91830	5	AL365436	AL365436 Homo sapi
C 604	233.6	10.2	117000	5	AC069222	AC069222 Homo sapi
C 605	233.6	10.2	126491	5	AL589784	AL589784 Human DNA
C 606	233.6	10.2	144041	12	AP001766	AP001766 Homo sapi
C 607	233.6	10.2	157358	5	AC009163	AC009163 Homo sapi
C 608	233.6	10.2	160552	2	AR635088	AR635088 Sequence
C 609	233.6	10.2	160552	2	AR897366	AR897366 Sequence
C 610	233.6	10.2	166992	12	AC022883	AC022883 Homo sapi
C 611	233.6	10.2	172744	5	AC183617	AC183617 Pan trogl
C 612	233.6	10.2	180080	5	CT737307	CT737307 CH251-89L
C 613	233.6	10.2	183263	5	AC092685	AC092685 Homo sapi
C 614	233.6	10.2	186168	12	AL391379	AL391379 Homo sapi
C 615	233.6	10.2	194447	5	AC150208	AC150208 Pan trogl
C 616	233.4	10.2	41461	5	AC010646	AC010646 Homo sapi
C 617	233.4	10.2	66992	12	AC091166	AC091166 Homo sapi
C 618	233.4	10.2	76481	5	AC096511	AC096511 Homo sapi
C 619	233.4	10.2	86973	5	AC079402	AC079402 Homo sapi
C 620	233.4	10.2	110000	12	BX322548_1	Continuation (2 of
C 621	233.4	10.2	110000	12	BX322548_2	Continuation (3 of
C 622	233.4	10.2	128800	5	AB053170	AB053170 Homo sapi
C 623	233.4	10.2	129711	5	AC110768	AC110768 Homo sapi
C 624	233.4	10.2	133568	5	HS16915	Z93015 Human DNA s
C 625	233.4	10.2	135762	12	AC139785	AC139785 Homo sapi
C 626	233.4	10.2	149061	5	AC098805	AC098805 Homo sapi
C 627	233.4	10.2	149578	12	AC139820	AC139820 Homo sapi
C 628	233.4	10.2	152336	12	AC009594	AC009594 Homo sapi
C 629	233.4	10.2	154295	5	AC087833	AC087833 Papio anu
C 630	233.4	10.2	155127	5	AC008532	AC008532 Homo sapi
C 631	233.4	10.2	157981	5	AC005184	AC005184 Homo sapi
C 632	233.4	10.2	158083	5	AL162493	AL162493 Human DNA
C 633	233.4	10.2	159707	5	AC013403	AC013403 Homo sapi
C 634	233.4	10.2	160466	12	AC139524	AC139524 Homo sapi
C 635	233.4	10.2	161608	12	AC140835	AC140835 Homo sapi
C 636	233.4	10.2	162750	5	AL355365	AL355365 Human DNA
C 637	233.4	10.2	165004	12	AC139465	AC139465 Homo sapi
C 638	233.4	10.2	165868	5	AC010651	AC010651 Homo sapi
C 639	233.4	10.2	170861	12	AC025698	AC025698 Homo sapi
C 640	233.4	10.2	172807	12	AC136617	AC136617 Homo sapi
C 641	233.4	10.2	176144	12	AC140872	AC140872 Homo sapi
C 642	233.4	10.2	177908	5	AC091817	AC091817 Homo sapi
C 643	233.4	10.2	177963	12	AC139461	AC139461 Homo sapi
C 644	233.4	10.2	180463	5	AC018978	AC018978 Homo sapi
C 645	233.4	10.2	180551	5	AC183296	AC183296 Pan trogl
C 646	233.4	10.2	180551	5	HUAC004158	AC004158 Homo sapi
C 647	233.4	10.2	181780	5	AC185245	AC185245 Pan trogl
C 648	233.4	10.2	182012	5	AL359846	AL359846 Human DNA
C 649	233.4	10.2	183430	5	AL391827	AL391827 Human DNA
C 650	233.4	10.2	184125	5	AC160650	AC160650 Pan trogl
C 651	233.4	10.2	185047	5	AC025289	AC025289 Homo sapi
C 652	233.4	10.2	185047	5	AC026472	AC026472 Homo sapi
C 653	233.4	10.2	188868	5	AC023232	AC023232 Homo sapi
C 654	233.4	10.2	194779	5	AC138811	AC138811 Homo sapi
C 655	233.4	10.2	196048	12	AC139469	AC139469 Homo sapi
C 656	233.4	10.2	202847	12	AC140713	AC140713 Homo sapi
C 657	233.4	10.2	203759	12	AC141601	AC141601 Homo sapi
C 658	233.4	10.2	206769	5	AC186385	AC186385 Pan trogl
C 659	233.4	10.2	202083	5	AC021443	AC021443 Homo sapi
C 660	233.4	10.2	232359	12	AC139825	AC139825 Homo sapi
C 661	233.4	10.2	288323	12	AC140887	AC140887 Homo sapi
C 662	233.2	10.2	778	7	BV566542	BV566542 rll18b09
C 663	233.2	10.2	1701	2	AX033917	AX033917 Sequence
C 664	233.2	10.2	3347	5	HSM804927	AL833614 Homo sapi
C 665	233.2	10.2	56458	5	HS342B11	AL008719 Human DNA
C 666	233.2	10.2	59211	5	AC006388	AC006388 Homo sapi
C 667	233.2	10.2	83039	5	AL137074	AL137074 Human DNA
C 668	233.2	10.2	126238	5	AC138472	AC138472 Homo sapi
C 669	233.2	10.2	126679	5	HSJ53488	AL121905 Human DNA
C 670	233.2	10.2	128444	12	AF214634	AF214634 Homo sapi
C 671	233.2	10.2	133021	12	CT476828	CT476828 Homo sapi
C 672	233.2	10.2	141612	5	AC079093	AC079093 Homo sapi
C 673	233.2	10.2	142790	5	AL445685	AL445685 Human DNA
C 674	233.2	10.2	151834	5	AP004195	AP004195 Homo sapi
C 675	233.2	10.2	152757	5	AC018475	AC018475 Homo sapi

C 676	233.2	10.2	157091	12	AC027772	AC027772 Homo sapi	749	232.8	10.2	188956	5	AL591493	Human DNA
C 677	233.2	10.2	158481	5	AL158063	AL158063 Human DNA	750	232.8	10.2	189539	5	AL357493	Human DNA
C 678	233.2	10.2	161366	5	AC090939	AC090939 Homo sapi	751	232.8	10.2	199785	5	AL355512	Human DNA
C 679	233.2	10.2	167294	12	AC013814	AC013814 Homo sapi	C 752	232.8	10.2	202383	5	AC009973	Homo sapi
C 680	233.2	10.2	170127	12	AC171648	AC171648 Macaca mu	C 753	232.8	10.2	202392	5	AC079061	Homo sapi
C 681	233.2	10.2	173411	5	AC092754	AC092754 Homo sapi	C 754	232.8	10.2	216457	5	CNS01RG1	Human chr
C 682	233.2	10.2	175263	5	AC023102	AC023102 Homo sapi	C 755	232.8	10.2	217081	5	AL182731	Pan trogl
C 683	233.2	10.2	180306	12	AC169845	AC169845 Macaca mu	C 756	232.8	10.2	254112	12	CR762382	Homo sapi
C 684	233.2	10.2	180531	5	AC008745	AC008745 Homo sapi	C 757	232.6	10.2	461	2	CQ517361	Sequence
C 685	233.2	10.2	185035	5	AC004770	AC004770 Homo sapi	C 758	232.6	10.2	766	7	BV569996	G591P6085
C 686	233.2	10.2	185624	5	AC013923	AC013923 Homo sapi	C 759	232.6	10.2	15835	5	AY338232	Homo sapi
C 687	233.2	10.2	185766	5	AP002754	AP002754 Homo sapi	C 760	232.6	10.2	51923	5	AL356983	Human DNA
C 688	233.2	10.2	188788	5	AP002380	AP002380 Homo sapi	C 761	232.6	10.2	62449	12	AC061985	Homo sapi
C 689	233.2	10.2	197136	5	AC146149	AC146149 Pan trogl	C 762	232.6	10.2	63332	5	AC024938	Homo sapi
C 690	233.2	10.2	199730	12	AC083940	AC083940 Homo sapi	C 763	232.6	10.2	67332	5	AP001468	Homo sapi
C 691	233.2	10.2	202607	5	AP002353	AP002353 Homo sapi	C 764	232.6	10.2	74429	5	AY523969	Homo sapi
C 692	233.2	10.2	218644	5	AC147079	AC147079 Pan trogl	C 765	232.6	10.2	100301	5	HS317E23	Human DNA
C 693	233.2	10.2	218724	12	AC025889	AC025889 Homo sapi	C 766	232.6	10.2	102509	5	AL953897	Human DNA
C 694	233.2	10.2	229379	5	AC010746	AC010746 Homo sapi	C 767	232.6	10.2	103608	5	AL139161	Human DNA
C 695	233.2	10.2	280473	12	AC068823	AC068823 Homo sapi	C 768	232.6	10.2	114532	12	AC016547	Homo sapi
C 696	233.2	10.2	328866	12	AC107203	AC107203 Homo sapi	C 769	232.6	10.2	129747	5	AL3465N24	Human DNA
C 697	233	10.2	662	7	BV584473	BV584473 G591P6286	C 770	232.6	10.2	132066	5	AL953882	Human DNA
C 698	233	10.2	90577	5	AL135912	AL135912 Human DNA	C 771	232.6	10.2	135668	5	AC139667	Homo sapi
C 699	233	10.2	96717	5	AL359182	AL359182 Human DNA	C 772	232.6	10.2	137496	5	AC005288	Homo sapi
C 700	233	10.2	102822	5	AC104407	AC104407 Homo sapi	C 773	232.6	10.2	138459	12	AC090795	Homo sapi
C 701	233	10.2	111990	5	AL360294	AL360294 Human DNA	C 774	232.6	10.2	143747	5	HS370M22	Human DNA s
C 702	233	10.2	122552	5	CNS01DRS	AL118555 Human chr	C 775	232.6	10.2	148504	5	AC138732	Pongo PY9
C 703	233	10.2	132720	5	AC093269	AC093269 Homo sapi	C 776	232.6	10.2	156365	12	AC183959	Homo sapi
C 704	233	10.2	151660	12	AC027450	AC027450 Homo sapi	C 777	232.6	10.2	160892	12	AC023910	Homo sapi
C 705	233	10.2	154102	12	AC183603	AC183603 Pan trogl	C 778	232.6	10.2	164330	12	AC016928	Homo sapi
C 706	233	10.2	154827	5	AL592221	AL592221 Human DNA	C 779	232.6	10.2	168833	12	AC021706	Homo sapi
C 707	233	10.2	156754	5	AC021055	AC021055 Homo sapi	C 780	232.6	10.2	169714	12	AC138876	Homo sapi
C 708	233	10.2	157777	12	AC114372	AC114372 Homo sapi	C 781	232.6	10.2	176975	12	AC008050	Homo sapi
C 709	233	10.2	157777	12	AC183683	AC183683 Pan trogl	C 782	232.6	10.2	179538	12	AC024740	Homo sapi
C 710	233	10.2	159504	5	AC104436	AC104436 Homo sapi	C 783	232.6	10.2	186330	5	AC007376	Homo sapi
C 711	233	10.2	164721	12	AC013657	AC013657 Homo sapi	C 784	232.6	10.2	187723	5	AC016889	Homo sapi
C 712	233	10.2	171617	12	AC016053	AC016053 Homo sapi	C 785	232.6	10.2	189149	12	AC046171	Homo sapi
C 713	233	10.2	172010	5	AC083876	AC083876 Homo sapi	C 786	232.6	10.2	201625	12	AC012144	Homo sapi
C 714	233	10.2	175064	12	AC012230	AC012230 Homo sapi	C 787	232.6	10.2	202233	5	AC003664	Homo sapi
C 715	233	10.2	180991	5	AC160056	AC160056 Pan trogl	C 788	232.6	10.2	202850	5	AC183546	Pan trogl
C 716	233	10.2	181074	12	AC146626	AC146626 Papio anu	C 789	232.6	10.2	203611	5	AC146448	Pan trogl
C 717	233	10.2	181673	5	AC148825	AC148825 Pan trogl	C 790	232.6	10.2	215960	12	AC144881	gorilla g
C 718	233	10.2	184730	12	AC146676	AC146676 Papio anu	C 791	232.6	10.2	224271	5	AC026803	Homo sapi
C 719	233	10.2	189694	12	AC187742	AC187742 Pan trogl	C 792	232.6	10.2	236109	5	CT009602	PTB-121B2
C 720	233	10.2	229612	12	AL161647	AL161647 Homo sapi	C 793	232.6	10.2	319064	12	CT009516	Homo sapi
C 721	233	10.2	251039	12	AL592290	AL592290 Homo sapi	C 794	232.6	10.2	340000	5	AP001759	Homo sapi
C 722	232.8	10.2	9846	5	AL359506	AL359506 Human DNA	C 795	232.4	10.2	62038	5	AC108469	Homo sapi
C 723	232.8	10.2	55442	5	BX119919	BX119919 Human DNA	C 796	232.4	10.2	69013	5	CR753842	Human DNA
C 724	232.8	10.2	61834	5	DQ314871	DQ314871 Homo sapi	C 797	232.4	10.2	90732	5	AL670886	Human DNA
C 725	232.8	10.2	79470	12	AL391000	AL391000 Homo sapi	C 798	232.4	10.2	94060	12	AF216673	Homo sapi
C 726	232.8	10.2	83111	5	HS12513	AL033528 Human DNA	C 799	232.4	10.2	100234	12	CR759702	Homo sapi
C 727	232.8	10.2	140292	5	CNS01D08	AL133223 Human chr	C 800	232.4	10.2	102215	12	CR933564	Homo sapi
C 728	232.8	10.2	144260	5	AC006299	AC006299 Homo sapi	C 801	232.4	10.2	105842	5	AC107387	Homo sapi
C 729	232.8	10.2	145937	12	AL355600	AL355600 Homo sapi	C 802	232.4	10.2	110000	5	BA000025_02	Continuation (3 of
C 730	232.8	10.2	146961	12	AL355525	AL355525 Homo sapi	C 803	232.4	10.2	113650	5	CR759787	Human DNA
C 731	232.8	10.2	150290	5	HS509L4	2999496 Human DNA s	C 804	232.4	10.2	116556	5	AC133435	Homo sapi
C 732	232.8	10.2	158466	5	AP004292	AP004292 Homo sapi	C 805	232.4	10.2	117338	5	HS173D1	Human DNA
C 733	232.8	10.2	159423	5	AC008429	AC008429 Homo sapi	C 806	232.4	10.2	127140	5	AL136137	Human DNA
C 734	232.8	10.2	160151	5	AC098595	AC098595 Homo sapi	C 807	232.4	10.2	132551	5	CR354443	Human DNA
C 735	232.8	10.2	160237	12	AC149093	AC149093 Pan trogl	C 808	232.4	10.2	135578	5	AF064861	Homo sapi
C 736	232.8	10.2	160815	12	AP001895	AP001895 Homo sapi	C 809	232.4	10.2	136493	5	AL662899	Human DNA
C 737	232.8	10.2	163372	12	AC087744	AC087744 Homo sapi	C 810	232.4	10.2	141372	12	AC011779	Homo sapi
C 738	232.8	10.2	166336	5	AL445467	AL445467 Human DNA	C 811	232.4	10.2	141843	5	AF129408	Homo sapi
C 739	232.8	10.2	172004	5	AL158032	AL158032 Human DNA	C 812	232.4	10.2	155113	5	BS000094	Pan trogl
C 740	232.8	10.2	174044	5	AC183799	AC183799 Pan trogl	C 813	232.4	10.2	159766	5	AC104942	Human DNA
C 741	232.8	10.2	176278	5	AC024028	AC024028 Homo sapi	C 814	232.4	10.2	163682	5	HS071117	Homo sapi
C 742	232.8	10.2	176709	5	AC011737	AC011737 Homo sapi	C 815	232.4	10.2	166239	12	AC078965	Homo sapi
C 743	232.8	10.2	179396	12	AC017056	AC017056 Homo sapi	C 816	232.4	10.2	168822	5	AC007511	Homo sapi
C 744	232.8	10.2	184129	5	AC083799	AC083799 Homo sapi	C 817	232.4	10.2	171427	2	CS200179	Sequence
C 745	232.8	10.2	186783	5	AC090355	AC090355 Homo sapi	C 818	232.4	10.2	173023	5	AL354898	Human DNA
C 746	232.8	10.2	187167	12	AP001563	AP001563 Homo sapi	C 819	232.4	10.2	173094	12	AL603629	Homo sapi
C 747	232.8	10.2	187215	12	AC013783	AC013783 Homo sapi	C 820	232.4	10.2	174551	5	AC010598	Homo sapi
C 748	232.8	10.2	188134	5	AL354797	AL354797 Human DNA	C 821	232.4	10.2	175104	5	AC130449	Homo sapi

822	232.4	10.2	175567	5	AC079447	AC079447 Homo sapi	895	232	10.2	171272	12	AC084707	AC084707 Homo sapi
823	232.4	10.2	175825	5	HS106H8	Z97195 Human DNA s	c 896	232	10.2	171426	12	AL391564	AL391564 Homo sapi
c 824	232.4	10.2	179485	5	AC005939	AC005939 Homo sapi	897	232	10.2	172969	5	AC090574	AC090574 Homo sapi
825	232.4	10.2	181946	12	AC097330	AC097330 Pan trogl	c 898	232	10.2	173025	12	AL391596	AL391596 Homo sapi
826	232.4	10.2	182123	12	AC002399	AC002399 Homo sapi	c 899	232	10.2	174074	5	AC018891	AC018891 Homo sapi
c 827	232.4	10.2	182509	5	AC112211	AC112211 Homo sapi	c 900	232	10.2	174162	5	AC099789	AC099789 Homo sapi
828	232.4	10.2	183097	12	AC027638	AC027638 Homo sapi	c 901	232	10.2	174396	12	AC021645	AC021645 Homo sapi
829	232.4	10.2	183773	5	AC087284	AC087284 Homo sapi	c 902	232	10.2	176742	5	AC007386	AC007386 Homo sapi
830	232.4	10.2	183827	5	AC005899	AC005899 Homo sapi	c 903	232	10.2	176806	12	AC090438	AC090438 Homo sapi
c 831	232.4	10.2	184666	5	DJ201624	AF129756 Homo sapi	904	232	10.2	176924	5	AC069410	AC069410 Homo sapi
832	232.4	10.2	189379	5	AC090930	AC090930 Homo sapi	c 905	232	10.2	182350	5	BS000243	BS000243 Pan trogl
833	232.4	10.2	190017	5	AC090589	AC090589 Homo sapi	c 906	232	10.2	187303	5	AC069226	AC069226 Homo sapi
c 834	232.4	10.2	190149	5	AC146327	AC146327 Pan trogl	c 907	232	10.2	189672	5	AL133480	AL133480 Human DNA
835	232.4	10.2	196319	5	CNS01DT4	AL132639 Human chr	908	232	10.2	190215	12	AC016975	AC016975 Homo sapi
c 836	232.4	10.2	208066	5	AC146483	AC146483 Pan trogl	c 909	232	10.2	192104	5	AC006994	AC006994 Homo sapi
837	232.4	10.2	211780	5	AC146006	AL163026 Pan trogl	c 910	232	10.2	193039	12	AC090690	AC090690 Homo sapi
c 838	232.4	10.2	340000	5	HS21C079	AL163279 Homo sapi	c 911	232	10.2	193369	12	AC114889	AC114889 Pan trogl
839	232.4	10.2	349980	2	CS039420	CS039420 Sequence	912	232	10.2	193421	5	AC107294	AC107294 Homo sapi
840	232.2	10.2	679	7	BV482411	BV482411 rmg13a12..	913	232	10.2	195600	12	AC079094	AC079094 Homo sapi
c 841	232.2	10.2	55870	5	AL645585	AL645585 Human DNA	c 914	232	10.2	207620	5	AP001331	AP001331 Homo sapi
c 842	232.2	10.2	55932	12	AC025791	AC025791 Homo sapi	c 915	232	10.2	212337	5	AC013746	AC013746 Homo sapi
c 843	232.2	10.2	83521	5	AC129510	AC129510 Homo sapi	c 916	232	10.2	226699	5	AC022146	AC022146 Homo sapi
844	232.2	10.2	84562	12	AC140700	AC140700 Homo sapi	917	232	10.2	260209	2	DD139819	DD139819 Sulfatase
c 845	232.2	10.2	84928	12	AC141231	AC141231 Homo sapi	918	232	10.2	260209	2	AX573201	AX573201 Sequence
c 846	232.2	10.2	98404	12	AL355676	AL355676 Homo sapi	c 919	232	10.2	309662	12	AC004469	AC004469 Homo sapi
c 847	232.2	10.2	108768	5	AL137126_0	AL137126 Homo sapi	920	232	10.2	340000	5	AP001759	AP001759 Homo sapi
c 848	232.2	10.2	110000	12	AL137126_0	AL137126 Homo sapi	921	231.8	10.1	601	2	AR665920	AR665920 Sequence
849	232.2	10.2	112168	5	BX572623	BX572623 Human DNA	922	231.8	10.1	702	7	BV474401	BV474401 G591P6293
c 850	232.2	10.2	122591	5	AL157786	AL157786 Human DNA	923	231.8	10.1	733	7	BV630049	BV630049 S217P6229
851	232.2	10.2	123530	12	AL356369	AL356369 Homo sapi	924	231.8	10.1	769	7	BV500774	BV500774 S222P6228
852	232.2	10.2	132725	12	AC046156	AC046156 Homo sapi	925	231.8	10.1	18396	2	AR659722	AR659722 Sequence
c 853	232.2	10.2	137924	12	AC026684	AC026684 Homo sapi	c 926	231.8	10.1	59731	5	AC068442	AC068442 Homo sapi
854	232.2	10.2	143291	5	AL137792	AL137792 Human DNA	927	231.8	10.1	105499	5	AC093335	AC093335 Homo sapi
855	232.2	10.2	148348	12	AC104074	AC104074 Homo sapi	928	231.8	10.1	106331	12	AC138226	AC138226 Homo sapi
856	232.2	10.2	151735	12	AC015611	AC015611 Homo sapi	c 929	231.8	10.1	115968	5	AL365277	AL365277 Human DNA
857	232.2	10.2	158867	5	AC109455	AC109455 Homo sapi	c 930	231.8	10.1	117751	5	AC020913	AC020913 Homo sapi
858	232.2	10.2	158905	5	AC005666	AC005666 Homo sapi	931	231.8	10.1	124524	5	BX255972	BX255972 Human DNA
c 859	232.2	10.2	161355	5	HS0760019	AL080314 Human DNA	c 932	231.8	10.1	127661	12	AP001261	AP001261 Homo sapi
c 860	232.2	10.2	165942	5	AC104943	AC104943 Homo sapi	c 933	231.8	10.1	133728	5	AL139220	AL139220 Human DNA
c 861	232.2	10.2	166256	5	AC173999	AC173999 Pan trogl	c 934	231.8	10.1	149163	12	AC073835	AC073835 Homo sapi
862	232.2	10.2	166985	5	AC009927	AC009927 Homo sapi	c 935	231.8	10.1	150660	5	AL157372	AL157372 Human DNA
c 863	232.2	10.2	170848	12	AC093630	AC093630 Homo sapi	c 936	231.8	10.1	155454	5	AC183281	AC183281 Pan trogl
864	232.2	10.2	174562	12	AC005848	AC005848 Homo sapi	937	231.8	10.1	160836	5	AP000729	AP000729 Homo sapi
865	232.2	10.2	178056	5	AC008536	AC008536 Homo sapi	c 938	231.8	10.1	160826	12	AC010354	AC010354 Homo sapi
866	232.2	10.2	178691	5	AC009704	AC009704 Homo sapi	c 939	231.8	10.1	162133	12	AC068569	AC068569 Homo sapi
c 867	232.2	10.2	181020	5	AC009119	AC009119 Homo sapi	c 940	231.8	10.1	164394	5	AL116904	AL116904 Homo sapi
c 868	232.2	10.2	189840	5	AC012320	AC012320 Homo sapi	c 941	231.8	10.1	167336	12	AC021350	AC021350 Homo sapi
c 869	232.2	10.2	192324	5	AC096920	AC096920 Homo sapi	942	231.8	10.1	167523	5	AC145983	AC145983 Pan trogl
870	232.2	10.2	196954	5	AC022148	AC022148 Homo sapi	943	231.8	10.1	168501	5	AC068594	AC068594 Homo sapi
c 871	232.2	10.2	197225	5	AC093835	AC093835 Homo sapi	944	231.8	10.1	169089	5	AC055725	AC055725 Homo sapi
c 872	232.2	10.2	212103	5	CNS01DV4	AL133453 Human chr	c 945	231.8	10.1	170696	12	AC137059	AC137059 Papio anu
c 873	232.2	10.2	215786	5	AC022916	AC022916 Homo sapi	946	231.8	10.1	171898	5	AC111182	AC111182 Homo sapi
c 874	232	10.2	34234	5	HS106H8	Z74019 Human DNA s	947	231.8	10.1	175023	5	AC011037	AC011037 Homo sapi
c 875	232	10.2	37194	5	HSV210B9	270280 Human DNA s	948	231.8	10.1	175827	5	AL358472	AL358472 Human DNA
876	232	10.2	39374	5	AC005256	AC005256 Homo sapi	949	231.8	10.1	181508	12	AC183643	AC183643 Pan trogl
877	232	10.2	40307	5	AC025155	AC025155 Homo sapi	c 950	231.8	10.1	184886	5	AC005358	AC005358 Homo sapi
878	232	10.2	40662	5	AL645758	AL645758 Human DNA	c 951	231.8	10.1	185820	5	HS1009524	HS1009524 Human DNA
879	232	10.2	58072	12	AC136758	AC136758 Homo sapi	952	231.8	10.1	189821	5	AL354735	AL354735 Human DNA
880	232	10.2	64359	5	AC005233	AC005233 Homo sapi	c 953	231.8	10.1	190155	12	AC105184	AC105184 Homo sapi
881	232	10.2	75008	5	AP000471	AP000471 Homo sapi	c 954	231.8	10.1	190558	12	AP001403	AP001403 Homo sapi
c 882	232	10.2	105583	12	AC084258	AC084258 Homo sapi	c 955	231.8	10.1	190744	5	AC005038	AC005038 Homo sapi
883	232	10.2	144834	5	AC073345	AC073345 Homo sapi	956	231.8	10.1	192296	5	AC009654	AC009654 Homo sapi
c 884	232	10.2	152339	12	AC083931	AC083931 Homo sapi	957	231.8	10.1	198410	12	AP000831	AP000831 Homo sapi
c 885	232	10.2	154034	5	AC087620	AC087620 Homo sapi	958	231.8	10.1	206329	12	AC017113	AC017113 Homo sapi
c 886	232	10.2	154599	12	AC016997	AC016997 Homo sapi	c 959	231.8	10.1	206647	5	AP002898	AP002898 Homo sapi
c 887	232	10.2	157021	12	AC020991	AC020991 Homo sapi	c 960	231.8	10.1	207433	2	AX326809	AX326809 Sequence
c 888	232	10.2	159863	5	AC002349	AC002349 Homo sapi	961	231.8	10.1	224761	5	AC026894	AC026894 Homo sapi
c 889	232	10.2	161406	5	AP002376	AP002376 Homo sapi	962	231.8	10.1	241278	5	AC097268	AC097268 Pan trogl
890	232	10.2	162554	5	AC079354	AC079354 Homo sapi	963	231.8	10.1	256164	5	HS4400877	HS4400877 Homo sapi
c 891	232	10.2	162996	12	AC051655	AC051655 Homo sapi	c 964	231.6	10.1	461	2	CQ487560	CQ487560 Sequence
c 892	232	10.2	167762	5	AL183682	AL183682 Pan trogl	965	231.6	10.1	31852	5	HS03689C5	HS03689C5 Human DNA
c 893	232	10.2	168963	12	AC009705	AC009705 Homo sapi	966	231.6	10.1	33417	5	AC104537	AC104537 Homo sapi
c 894	232	10.2	170245	5	HS109F14	AL022721 Human DNA	967	231.6	10.1	37001	5	AC005513	AC005513 Homo sapi

c 968	231.6	10.1	44219	5	AC005512	AC005512 Homo sapi	1041	231.6	10.1	200493	5	AP005270	AP005270 Homo sapi
c 969	231.6	10.1	44717	5	AY207046	AY207046 Homo sapi	c1043	231.6	10.1	206860	12	AC025689	AC025689 Homo sapi
c 970	231.6	10.1	48852	5	CR936875	CR936875 Human DNA	1043	231.6	10.1	209545	12	AC087848	AC087848 Homo sapi
c 971	231.6	10.1	57896	12	AC090775	AC090775 Homo sapi	1044	231.6	10.1	211627	5	AL161651	AL161651 Human DNA
c 972	231.6	10.1	61698	5	AL662870	AL662870 Human DNA	1045	231.6	10.1	212999	5	DQ436495	DQ436495 Homo sapi
c 973	231.6	10.1	62449	12	AC061985	AC061985 Homo sapi	1046	231.6	10.1	215273	5	AC126121	AC126121 Homo sapi
c 974	231.6	10.1	65544	12	AC120025	AC120025 Homo sapi	c1047	231.6	10.1	232696	5	AC007221	AC007221 Homo sapi
c 975	231.6	10.1	65612	12	AC087452	AC087452 Homo sapi	c1048	231.6	10.1	232574	12	AL158037	AL158037 Homo sapi
c 976	231.6	10.1	68984	5	AC135592	AC135592 Homo sapi	c1049	231.6	10.1	280140	12	AC055751	AC055751 Homo sapi
c 977	231.6	10.1	85787	5	AC073069	AC073069 Homo sapi	1050	231.6	10.1	305000	5	HSXDPA	CS039418 Sequence
c 978	231.6	10.1	91830	5	AL365436	AL365436 Human DNA	1051	231.6	10.1	349980	2	CS039418	CS039418 Sequence
c 979	231.6	10.1	103780	5	AL773541	AL773541 Human DNA	1052	231.6	10.1	601	2	AR665921	AR665921 Sequence
c 980	231.6	10.1	104070	5	AC008955	AC008955 Homo sapi	1053	231.4	10.1	752	7	BV589457	BV589457 G591P6335
c 981	231.6	10.1	105045	2	AR659622	AR659622 Sequence	c1054	231.4	10.1	29848	5	U73023	U73023 Homo sapien
c 982	231.6	10.1	107045	2	AR659731	AR659731 Sequence	c1055	231.4	10.1	102101	5	AL359816	AL359816 Human DNA
c 983	231.6	10.1	109891	5	HS112K5	Z85987 Human DNA	c1056	231.4	10.1	107000	5	AC069417	AC069417 Homo sapi
c 984	231.6	10.1	110000	5	BA000025_10	Continuation (11 o	1057	231.4	10.1	111566	5	AL357314	AL357314 Human DNA
c 985	231.6	10.1	110208	5	BS2727194	BS2727194 Human DNA	1058	231.4	10.1	119147	5	AC098873	AC098873 Homo sapi
c 986	231.6	10.1	112018	5	AB023050	AB023050 Homo sapi	c1059	231.4	10.1	131716	12	AC025833	AC025833 Homo sapi
c 987	231.6	10.1	118508	5	AL929236	AL929236 Human DNA	c1060	231.4	10.1	134793	5	AC020922	AC020922 Homo sapi
c 988	231.6	10.1	118699	5	AC130004	AC130004 Homo sapi	c1061	231.4	10.1	135928	2	CS351346	CS351346 Sequence
c 989	231.6	10.1	120825	5	HSJ733M16	AL109627 Human DNA	c1062	231.4	10.1	135928	5	HS434014	AL022398 Human DNA
c 990	231.6	10.1	122073	12	AC090831	AC090831 Homo sapi	c1063	231.4	10.1	141168	12	AC147432	AC147432 Pan trogl
c 991	231.6	10.1	125719	5	AC027702	AC027702 Homo sapi	1064	231.4	10.1	143618	5	AL137856	AL137856 Human DNA
c 992	231.6	10.1	125882	12	AC087733	AC087733 Homo sapi	1065	231.4	10.1	146370	12	AC006595	AC006595 Homo sapi
c 993	231.6	10.1	129625	5	AC009301	AC009301 Homo sapi	c1066	231.4	10.1	147029	5	AL137068	AL137068 Human DNA
c 994	231.6	10.1	132033	5	AC099796	AC099796 Homo sapi	c1067	231.4	10.1	147924	12	AC036186	AC036186 Homo sapi
c 995	231.6	10.1	141579	12	AC044793	AC044793 Homo sapi	c1068	231.4	10.1	154622	12	AL592082	AL592082 Homo sapi
c 996	231.6	10.1	144383	5	AC117498	AC117498 Homo sapi	1069	231.4	10.1	155439	5	AC008626	AC008626 Homo sapi
c 997	231.6	10.1	148008	12	AC130471	AC130471 Homo sapi	1070	231.4	10.1	156314	5	AC007671	AC007671 Homo sapi
c 998	231.6	10.1	148450	12	AC068184	AC068184 Homo sapi	c1071	231.4	10.1	156655	12	AP002417	AP002417 Homo sapi
c 999	231.6	10.1	148688	5	AL385985	AL385985 Pan trogl	1072	231.4	10.1	157463	5	AC091529	AC091529 Homo sapi
c1000	231.6	10.1	148984	5	HS105D16	AL031311 Human DNA	c1073	231.4	10.1	158500	12	AL359206	AL359206 Macaca mu
c1001	231.6	10.1	154732	12	AC023236	AC023236 Homo sapi	1074	231.4	10.1	162439	12	AC153302	AC153302 Macaca mu
c1002	231.6	10.1	155365	5	AC107970	AC107970 Homo sapi	1075	231.4	10.1	166256	5	AC018922	AC018922 Homo sapi
c1003	231.6	10.1	156265	5	AC079140	AC079140 Homo sapi	c1076	231.4	10.1	166527	12	AC140897	AC140897 Homo sapi
c1004	231.6	10.1	159273	12	AC025001	AC025001 Homo sapi	c1077	231.4	10.1	167075	5	HS742J24	AL035448 Human DNA
c1005	231.6	10.1	159611	5	AC009335	AC009335 Homo sapi	c1078	231.4	10.1	168262	12	AC140562	AC140562 Macaca mu
c1006	231.6	10.1	160193	5	AC092442	AC092442 Homo sapi	1079	231.4	10.1	168993	12	AC153301	AC153301 Macaca mu
c1007	231.6	10.1	161578	5	AC023595	AC023595 Homo sapi	1080	231.4	10.1	169212	5	AP002392	AP002392 Homo sapi
c1008	231.6	10.1	161711	12	AC008025	AC008025 Homo sapi	1081	231.4	10.1	170245	5	HS109F14	AL022721 Human DNA
c1009	231.6	10.1	162527	12	AC020643	AC020643 Homo sapi	1082	231.4	10.1	171162	2	CS200157	CS200157 Sequence
c1010	231.6	10.1	164702	2	DD134569	DD134569 Means and	1083	231.4	10.1	171805	5	AC020716	AC020716 Homo sapi
c1011	231.6	10.1	164702	2	DD142671	DD142671 Means and	1084	231.4	10.1	176513	12	AC021885	AC021885 Homo sapi
c1012	231.6	10.1	164702	2	DD144740	DD144740 Means and	1085	231.4	10.1	176594	12	AC139480	AC139480 Homo sapi
c1013	231.6	10.1	164702	2	DD156328	DD156328 Means and	1086	231.4	10.1	177219	5	HS179D22	AL355433 Homo sapi
c1014	231.6	10.1	164702	2	DD156880	DD156880 Means and	c1087	231.4	10.1	178311	5	AC092910	AC092910 Homo sapi
c1015	231.6	10.1	164702	2	AX706960	AX706960 Sequence	1088	231.4	10.1	178688	5	AC068644	AC068644 Homo sapi
c1016	231.6	10.1	164702	2	AX707890	AX707890 Sequence	c1089	231.4	10.1	181300	12	AC142387	AC142387 Homo sapi
c1017	231.6	10.1	166451	12	AL36430	AL36430 Homo sapi	c1090	231.4	10.1	181340	12	AC009270	AC009270 Homo sapi
c1018	231.6	10.1	166517	12	AL591663	AL591663 Homo sapi	1091	231.4	10.1	183478	5	AC095055	AC095055 Homo sapi
c1019	231.6	10.1	169740	12	AF186193	AF186193 Homo sapi	1092	231.4	10.1	184296	5	AC099047	AC099047 Homo sapi
c1020	231.6	10.1	170240	12	AL160279	AL160279 Human DNA	c1093	231.4	10.1	184313	12	AC136509	AC136509 Pan trogl
c1021	231.6	10.1	173797	12	AC027289	AC027289 Homo sapi	1094	231.4	10.1	188491	5	HS56F10	AL355432 Homo sapi
c1022	231.6	10.1	174955	5	AL365502	AL365502 Human DNA	c1095	231.4	10.1	193790	5	AC009036	AC009036 Homo sapi
c1023	231.6	10.1	175905	12	AC127485	AC127485 Homo sapi	c1096	231.4	10.1	196730	5	AL391001	AL391001 Human DNA
c1024	231.6	10.1	177100	5	AC104437	AC104437 Homo sapi	1097	231.4	10.1	200418	5	AC074138	AC074138 Homo sapi
c1025	231.6	10.1	177950	5	AC019103	AC019103 Homo sapi	1098	231.4	10.1	201144	5	AF287262	AF287262 Homo sapi
c1026	231.6	10.1	180746	12	AL138803	AL138803 Homo sapi	1099	231.4	10.1	227139	12	AP001780	AP001780 Homo sapi
c1027	231.6	10.1	182105	5	AC009136	AC009136 Homo sapi	c1100	231.4	10.1	228390	12	AC141079	AC141079 Homo sapi
c1028	231.6	10.1	182256	5	AC005058	AC005058 Homo sapi	1101	231.4	10.1	252248	12	AC023238	AC023238 Homo sapi
c1029	231.6	10.1	183858	5	AL161626	AL161626 Human DNA	1102	231.2	10.1	286758	5	AC006449	AC006449 Homo sapi
c1030	231.6	10.1	188519	5	AC104041	AC104041 Homo sapi	1103	231.2	10.1	15399	5	AY566236	AY566236 Homo sapi
c1031	231.6	10.1	189008	12	AP001491	AP001491 Homo sapi	c1104	231.2	10.1	38000	5	AC008974	AC008974 Homo sapi
c1032	231.6	10.1	193456	12	AL492228	AL492228 Pan trogl	1105	231.2	10.1	39925	5	AC130897	AC130897 Homo sapi
c1033	231.6	10.1	194429	12	AC146061	AC146061 Pan trogl	1106	231.2	10.1	62693	5	AC140058	AC140058 Homo sapi
c1034	231.6	10.1	195029	12	AC007902	AC007902 Homo sapi	c1107	231.2	10.1	62836	5	AC004811	AC004811 Homo sapi
c1035	231.6	10.1	195741	5	AC132808	AC132808 Homo sapi	c1108	231.2	10.1	82827	5	AC079395	AC079395 Homo sapi
c1036	231.6	10.1	199889	12	AC120211	AC120211 Pan trogl	1109	231.2	10.1	92029	12	AL357492	AL357492 Homo sapi
c1037	231.6	10.1	200000	12	AC004624	AC004624 Homo sapi	c1110	231.2	10.1	101224	5	AC106750	AC106750 Homo sapi
c1038	231.6	10.1	200000	12	AC004670	AC004670 Homo sapi	c1111	231.2	10.1	102351	12	AL138848	AL138848 Homo sapi
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c1040	231.6	10.1	200254	12	AC135949	AC135949 Homo sapi	1113	231.2	10.1	124000	5	AC026310	AC026310 Homo sapi

c1114	231.2	10.1	125983	5	HS30760D1	283822 Human DNA s	1187	231	10.1	190771	5	AC113385	AC113385 Homo sapi
c1115	231.2	10.1	147862	5	AC079317	AC079317 Homo sapi	c1188	231	10.1	190982	5	AL133355	AL133355 Human DNA
c1116	231.2	10.1	148493	5	HS1061C18	AL121981 Human DNA	c1189	231	10.1	190912	12	AC080170	AC080170 Homo sapi
c1117	231.2	10.1	148750	5	AL596225	AL596225 Human DNA	c1190	231	10.1	192096	5	AL590133	AL590133 Human DNA
c1118	231.2	10.1	148930	5	AC073316	AC073316 Homo sapi	c1191	231	10.1	194367	5	AC022973	AC022973 Homo sapi
c1119	231.2	10.1	156422	5	AC0933579	AC0933579 Homo sapi	c1192	231	10.1	197484	5	AC068989	AC068989 Homo sapi
c1120	231.2	10.1	159059	12	AC0933000	AC0933000 Homo sapi	c1193	231	10.1	198456	12	AC003115	AC003115 Homo sapi
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c1122	231.2	10.1	160643	5	AC0102771	AC0102771 Homo sapi	c1195	231	10.1	202381	5	AC091167	AC091167 Homo sapi
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c1124	231.2	10.1	166013	12	AC016328	AC016328 Homo sapi	c1197	231	10.1	212858	12	AC036172	AC036172 Homo sapi
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c1126	231.2	10.1	172615	12	AC139765	AC139765 Homo sapi	c1199	230.8	10.1	675	7	BV604877	BV604877 S217P6043
c1127	231.2	10.1	173331	5	AC128639	AC128639 Papio anu	c1200	230.8	10.1	720	2	BD411360	BD411360 Method fo
c1128	231.2	10.1	174041	5	AL356423	AL356423 Human DNA	c1201	230.8	10.1	4008	5	AL112772	AL112772 Homo sapi
c1129	231.2	10.1	174253	12	AC068590	AC068590 Homo sapi	c1202	230.8	10.1	24031	5	AC084036	AC084036 Homo sapi
c1130	231.2	10.1	178970	5	AC159218	AC159218 Pan trogl	c1203	230.8	10.1	51720	12	AC027294	AC027294 4
c1131	231.2	10.1	185754	12	AC149082	AC149082 Papio anu	c1204	230.8	10.1	71591	5	AL772369	AL772369 Human DNA
c1132	231.2	10.1	186291	5	AC098932	AC098932 Homo sapi	c1205	230.8	10.1	73645	12	AC133545	AC133545 Homo sapi
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c1134	231.2	10.1	202308	5	AC1591108	AC1591108 Pan trogl	c1207	230.8	10.1	87878	2	AX695467	AX695467 Sequence
c1135	231.2	10.1	208239	12	AC021988	AC021988 Homo sapi	c1208	230.8	10.1	93390	2	BD411378	BD411378 Method fo
c1136	231.2	10.1	208642	5	HS4508N22	AL117339 Human DNA	c1209	230.8	10.1	101422	5	CR753892	CR753892 Human DNA
c1137	231.2	10.1	218724	12	AC025889	AC025889 Homo sapi	c1210	230.8	10.1	107314	5	AC005000	AC005000 Homo sapi
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c1139	231	10.1	783	7	BV531489	BV531489 G591P6238	c1212	230.8	10.1	110000	12	AC125619	AC125619 2
c1140	231	10.1	868	7	BV523651	BV523651 G591P6002	c1213	230.8	10.1	110000	12	AC125619	AC125619 3
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c1142	231	10.1	63412	5	AC093367	AC093367 Homo sapi	c1215	230.8	10.1	112705	12	AP002025	AP002025 Homo sapi
c1143	231	10.1	63432	5	BX004859	BX004859 Human DNA	c1216	230.8	10.1	113761	12	AL355494	AL355494 Homo sapi
c1144	231	10.1	63682	5	CR381640	CR381640 Human DNA	c1217	230.8	10.1	115952	5	AL772267	AL772267 Human DNA
c1145	231	10.1	84129	5	AC103813	AC103813 Homo sapi	c1218	230.8	10.1	116131	5	AL139324	AL139324 Human DNA
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c1147	231	10.1	118291	12	AC021469	AC021469 Homo sapi	c1220	230.8	10.1	123004	5	AC073846	AC073846 Homo sapi
c1148	231	10.1	120169	5	AC005060	AC005060 Homo sapi	c1221	230.8	10.1	123817	5	AL713980	AL713980 Human DNA
c1149	231	10.1	123668	5	AL390728	AL390728 Human DNA	c1222	230.8	10.1	13742	12	AC067727	AC067727 Homo sapi
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c1151	231	10.1	125133	5	AC013274	AC013274 Homo sapi	c1224	230.8	10.1	139203	12	AC068311	AC068311 Homo sapi
c1152	231	10.1	125585	5	HSDJ62D2	AL121955 Human DNA	c1225	230.8	10.1	139604	5	AC090639	AC090639 Homo sapi
c1153	231	10.1	133751	12	AL138843	AL138843 Homo sapi	c1226	230.8	10.1	142916	5	AL928921	AL928921 Human DNA
c1154	231	10.1	134250	5	AL139044	AL139044 Human DNA	c1227	230.8	10.1	145253	5	AC006329	AC006329 Homo sapi
c1155	231	10.1	134425	5	AP005715	AP005715 Homo sapi	c1228	230.8	10.1	146208	5	AL354776	AL354776 Human DNA
c1156	231	10.1	138177	5	AL139286	AL139286 Human DNA	c1229	230.8	10.1	146466	5	AL353637	AL353637 Human DNA
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c1158	231	10.1	148002	12	AL137838	AL137838 Homo sapi	c1231	230.8	10.1	153762	5	AL355338	AL355338 Human DNA
c1159	231	10.1	148285	12	AL451053	AL451053 Homo sapi	c1232	230.8	10.1	157173	5	AC009501	AC009501 Homo sapi
c1160	231	10.1	150481	5	HSDJ61404	AL121753 Human DNA	c1233	230.8	10.1	160013	5	AL133325	AL133325 Human DNA
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c1162	231	10.1	158135	5	AC025682	AC025682 Homo sapi	c1235	230.8	10.1	160277	5	AC009082	AC009082 Homo sapi
c1163	231	10.1	163520	5	AL391259	AL391259 Human DNA	c1236	230.8	10.1	166372	5	AL353705	AL353705 Human DNA
c1164	231	10.1	164304	5	BS000061	BS000061 Pan trogl	c1237	230.8	10.1	172151	5	HSAC000114	AC000114 Human PAC
c1165	231	10.1	165178	12	AC025355	AC025355 Homo sapi	c1238	230.8	10.1	173670	5	AL133351	AL133351 Human DNA
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c1168	231	10.1	172709	5	AC032019	AC032019 Homo sapi	c1241	230.8	10.1	176712	12	AC019290	AC019290 Homo sapi
c1169	231	10.1	173817	12	AC012141	AC012141 Homo sapi	c1242	230.8	10.1	177841	5	AC146018	AC146018 Pan trogl
c1170	231	10.1	174874	5	AL355674	AL355674 Human DNA	c1243	230.8	10.1	178932	12	AC146374	AC146374 Pan trogl
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c1172	231	10.1	176206	5	AC009867	AC009867 Homo sapi	c1245	230.8	10.1	179969	5	AC016643	AC016643 Homo sapi
c1173	231	10.1	176503	5	AL512604	AL512604 Human DNA	c1246	230.8	10.1	180548	5	AL596223	AL596223 Human DNA
c1174	231	10.1	177277	5	AL353668	AL353668 Human DNA	c1247	230.8	10.1	182020	5	AC113170	AC113170 Homo sapi
c1175	231	10.1	178256	5	AC009027	AC009027 Homo sapi	c1248	230.8	10.1	182865	12	AC171262	AC171262 Pan trogl
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c1179	231	10.1	180835	5	AC0091131	AC0091131 Homo sapi	c1252	230.8	10.1	187806	12	AC169997	AC169997 Macaca mu
c1180	231	10.1	180962	12	AC016415	AC016415 Homo sapi	c1253	230.8	10.1	204843	5	AC010359	AC010359 Homo sapi
c1181	231	10.1	182381	12	AC021725	AC021725 Homo sapi	c1254	230.8	10.1	212752	5	AC063977	AC063977 Homo sapi
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c1185	231	10.1	185415	5	HS121M24	AL354046 Homo sapi	c1258	230.6	10.1	43902	5	HSU12082	Z73496 Human DNA s
c1186	231	10.1	187160	5	AC138230	AC138230 Homo sapi	c1259	230.6	10.1	49373	5	AC104061	AC104061 Homo sapi

c1260	230.6	10.1	65114	5	AL590225	AL590225 Human DNA	1333	230.6	10.1	202360	5	AC055872	AC055872 Homo sapi
1261	230.6	10.1	70515	12	AL136332	AL136332 Homo sapi	1334	230.6	10.1	202414	12	AC135051	AC135051 Homo sapi
1262	230.6	10.1	71903	5	AL607035	AL607035 Human DNA	1335	230.6	10.1	216379	5	AL954243	AL954243 Pan trogl
1263	230.6	10.1	74284	12	AC034277	AC034277 Homo sapi	c1336	230.6	10.1	217746	5	AC015909	AC015909 Homo sapi
1264	230.6	10.1	75022	5	AF452638	AF452638 Homo sapi	1337	230.6	10.1	225423	12	AC167289	AC167289 Gorilla g
1265	230.6	10.1	77266	12	AL1390861	AL1390861 Homo sapi	1338	230.6	10.1	275197	5	AC004166	AC004166 Homo sapi
1266	230.6	10.1	81082	5	AY623113	AY623113 Homo sapi	1339	230.6	10.1	13949	5	HS745C22	HS745C22 Human DNA
1267	230.6	10.1	82486	5	AL133211	AL133211 Human DNA	1340	230.6	10.1	68122	5	AP000998	AP000998 Homo sapi
c1268	230.6	10.1	110000	12	AC008576	AC008576 Homo sapi	c1341	230.6	10.1	68759	5	AL136111	AL136111 Human DNA
c1269	230.6	10.1	110000	12	AC079517	AC079517 Mus muscu	1342	230.6	10.1	101299	12	AC022423	AC022423 Homo sapi
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c1273	230.6	10.1	124949	5	AL358794	AL358794 Human DNA	1346	230.6	10.1	124211	5	AC016593	AC016593 Homo sapi
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c1276	230.6	10.1	131359	5	AC004883	AC004883 Homo sapi	1349	230.6	10.1	140020	12	AC046162	AC046162 Homo sapi
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c1278	230.6	10.1	140026	5	AC005840	AC005840 Homo sapi	c1351	230.6	10.1	144273	12	AC024487	AC024487 Homo sapi
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c1280	230.6	10.1	145442	5	AC004859	AC004859 Homo sapi	c1353	230.6	10.1	147556	12	AC011007	AC011007 Homo sapi
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c1282	230.6	10.1	148933	5	AC104232	AC104232 Homo sapi	1355	230.6	10.1	151123	5	AC005520	AC005520 Homo sapi
1283	230.6	10.1	149831	12	AC026593	AC026593 Homo sapi	1356	230.6	10.1	151182	5	AL356010	AL356010 Human DNA
1284	230.6	10.1	150228	5	AC003071	AC003071 Homo sapi	c1357	230.6	10.1	151841	5	AC013408	AC013408 Homo sapi
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1286	230.6	10.1	152867	5	AC027671	AC027671 Homo sapi	1359	230.6	10.1	157208	5	AC113409	AC113409 Homo sapi
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1289	230.6	10.1	159123	5	AC007739	AC007739 Homo sapi	1362	230.6	10.1	160406	12	AC151370	AC151370 Aotus nan
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1292	230.6	10.1	161524	5	AC146451	AC146451 Pan trogl	1365	230.6	10.1	168690	12	AC024043	AC024043 Homo sapi
1293	230.6	10.1	163389	5	AL589765	AL589765 Human DNA	1366	230.6	10.1	172606	5	AL358972	AL358972 Human DNA
1294	230.6	10.1	163499	12	AC021109	AC021109 Homo sapi	c1367	230.6	10.1	173958	12	AC087351	AC087351 Homo sapi
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c1296	230.6	10.1	164914	5	AC027801	AC027801 Homo sapi	1369	230.6	10.1	177055	5	AC090360	AC090360 Homo sapi
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1300	230.6	10.1	167672	12	AC132806	AC132806 Homo sapi	1373	230.6	10.1	181443	5	AC099775	AC099775 Homo sapi
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1302	230.6	10.1	169604	5	AC083884	AC083884 Homo sapi	c1375	230.6	10.1	187406	12	AC169977	AC169977 Pan trogl
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c1306	230.6	10.1	176544	12	AL138877	AL138877 Homo sapi	c1379	230.6	10.1	190044	5	AC021842	AC021842 Homo sapi
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c1308	230.6	10.1	177531	2	DD134571	DD134571 Means and	c1381	230.6	10.1	198665	12	AC135612	AC135612 Pan trogl
c1309	230.6	10.1	177531	2	DD142673	DD142673 Means and	c1382	230.6	10.1	199268	12	AC099523	AC099523 Homo sapi
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c1311	230.6	10.1	177531	2	DD156330	DD156330 Means and	1384	230.6	10.1	202544	5	AC104447	AC104447 Homo sapi
c1312	230.6	10.1	177531	2	DD156882	DD156882 Means and	c1385	230.6	10.1	203448	12	AC063958	AC063958 Homo sapi
c1313	230.6	10.1	177531	2	AX706962	AX706962 Sequence	1386	230.6	10.1	204746	5	AC055866	AC055866 Homo sapi
c1314	230.6	10.1	177531	2	AX707892	AX707892 Sequence	c1387	230.6	10.1	216161	5	AC024558	AC024558 Homo sapi
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1316	230.6	10.1	177719	5	AC135048	AC135048 Homo sapi	c1389	230.6	10.1	218497	5	AC158241	AC158241 Pan trogl
c1317	230.6	10.1	177756	5	AC034111	AC034111 Homo sapi	c1390	230.6	10.1	218859	12	AC022912	AC022912 Homo sapi
1318	230.6	10.1	178733	12	AC068786	AC068786 Homo sapi	c1391	230.6	10.1	218859	12	AC093623	AC093623 Homo sapi
c1319	230.6	10.1	180133	5	AL138885	AL138885 Human DNA	1392	230.6	10.1	274349	12	AP001671	AP001671 Homo sapi
c1320	230.6	10.1	181400	5	AC084251	AC084251 Homo sapi	c1393	230.6	10.1	340000	5	SV624051	SV624051 S215P6991
1321	230.6	10.1	181823	12	AC145526	AC145526 Homo sapi	1394	230.6	10.1	2291	5	BC041339	BC041339 Homo sapi
1322	230.6	10.1	182892	5	AC034244	AC034244 Homo sapi	c1395	230.6	10.1	3116	5	BSM809067	BSM809067 Homo sapi
1323	230.6	10.1	183521	5	AC091609	AC091609 Homo sapi	1396	230.6	10.1	3757	5	BC035187	BC035187 Homo sapi
c1324	230.6	10.1	184026	12	AC026638	AC026638 Homo sapi	c1397	230.6	10.1	4471	2	CS124343	CS124343 Sequence
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c1326	230.6	10.1	185173	12	AC009056	AC009056 Homo sapi	c1399	230.6	10.1	23948	5	AL355505	AL355505 Human DNA
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1329	230.6	10.1	190477	5	FTB109N16	AL954242 Pan trogl	c1402	230.6	10.1	36377	5	AC011531	AC011531 Homo sapi
1330	230.6	10.1	190648	5	CNS01DXI	AL139317 Human chr	c1403	230.6	10.1	39255	5	AC002496	AC002496 Human cos
c1331	230.6	10.1	192464	5	AC090971	AC090971 Homo sapi	c1404	230.6	10.1	45347	5	HSAC002057	HSAC002057 Human cos
c1332	230.6	10.1	199454	12	AC117180	AC117180 Homo sapi	1405	230.6	10.1	56408	5	AF527418	AF527418 Homo sapi

1406	230.2	10.1	65245	5	AV785359	AY785359 Homo sapi
1407	230.2	10.1	90906	5	AC079767	AC079767 Homo sapi
1408	230.2	10.1	94000	5	AC138336	AC138336 Homo sapi
1409	230.2	10.1	97477	5	AL359257	AL359257 Human DNA
1410	230.2	10.1	100000	5	AP000049	AP000049 Homo sapi
1411	230.2	10.1	100000	5	AP000116	AP000116 Homo sapi
1412	230.2	10.1	100000	5	AP000192	AP000192 Homo sapi
1413	230.2	10.1	101352	5	AC008902	AC008902 Homo sapi
1414	230.2	10.1	104309	5	AL138717	AL138717 Human DNA
1415	230.2	10.1	106034	5	AL134028	AL134028 Homo sapi
1416	230.2	10.1	106988	5	AC001226	AC001226 Genomic s
1417	230.2	10.1	111026	12	AL157403	AL157403 Homo sapi
1418	230.2	10.1	125242	5	AP000311	AP000311 Homo sapi
1419	230.2	10.1	126581	5	AC003957	AC003957 Homo sapi
1420	230.2	10.1	127709	12	CNS05TC1	AL352983 Homo sapi
1421	230.2	10.1	129272	5	AL451125	AL451125 Human DNA
1422	230.2	10.1	131990	5	AC008925	AC008925 Homo sapi
1423	230.2	10.1	132953	5	AC024221	AC024221 Homo sapi
1424	230.2	10.1	142890	5	AC097492	AC097492 Homo sapi
1425	230.2	10.1	143340	5	AF215937	AF215937 Homo sapi
1426	230.2	10.1	143754	12	AL359093	AL359093 Homo sapi
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1429	230.2	10.1	153267	12	AC011212	AC011212 Homo sapi
1430	230.2	10.1	153609	5	HSJA9617	AJ009617 Homo sapi
1431	230.2	10.1	154353	5	AC027820	AC027820 Homo sapi
1432	230.2	10.1	157878	12	AP001367	AP001367 Homo sapi
1433	230.2	10.1	160256	5	AC183108	AC183108 Pan trogl
1434	230.2	10.1	161087	5	AC018850	AC018850 Homo sapi
1435	230.2	10.1	162451	5	AL353597	AL353597 Human DNA
1436	230.2	10.1	165215	5	AC185986	AC185986 Pan trogl
1437	230.2	10.1	166857	12	CNS01RG5	AL157757 Homo sapi
1438	230.2	10.1	167127	5	CNS01RHR	AL162311 Human chr
1439	230.2	10.1	167272	5	AC011466	AC011466 Homo sapi
1440	230.2	10.1	167746	5	AC011120	AC011120 Homo sapi
1441	230.2	10.1	168956	5	AC090286	AC090286 Homo sapi
1442	230.2	10.1	169950	12	AC084049	AC084049 Homo sapi
1443	230.2	10.1	170067	12	AC124946	AC124946 Homo sapi
1444	230.2	10.1	170758	5	AC004965	AC004965 Homo sapi
1445	230.2	10.1	172191	12	AC034173	AC034173 Homo sapi
1446	230.2	10.1	172579	12	AC168953	AC168953 Actus nan
1447	230.2	10.1	174634	12	AC140513	AC140513 Homo sapi
1448	230.2	10.1	174937	5	AC027233	AC027233 Homo sapi
1449	230.2	10.1	176257	5	CNS01RHJ	AL161756 Human chr
1450	230.2	10.1	180445	5	AC019171	AC019171 Homo sapi
1451	230.2	10.1	182320	12	AC016808	AC016808 Homo sapi
1452	230.2	10.1	183023	5	AC183803	AC183803 Pan trogl
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1454	230.2	10.1	184595	12	AC015913	AC015913 Homo sapi
1455	230.2	10.1	186108	5	AL158827	AL158827 Human DNA
1456	230.2	10.1	186233	5	AC092329	AC092329 Homo sapi
1457	230.2	10.1	187359	12	AC140518	AC140518 Homo sapi
1458	230.2	10.1	187431	5	AC107219	AC107219 Homo sapi
1459	230.2	10.1	187514	12	AC019267	AC019267 Homo sapi
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1461	230.2	10.1	187929	12	AC163245	AC163245 Papio anu
1462	230.2	10.1	188290	5	AC187773	AC187773 Pongo pyg
1463	230.2	10.1	188526	12	AC012342	AC012342 Homo sapi
1464	230.2	10.1	189317	12	AC024483	AC024483 Homo sapi
1465	230.2	10.1	190714	5	AC145863	AC145863 Pan trogl
1466	230.2	10.1	190943	12	AC130424	AC130424 Homo sapi
1467	230.2	10.1	192336	5	AL158155	AL158155 Human DNA
1468	230.2	10.1	192524	12	AC153752	AC153752 Papio anu
1469	230.2	10.1	193041	5	AC092017	AC092017 Homo sapi
1470	230.2	10.1	193633	5	AC009167	AC009167 Homo sapi
1471	230.2	10.1	194473	12	AC183982	AC183982 Pan trogl
1472	230.2	10.1	195052	12	AC145040	AC145040 Gorilla g
1473	230.2	10.1	195494	5	AC091153	AC091153 Homo sapi
1474	230.2	10.1	196216	5	AC099343	AC099343 Homo sapi
1475	230.2	10.1	196341	12	AC140517	AC140517 Homo sapi
1476	230.2	10.1	205443	12	AC140505	AC140505 Homo sapi
1477	230.2	10.1	206587	5	AL138898	AL138898 Human DNA
1478	230.2	10.1	208155	5	AC124254	AC124254 Homo sapi
1479	230.2	10.1	210528	12	AC169135	AC169135 Actus nan
1480	230.2	10.1	211116	12	AC168952	AC168952 Actus nan
1481	230.2	10.1	222273	5	AC185243	AC185243 Pan trogl
1482	230.2	10.1	223468	12	AC187617	AC187617 Pan trogl
1483	230.2	10.1	231174	5	AL139264	AL139264 Homo sapi
1484	230.2	10.1	251187	12	AL359875	AL359875 Homo sapi
1485	230.2	10.1	255427	12	AC171374	AC171374 Saimiri b
1486	230.2	10.1	290040	2	CQ955690	CQ955690 Sequence
1487	230.2	10.1	290040	2	CQ955720	CQ955720 Sequence
1488	230.2	10.1	290040	2	CQ969957	CQ969957 Sequence
1489	230.2	10.1	290040	2	CQ970012	CQ970012 Sequence
1490	230.2	10.1	290420	12	AC020873	AC020873 Mus muscu
1491	230.2	10.1	325791	2	DD010238	DD010238 Estrogen
1492	230.2	10.1	325791	2	AR606191	AR606191 Sequence
1493	230.2	10.1	325791	2	AX234657	AX234657 Sequence
1494	230.2	10.1	328187	12	AC117393	AC117393 Homo sapi
1495	230.2	10.1	340000	5	AP001718	AP001718 Homo sapi
1496	230.2	10.1	955	2	AR338737	AR338737 Sequence
1497	230.2	10.1	26133	5	CR385036	CR385036 Human DNA
1498	230.2	10.1	29186	5	AL357560	AL357560 Human DNA
1499	230.2	10.1	37991	5	AC005101	AC005101 Homo sapi
1500	230.2	10.1	40629	12	AC006105	AC006105 Homo sapi

ALIGNMENTS

RESULT 1

BD140585

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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Query Match									
Best Local Similarity 100.0%; Score 2284; DB 2; Length 2284;									
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCGGACATCCGTCGGTCTCGCGAGACCCCGCGGATTCGCGGTCTCTCCGC	60						
Db	1	GCGGAGCATCCGTCGGTCTCGCGAGACCCCGCGGATTCGCGGTCTCTCCGC	60						
Qy	61	GCGCGGACAGAGCTGTCCTCGACCTGGATGGCAGCGGGCGCGGGTCTCTCGAC	120						
Db	61	GCGCGGACAGAGCTGTCCTCGACCTGGATGGCAGCGGGCGCGGGTCTCTCGAC	120						
Qy	121	GCAGAGAGAAATCTCATCATCTGTGCGCTTCTTAAAGCAAACTAAGACGAGGGAG	180						
Db	121	GCAGAGAGAAATCTCATCATCTGTGCGCTTCTTAAAGCAAACTAAGACGAGGGAG	180						
Qy	181	GATTATCTTACCTTTGAAGCAAACTAAGACGAGGGAG	240						
Db	181	GATTATCTTACCTTTGAAGCAAACTAAGACGAGGGAG	240						
Qy	241	GAAGGAGCTTGACTTACCTTTGGTAAATTTGCTTCTGACACTAAGGCTGTCTGCT	300						
Db	241	GAAGGAGCTTGACTTACCTTTGGTAAATTTGCTTCTGACACTAAGGCTGTCTGCT	300						
Qy	301	AGTCAGAAATTCCTCAAAAAGAGCTAGAAAGATGTTGTCATTTGACATCCAGTCTCTT	360						
Db	301	AGTCAGAAATTCCTCAAAAAGAGCTAGAAAGATGTTGTCATTTGACATCCAGTCTCTT	360						
Qy	361	TCTAAGGAAATCAGAGCAATGAGCCGCTATATCTCAACTCAAGAGACTGATTAAT	420						
Db	361	TCTAAGGAAATCAGAGCAATGAGCCGCTATATCTCAACTCAAGAGACTGATTAAT	420						
Qy	421	TCTTGTCTTCAACAAAAACATATCAGGCGACAAAGCATGTAACTTGTATCTTCGAC	480						
Db	421	TCTTGTCTTCAACAAAAACATATCAGGCGACAAAGCATGTAACTTGTATCTTCGAC	480						
Qy	481	ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGTCCTCAACGAGGAAGCC	540						
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Qy	601	TTGACAGAAATTTGCAAGCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAA	660						
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Qy	661	TTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTTATCAAGGCCCCACCGAT	720						
Db	661	TTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTTATCAAGGCCCCACCGAT	720						
Qy	721	ATCTCATGGAGACACATTTCTCAGAAATTTGGATCTCAGATCACTGGAGAACTA	780						
Db	721	ATCTCATGGAGACACATTTCTCAGAAATTTGGATCTCAGATCACTGGAGAACTA	780						
Qy	781	TTTTAAGATGATGAGCAAGTCCCGCTGCTTATTAAGGAAAGGCCATTTCTCAG	840						
Db	781	TTTTAAGATGATGAGCAAGTCCCGCTGCTTATTAAGGAAAGGCCATTTCTCAG	840						
Qy	841	AGTTTCAAAATTTCTCTGATCAAGAAATAGTCTATCTGCTCTGAAATTTGAGTGGC	900						
Db	841	AGTTTCAAAATTTCTCTGATCAAGAAATAGTCTATCTGCTCTGAAATTTGAGTGGC	900						
Qy	901	CTCCAGCTAGGTGGAGTTGCTTCTCCATACCACTCGGCTACTTCCAAAGCCCGCC	960						
Db	901	CTCCAGCTAGGTGGAGTTGCTTCTCCATACCACTCGGCTACTTCCAAAGCCCGCC	960						
Qy	961	ACCTTCTACCCCAATGCTTCAAGTACAGCTTCTGGGACTTCCGAGCACAGCTGGCC	1020						
Db	961	ACCTTCTACCCCAATGCTTCAAGTACAGCTTCTGGGACTTCCGAGCACAGCTGGCC	1020						

Qy	1021	ACCACAGCTCCAGCTGTAAACCACTGTCTCAGCTTCCACAGACCTCATTTCTACA	1080
Db	1021	ACCACAGCTCCAGCTGTAAACCACTGTCTCAGCTTCCACAGACCTCATTTCTACA	1080
Qy	1081	GTTTTACACGGGCTCGGCTACACTCAAGCAATGGCTACAAACAGCAGTTCTGACTACC	1140
Db	1081	GTTTTACACGGGCTCGGCTACACTCAAGCAATGGCTACAAACAGCAGTTCTGACTACC	1140
Qy	1141	ACCTTTACAGGACCTACGAGCTCGAAAGGAGCTTTAGAAACCATACCTTTACAGAAATC	1200
Db	1141	ACCTTTACAGGACCTACGAGCTCGAAAGGAGCTTTAGAAACCATACCTTTACAGAAATC	1200
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Db	1261	GTGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGTAGGGAGCCAGTCCAGGC	1320
Qy	1321	AGTTCTTCCAGGACGTGTTCCAGAAATCAGTACGGCTTCCATTTGAAAAATGGCTT	1380
Db	1321	AGTTCTTCCAGGACGTGTTCCAGAAATCAGTACGGCTTCCATTTGAAAAATGGCTT	1380
Qy	1381	CTTATCGGGTCCCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440
Db	1381	CTTATCGGGTCCCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440
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Qy	1501	GGGATCTATGTGGACATTAAGAGTGAATTCGGTGTCTTAAATTCATTTAGTAAACAG	1560
Db	1501	GGGATCTATGTGGACATTAAGAGTGAATTCGGTGTCTTAAATTCATTTAGTAAACAG	1560
Qy	1561	AAGCCCAAAATGCAATGAGTTTCTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
Db	1561	AAGCCCAAAATGCAATGAGTTTCTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
Qy	1621	AGACAGAAATGCGCTTCTGCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT	1680
Db	1621	AGACAGAAATGCGCTTCTGCTGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCT	1680
Qy	1681	TTGCCCCAGGCTGGAGTGCAGTACGATCTCGGCTCTCACGCAACCTCCGCTCTCTGG	1740
Db	1681	TTGCCCCAGGCTGGAGTGCAGTACGATCTCGGCTCTCACGCAACCTCCGCTCTCTGG	1740
Qy	1741	GTTCAAGCGATTTCTCTGCTCAGCTCCTAAGTATCTGGGATTTACAGGCATGTGCCACC	1800
Db	1741	GTTCAAGCGATTTCTCTGCTCAGCTCCTAAGTATCTGGGATTTACAGGCATGTGCCACC	1800
Qy	1801	ACACTGGGTGATTTTGTATTTTGTAGAGAGGGGTTTCCACATGTTGCTCAGGCTG	1860
Db	1801	ACACTGGGTGATTTTGTATTTTGTAGAGAGGGGTTTCCACATGTTGCTCAGGCTG	1860
Qy	1861	GTCTCAAACTCCTGACCTAGTATCCACCTCTCGGCTCCCAAGTGTGGGATTTACA	1920
Db	1861	GTCTCAAACTCCTGACCTAGTATCCACCTCTCGGCTCCCAAGTGTGGGATTTACA	1920
Qy	1921	GGCATGAGCCACCAAGCTGGCCCTCTGTTTATTTGTTGTTTGTAGAGGAATGA	1980
Db	1921	GGCATGAGCCACCAAGCTGGCCCTCTGTTTATTTGTTGTTTGTAGAGGAATGA	1980
Qy	1981	AGTGGGAACCAATTTAGTATTTGGTATCTGCTCTAATAATTTAGCTTAAACAA	2040
Db	1981	AGTGGGAACCAATTTAGTATTTGGTATCTGCTCTAATAATTTAGCTTAAACAA	2040
Qy	2041	AGCTCTATGTAAGTAAATAAAGTAAATTTGCCATATAAATTTCAAAATTTCAACTGGCTTT	2100
Db	2041	AGCTCTATGTAAGTAAATAAAGTAAATTTGCCATATAAATTTCAAAATTTCAACTGGCTTT	2100
Qy	2101	TATCAAAAGAAACAGGTTAGGACATCTAGTTTCAATTTCAATTTCTTGGTCCAGA	2160

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Db      2101  |||||TATGCAAGAAACAGGTAGGACATCTAGTTCCTCAATTCATTCACATCTTGGTCCAGA 2160
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QY      2221  TTAATACTATTTCAGATGCTCTCTCCCAATTAATATTTGAATAAATCTTTGTTTAC 2280
Db      2221  TTAATACTATTTCAGATGCTCTCTCCCAATTAATATTTGAATAAATCTTTGTTTAC 2280
QY      2281  TCAA 2284
Db      2281  |||||TCAA 2284

RESULT 2
LOCUS   BD378361          2284 bp      DNA      linear      PAT 04-NOV-2005
DEFINITION SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
          THE SAME.
ACCESSION BD378361
VERSION   BD378361.1 GI:92277455
KEYWORDS  JP 2003524387-A/68.
SOURCE   unidentified
          unclassified sequences.
REFERENCE 1 (bases 1 to 2284)
          Roy,M.A., Napier M.A., Tumas,D., Kljavin,I.J., Hillan,K.J.,
          Gurney,A.L., Grimaldi,C.J., Godowski,P.J., Goddard,A.,
          Gerritsen,M.E., Filvaroff,E., Dan, Eaton,L., Botstein,D.,
          Baker,K.P., Ferrara,N. and Wood,W.I.
          SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
          THE SAME
JOURNAL  Patent: JP 2003524387-A 68 19-AUG-2003;
          Genentech Inc,Kevin P Baker,David Botstein,Dan L Eaton, Napoleone
          Ferrara, Ellen Filvaroff,Mary E Gerritsen,Audrey Goddard,Paul J
          Godowski, Christopher J Grimaldi,Austin L Gurney,Kenneth J Hillan,
          Ivar J Kljavin, Mary A Napier,Margaret Ann Roy,Daniel Tumas,William
          I Wood
COMMENT  OS Homo Sapien
          PN JP 2003524387-A/68
          PD 19-AUG-2003
          PF 01-DEC-1999 JP 2000585407
          PR 01-DEC-1998 US US9825108,16-DEC-1998 US 60/112850, PR
          22-DEC-1998 US 60/113296
          PI margaret ann roy,mary a napier,daniel tumas,ivar j kljavin, PI
          kenneth j hillan,austin l gurney,christopher
          PI j grimaldi,paul j
          PI godowski,
          PI audrey goddard,mary e gerritsen,ellen filvaroff,dan PI 1
          eaton,david botstein,
          PI kevin p baker,napoleone ferrara,william i wood CC
          FH key Location/Qualifiers
          source      1. .2284
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Query Match 100.0%; Score 2284; DB 2; Length 2284;
Best Local Similarity 100.0%; Pred NO. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCGAGCATCCGTCGGTCTCTCGCCGAGACCCCGCGGATTCGCCGTCCTCCCGC 60
Db      1 GCGAGCATCCGTCGGTCTCTCGCCGAGACCCCGCGGATTCGCCGTCCTCCCGC 60
QY      61 GGGCGGACAGAGCTGCTCTCGCACTTGGATGCGAGCGGGCGCGGGTCTCTTCGAC 120
Db      61 GGGCGGACAGAGCTGCTCTCGCACTTGGATGCGAGCGGGCGCGGGTCTCTTCGAC 120

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QY      121 GCCAGAGAGAAATCTCATCTGTGTGAGCCTTCTTAAAGCAAACTAAGACCAGGGAG 180
Db      121 GCCAGAGAGAAATCTCATCTGTGTGAGCCTTCTTAAAGCAAACTAAGACCAGGGAG 180
QY      181 GATTATCTTTGACCTTTGAAAGACCAAACTAAACTGAAATTTAAATTTCTTCGGGGGA 240
Db      181 GATTATCTTTGACCTTTGAAAGACCAAACTAAACTGAAATTTAAATTTCTTCGGGGGA 240
QY      241 GAAGGGAGCTTGACTTACACTTTGGTGAATTAATTTGCTTCTTGACACTTAAGGCTGTCTCT 300
Db      241 GAAGGGAGCTTGACTTACACTTTGGTGAATTAATTTGCTTCTTGACACTTAAGGCTGTCTCT 300
QY      301 AGTCAGAATTTGCTCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCT 360
Db      301 AGTCAGAATTTGCTCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCT 360
QY      361 TCTAAGGGAATCAGAGGCAATGAGCCGCTATATATCTTCAACTCAAGAAGACTGCAATTAAT 420
Db      361 TCTAAGGGAATCAGAGGCAATGAGCCGCTATATATCTTCAACTCAAGAAGACTGCAATTAAT 420
QY      421 TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 480
Db      421 TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 480
QY      481 ACTCGAAAAACAGCTAGACCAACCCACTGTCTACTTATTTTCTGTCCCAACGAGGAAGCC 540
Db      481 ACTCGAAAAACAGCTAGACCAACCCACTGTCTACTTATTTTCTGTCCCAACGAGGAAGCC 540
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QY      601 TTGACCAAGAAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTTCTCTTACATGCCCCAA 660
Db      601 TTGACCAAGAAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTTCTCTTACATGCCCCAA 660
QY      661 TTTTCAAGAGTCACTCCCTAGCCCATCATCACACAGATTTATTTCAAGGCCACCGAT 720
Db      661 TTTTCAAGAGTCACTCCCTAGCCCATCATCACACAGATTTATTTCAAGGCCACCGAT 720
QY      721 ATCTCATGGAGAGACACACTTTCTCAGAAATTTGGATCCTCAGATCACTCGAGAAACTA 780
Db      721 ATCTCATGGAGAGACACACTTTCTCAGAAATTTGGATCCTCAGATCACTCGAGAAACTA 780
QY      781 TTTAAGATGATGAAGCAAGTGCCAGCTCTTGCTTATAAGGAAAAAGGCCATTTCTCAG 840
Db      781 TTTAAGATGATGAAGCAAGTGCCAGCTCTTGCTTATAAGGAAAAAGGCCATTTCTCAG 840
QY      841 AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGTGCTGCTGAAATTTGAGTGG 900
Db      841 AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGTGCTGCTGAAATTTGAGTGG 900
QY      901 CTCCAGCTAGGTGGGAGTGTCTTCTCCACATACCACCTCGGCTACTCCAAAGCCGCC 960
Db      901 CTCCAGCTAGGTGGGAGTGTCTTCTCCACATACCACCTCGGCTACTCCAAAGCCGCC 960
QY      961 ACCCTTCTACCCCAATGCTTTCAGTGACACCTTCTGGGACTTCCAGCACAGCTGGCC 1020
Db      961 ACCCTTCTACCCCAATGCTTTCAGTGACACCTTCTGGGACTTCCAGCACAGCTGGCC 1020
QY      1021 ACCACAGCTCCACCTGTAAACCACTGTCTCTCAGCCTCCACGACCTCAATTTCTACA 1080
Db      1021 ACCACAGCTCCACCTGTAAACCACTGTCTCTCAGCCTCCACGACCTCAATTTCTACA 1080
QY      1081 GTTTTTCACGGGCTGGGCTTACCTCAAGCAATGGCTACACAGCAGTTCCTGATACC 1140
Db      1081 GTTTTTCACGGGCTGGGCTTACCTCAAGCAATGGCTTACACAGCAGTTCCTGATACC 1140
QY      1141 ACCTTTTCAGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCT 1200
Db      1141 ACCTTTTCAGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCT 1200
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Db      1261  |||||GTGGAGCTTCCACATATGAATAAACTGCTTCTGGGAAAGTAGGAGGCCAGTCCAGGC||| 1320
Qy      1321  |||||AGTTCTCCAGGCGAGTGTTCAGAAAATCAGTACGGCTTCCATTTGAAAATGGCTT||| 1380
Db      1321  |||||AGTTCTCCAGGCGAGTGTTCAGAAAATCAGTACGGCTTCCATTTGAAAATGGCTT||| 1380
Qy      1381  |||||CTTATCGGCTCCCTGCTCTTGTGTCCTGTCCTGCTGATAGGCTCGTCCCTCGGCT||| 1440
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Qy      1441  |||||AGAATCTTTGGAATCACTCCGACGAAACGTTACTCAAGACTGGAATATTGATCAAT||| 1500
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Qy      1501  |||||GGGATCTATGAGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCATTTAGTAACAG||| 1560
Db      1501  |||||GGGATCTATGAGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCATTTAGTAACAG||| 1560
Qy      1561  |||||AAGCCCAATGCATGAGTCTTCTGCTGACTTGTCTAGTCTTAGCAGGAGTGTATTGTA||| 1620
Db      1561  |||||AAGCCCAATGCATGAGTCTTCTGCTGACTTGTCTAGTCTTAGCAGGAGTGTATTGTA||| 1620
Qy      1621  |||||AGACAGAAAATGCCCCCTTCTGCTTCTTCTTTTGGAGACAGAGTCTTGTCTG||| 1680
Db      1621  |||||AGACAGAAAATGCCCCCTTCTGCTTCTTCTTTTGGAGACAGAGTCTTGTCTG||| 1680
Qy      1681  |||||TTGCCAGGCTGGAGTGCAGTAGCAGATCTGGCTCTCACGCCAACCTCCGCTCCTGG||| 1740
Db      1681  |||||TTGCCAGGCTGGAGTGCAGTAGCAGATCTGGCTCTCACGCCAACCTCCGCTCCTGG||| 1740
Qy      1741  |||||GTTCAAGCGATTCCTGCTCCTAGCTCTTAAGTATCTGGGATTCAGGATGTGCCACC||| 1800
Db      1741  |||||GTTCAAGCGATTCCTGCTCCTAGCTCTTAAGTATCTGGGATTCAGGATGTGCCACC||| 1800
Qy      1801  |||||ACACCTGGGTGATTTTGTATTTTGTAGTAGAGAGCGGGTTTCCACATGTTGGTCAGGCTG||| 1860
Db      1801  |||||ACACCTGGGTGATTTTGTATTTTGTAGTAGAGAGCGGGTTTCCACATGTTGGTCAGGCTG||| 1860
Qy      1861  |||||GTCTCAAACTCCGACCTAGTATGATCACCTCTCGGCTCTCCAAAGTGTGGGATTACA||| 1920
Db      1861  |||||GTCTCAAACTCCGACCTAGTATGATCACCTCTCGGCTCTCCAAAGTGTGGGATTACA||| 1920
Qy      1921  |||||GGCATGAGCCACACAGCTGGCCCCCTTCTGTTTTATGTTGTTTGTAGAGAGGAATGA||| 1980
Db      1921  |||||GGCATGAGCCACACAGCTGGCCCCCTTCTGTTTTATGTTGTTTGTAGAGAGGAATGA||| 1980
Qy      1981  |||||AGTGGGAACCAATTTAGGTAATTTGGGTAATCTGTCTTAAATATTTAGCTAAAAACAA||| 2040
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Qy      2041  |||||AGCTCTATGTAAAGTAAATTAAGTATAATTCGCCATATAAAATTCAAATTCAGCTGGCTTT||| 2100
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Qy      2101  |||||TATGCAAGAAACAGGTTAGGACATCTAGTTCCTTCAATTCATTCATTCCTGGTTCAGA||| 2160
Db      2101  |||||TATGCAAGAAACAGGTTAGGACATCTAGTTCCTTCAATTCATTCATTCCTGGTTCAGA||| 2160
Qy      2161  |||||TAAATCACTGTTTATATCAATTTCTAATGGAATTCCTTTTCTTTTATATGATTCCT||| 2220
Db      2161  |||||TAAATCACTGTTTATATCAATTTCTAATGGAATTCCTTTTCTTTTATATGATTCCT||| 2220
Qy      2221  |||||TTAAACTTATTCAGATGTAGTTCCTTCCAAATTAATATTTGAATAAATCTTTTGTAC||| 2280
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Qy      2281  |||||TCAA 2284

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Db      2281  TCAA 2284

RESULT 3
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LOCUS      2284 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 514 from patent US 6478825.
ACCESSION AR252736
VERSION   AR252736.1 GI:27300644
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE     Implant, method of making same and use of the implant for the
          treatment of bone defects
JOURNAL   Patent: US 6478825-A 514 12-NOV-2002;
          Osteotech, Inc.; Batontown, NJ
FEATURES  Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 2284; DB 2; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1   GCGGAGCATCCGCTGGCTCCTCGCCGAGACCCCGCGGATTCGCGGTCCTTCCGCG 60
Db      1   GCGGAGCATCCGCTGGCTCCTCGCCGAGACCCCGCGGATTCGCGGTCCTTCCGCG 60
Qy      61   GCGCGCGACAGAGCTGCTCGCACCTGGATGGCAGAGGGCGCGCGGGTCTCTCGAC 120
Db      61   GCGCGCGACAGAGCTGCTCGCACCTGGATGGCAGAGGGCGCGCGGGTCTCTCGAC 120
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Qy      181  GATTATCTTGACCTTTGAAGCAAACTAAACTGAATTTAAATTTCTTCGGGGA 240
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Qy      361  TCTAAGGGAATCAGAGCAATAGCCCGTATATCTTCAACTCAAGAGAGTGCATTAAT 420
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Qy      421  TCTTGTCTGTTCAACAAAACATATCAGGGGACAAAGCATGTGATGATCTTTCGAC 480
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Db	841		
Qy	901	TTTAAAGATGGATGAACAAAGTGCCAGCTCCTTGTCTTATAAGGAAAAAGGCCATTTCTCAG	960
Db	901		
Qy	961	TTTAAAGATGGATGAACAAAGTGCCAGCTCCTTGTCTTATAAGGAAAAAGGCCATTTCTCAG	1020
Db	961		
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Db	1021		
Qy	1081	AGTTTCAAAATTTTCCTCTGATCAAGAAATAGTCTATCTGCTGCCTGAAATGTGAGTGGC	1140
Db	1081		
Qy	1141	CTCCGAGCTACGGTGGCAGTTGCTTCTCCACATACACACTCGGCTACTCCAAAGCCGCGC	1200
Db	1141		
Qy	1201	CTCCGAGCTACGGTGGCAGTTGCTTCTCCACATACACACTCGGCTACTCCAAAGCCGCGC	1260
Db	1201		
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Db	1321		
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1861	Qy	GTCTCAAACTCCTGACCTAGTGATCCACCCCTCTCGGCCCTCCAAAGTGTGGGATTCACA	1920
1861	Db	GTCTCAAACTCCTGACCTAGTGATCCACCCCTCTCGGCCCTCCAAAGTGTGGGATTCACA	1920
1921	Qy	GGCATGAGCCACACACAGCTGGCCCCCTTCGTGTTTATGTTGGTTCAGAGAGGAATGA	1980
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DEFINITION	the same.								
ACCESSION	DD028540								
VERSION	DD028540.1	GI:92561177							
KEYWORDS	JP 2004203742-A/369.								
SOURCE	unidentified								
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AUTHORS	1 (bases 1 to 2284)								
	Grimaldi,C.J., Ashkenazi,A.J., Desnoyers,L., Baker,K.P.,								
	Godowski,P.J., Goddard,A., Gerstitsen,M.E., Gerber,H., Fong,S.,								
	Ferrara,N., Eaton,D.L., Botstein,D., Gurney,A.L., Kljavin,I.J.,								
	Napier,M.A., Zhang,Z., Wood,W.I., Williams,M.P., Tumas,D.,								
	Watanabe,C.K., Stewart,T.A., Roy,M.A., Paoni,N.F. and Pan,J.								
	Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding								
TITLE	the same								
JOURNAL	Patent: JP 2004203742-A 369 22-JUL-2004;								
	Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney,								
	Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan								
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17-AUG-1999	US	60/149396, 15-SEP-1999	US	US9921090,	PR
15-SEP-1999	US	US9921547, 08-OCT-1999	US	60/158663,	PR
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christopher j grimaldi, avi j askenazi, luc desnoyers, kevin p PI					
baker,					
PI	paul j	godowski, audrey goddard, mary e	gerritsen, hanspeter	PI	
gerber,					
PI	sherman fong, napoleone ferrara, dan l	eaton, david	botstein,	PI	
austin l gurney,					
PI	ivar j	kljavin, mary a	napier, zemin zhang,	william PI	i
wood, mickey					
PI	p	williams,			
PI	daniel	tumas, colin k	watanabe, timothy a	stewart, margaret	ann
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Db	61	GGCGCGACAGAGTCTCCGACCTGGATGGCAGCGGGCGCGGTCTCTCGAC	120		
Qy	121	GCAGAGAGAAATCTCATCTGTGAGCTTCTTAAAGCAAACTAAGACGAGGGAG	180		
Db	121	GCAGAGAGAAATCTCATCTGTGAGCTTCTTAAAGCAAACTAAGACGAGGGAG	180		
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Qy	241	GAAGGAGCTTGACTTACCTTTGGTAAATTAATTTGCTTCTGACACTAAGGCTGTCTGCT	300		
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Qy	301	AGTCAGAAATTCCTCAAAAGAGCTAGAGAGTCTGATGATCTGATGACATCCAGTCACTCTT	360		
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Db	1681	TTGCCAGGCTGGAGTGCAGTACGAGTCTCGGCTCTCACCGCAACTCCCTCTCTCTCG	1740		

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Db	1861	GTCTCAACTCTGACCTAGTATGATCACCCTCTCGGCTCCCAAGTCTCTGGATTACA	1920
QY	1921	GCATGAGCCACACAGCTGGCCCTCTCTGTTTATGTTTGTGTTTTCAGAGGAATGA	1980
Db	1921	GCATGAGCCACACAGCTGGCCCTCTCTGTTTATGTTTGTGTTTTCAGAGGAATGA	1980
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DEFINITION			
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ACCESSION			
DD031661			
VERSION			
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KEYWORDS			
JP 2004516227-A/57.			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Watanabe,C.K., Yan,M., Shelton,D.L., Smith,V., Stewart,T.A., Wood,W.I., Tumas,D., Gurney,A.L., Pennica,D., Ashkenazi,A.J., Baker,K.P., Lu,Y., Pan,J., Kabakoff,R.C., Henzel,W., Hebert,C. and Goddard,A.			
TITLE			
COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED			
Patent: JP 2004516227-A 57 03-JUN-2004;			
Genentech Inc et al			
OS Homo sapiens			
PN JP 2004516227-A/57			
PD 03-JUN-2004			
PF 02-MAR-2000 JP 2000603379			
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16-DEC-1999 US US9930095,20-DEC-1999 US US9930999, PR			
30-DEC-1999 US US9931274,05-JAN-2000 US US0000219, PR			

06-JAN-2000	US	US0000277,06-JAN-2000	US	US0000376, PR
11-FEB-2000	US	US0003565,29-NOV-1999	US	US9928214, PR
15-SEP-1999	US	US9921090,05-OCT-1999	US	US9923089, PR
04-MAY-1999	US	60/132371,14-MAY-1999	US	60/134287, PR
02-JUN-1999	US	US9912252,23-JUN-1999	US	60/141037, PR
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28-JUL-1999	US	60/146222,20-APR-1999	US	US9908615, PR
23-MAR-1999	US	60/125775,12-MAR-1999	US	60/123957, PR
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29-OCT-1999	US	60/162506		
PI	colin k watanabe,minhong yan,david l shelton,victoria smith,			
PI	timothy a steward,william i wood,daniel tumas,austin l gurney,			
PI	diane pennica,avi j ashkenazi,kevin p baker,yanmei lu,james			
PI	pan,			
PI	rhona c kabakoff,william henzel,carolyn hebert,audrey goddard			
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REFERENCE
AUTHORS
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JOURNAL
COMMENT

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JP 2004522402-A/369.
unidentified
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1 (bases 1 to 2284)
Zhang, Z., Wood, W.I., Ashkenazi, A.J., Botstein, D., Napier, M.A.,
Kjavin, I.J., Gurney, A.L., Grimaldi, C.J., Godowski, P.J.,
Goddard, A., Paoni, N.F., Stewart, T.A., Tamas, D., Watanabe, C.K.,
Williams, M.P., Baker, K.P., Pan, J., Roy, M.A., Gerritsen, M.E.,
Gerber, H., Fong, S., Ferrara, N., Eaton, D.L. and Desnoyers, L.
Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
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Patent: JP 2004522402-A 369 29-JUL-2004;
Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney,
Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan
OS Homo Sapien
PN JP 2004522402-A/369
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AUTHORS	Napier,M.A., Kljavin,I.J., Gurney,A.L., Grimaldi,C.J., Watanabe,C.K., Stewart,T.A., Zhang,Z., Wood,W.I., Williams,P.M., Tumas,D., Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H., Fong,S., Paoni,N.F., Pan,J., Roy,M.A., Ferrara,N., Eaton,D.L., Desnoyers,I., Botstein,D., Baker,K.P. and Ashkenazi,A.J.		
TITLE	Secreted and Transmembrane Polypeptides and Nucleic Acids		Encoding the Same
JOURNAL	Patent: JP 2005304500-A 369 04-NOV-2005; Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney, Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan		
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LOCUS AR429104
DEFINITION Sequence 82 from patent US 6642360.
ACCESSION AR429104
VERSION AR429104.1 GI:40189199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.
and Wood,W.I.
TITLE Secreted polypeptides that stimulate release of proteoglycans from cartilage
JOURNAL Patent: US 6642360-A 82 04-NOV-2003;
Genentech, Inc.; South San Francisco, CA
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LOCUS AR534995 2284 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 82 from patent US 6734288.
ACCESSION AR534995
VERSION AR534995.1 GI:53925785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
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AUTHORS Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.
and Wood,W.I.
TITLE Antibodies against a secreted polypeptide that stimulates release
of proteoglycans from cartilage
JOURNAL Patent: US 6734288-A 82 11-MAY-2004;
Genentech, Inc.; San Francisco, CA
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RESULT 10
AR691142 2284 bp DNA linear PAT 13-SBP-2005
LOCUS AR691142
DEFINITION Sequence 82 from patent US 6908993.
ACCESSION AR691142
VERSION AR691142.1 GI:74478541
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.,
Hillan,K.J., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6908993-A 82 21-JUN-2005;
Genentech, Inc.; South San Francisco, CA
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Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 514 from patent US 6913919.
DEFINITION AR693626
ACCESSION AR693626
VERSION AR693626.1 GI:75184121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6913919-A 514 05-JUL-2005;
Genetech, Inc.; South San Francisco, CA
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Db 2281 |TCAA 2284

RESULT 12
LOCUS AR705580 2284 bp DNA linear PAT 20-SEP-2005
DEFINITION Sequence 82 from patent US 6929947.
ACCESSION AR705580
VERSION AR705580.1 GI:75924126
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6929947-A 82 16-AUG-2005; Genentech, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
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Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION     AR706178
VERSION       AR706178.1  GI:75924899
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 2284)
AUTHORS       Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
TITLE         PRO1184 polypeptides
JOURNAL       Patent: US 6930170-A 514 16-AUG-2005;
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RESULT 14
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DEFINITION Sequence 82 from patent US 6936254.
ACCESSION AR708652
VERSION AR708652.1 GI:75998546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Baker, K.P., Botstein, D., Eaton, D.L., Ferrara, N., Filvaroff, E., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Guney, A.L., Hillan, K.J., Kijavina, I.J., Napier, M.A., Roy, M.A., Tumas, D. and Wood, W.I.
TITLE Method of inducing fetal hemoglobin synthesis
JOURNAL Patent: US 6936254-A 82 30-AUG-2005;
Genentech, Inc.; South San Francisco, CA
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LOCUS AR757551 2284 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 514 from patent US 6953836.
ACCESSION AR757551
VERSION AR757551.1 GI:83322728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
TITLE PRO844 polypeptides
JOURNAL Patent: US 6953836-A 514 11-OCT-2005;
Genentech, Inc.; South San Francisco, CA
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PD 08-JUN-2000.
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PD 02-JAN-2003.
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PN US2002127576-A1.
PD 12-SEP-2002.
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PD 14-NOV-2002.
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PN US2003022187-A1.
PD 30-JAN-2003.
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DE Novel human secreted or transmembrane protein PRO846 DNA.
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PN US2002165143-A1.
PD 07-NOV-2002.
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PN US2002177164-A1.
PD 28-NOV-2002.
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PA (GETH) GENENTECH INC.
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PD 20-MAR-2003.
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PN US2003054359-A1.
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Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA94730 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA38955 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA93076 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ACH65633 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA22637 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ACD39623 standard; cDNA; 2284 BP.
DE Human cDNA encoding PRO846.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA06803 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #146.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
ID ADA39496 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 35
ID ADB96522 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2284; DB 9; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ADC57994 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADC25838 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADC35596 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADC53358 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADC12225 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADC56647 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADC11692 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADC25717 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ADC14814 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADD08346 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADC82171 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADD07813 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADC82704 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADD08884 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADD07133 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADC83380 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADD55487 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADD56445 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADD54883 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2002132553-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 55
ID ADE31902 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADE27037 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ADE26504 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ADF67441 standard; cDNA; 2284 BP.
DE Human PRO361 nucleotide sequence SEQ ID NO:514.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADH27502 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADI35695 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADI00188 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ABX75504 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein PRO361 cDNA.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABX78062 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ABX80474 standard; DNA; 2284 BP.
DE Novel human secreted or transmembrane protein PRO846 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ACA69380 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ABX90451 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein cDNA, #182.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ABX64297 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ABX89495 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #15.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 10; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADE71551 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADF35640 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADG11890 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADG63494 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003211570-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADH19760 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADH21253 standard; cDNA; 2284 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US200324358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADH20293 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADH43223 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003207401-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADN00461 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2004091972-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 12; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADU25385 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2004220385-A1.
PD 04-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 13; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADY39548 standard; cDNA; 2284 BP.
DE Human mucin/chitinase homolog PRO361 precursor cDNA.
PN US2005048613-A1.
PD 03-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 14; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADY73829 standard; cDNA; 2284 BP.
DE Human PRO361 cDNA, SEQ ID NO: 82.
PN US2005059115-A1.
PD 17-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 14; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID AEA38662 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein cDNA, #215.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 14; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID AEH50178 standard; cDNA; 2284 BP.
DE Human cDNA clone DNA45410-1250 SEQ ID NO: 82.
PN US2006105427-A1.
PD 18-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 15; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID AEI36386 standard; cDNA; 2284 BP.
DE Human PRO protein coding sequence - SEQ ID 82.
PN US2006127983-A1.

PD 15-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 15; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID AAC58593 standard; cDNA; 2418 BP.
DE Human PRO361 protein UNQ316 encoding cDNA SEQ ID NO:71.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2284; DB 3; Length 2418;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID AAC59840 standard; DNA; 2342 BP.
DE Human secreted protein encoding DNA clone vo27 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match 99.4%; Score 2271.4; DB 3; Length 2342;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 86
ID AAH18096 standard; cDNA; 2297 BP.
DE Human cDNA sequence SEQ ID NO:17949.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 98.3%; Score 2245.6; DB 4; Length 2297;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 87
ID AAH13971 standard; cDNA; 2221 BP.
DE Human cDNA sequence SEQ ID NO:11027.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 89.6%; Score 2045.8; DB 4; Length 2221;
Best Local Similarity 95.2%; Pred. No. 0;
RESULT 88
ID ADJ75252 standard; DNA; 2221 BP.
DE Marker Gene SEQ ID NO:504.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 89.6%; Score 2045.8; DB 12; Length 2221;
Best Local Similarity 95.2%; Pred. No. 0;
RESULT 89
ID ADN05895 standard; cDNA; 2221 BP.
DE Antipsoriatic cDNA sequence #1179.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 89.6%; Score 2045.8; DB 12; Length 2221;
Best Local Similarity 95.2%; Pred. No. 0;
RESULT 90
ID AAA16637 standard; cDNA; 2015 BP.
DE Human secreted protein clone cf85_1 nucleotide sequence SEQ ID NO:39.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 84.9%; Score 1939.4; DB 3; Length 2015;
Best Local Similarity 99.5%; Pred. No. 0;
RESULT 91
ID AAH99840 standard; cDNA; 1423 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:675.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 58.4%; Score 1333.2; DB 4; Length 1423;
Best Local Similarity 97.3%; Pred. No. 0;
RESULT 92
ID AAS78315 standard; cDNA; 2487 BP.
DE DNA encoding novel human diagnostic protein #14119.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC. 46.9%; Score 1071.2; DB 5; Length 2487;
 Query Match 99.7%; Pred. No. 1.9e-263;
 Best Local Similarity 99.7%; Pred. No. 1.9e-263;
 RESULT 93
 ID ABL89648 standard; cDNA; 842 BP.
 DE Human polynucleotide SEQ ID NO 210.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 34.8%; Score 795.4; DB 6; Length 842;
 Best Local Similarity 98.0%; Pred. No. 5e-193;
 RESULT 94
 ID ADJ76101 standard; cDNA; 2286 BP.
 DE Marker Gene SEQ ID NO:1353.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INST.
 Query Match 29.4%; Score 670.6; DB 12; Length 2286;
 Best Local Similarity 62.7%; Pred. No. 7.1e-161;
 RESULT 95
 ID AAH07904 standard; cDNA; 805 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:4739.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 29.0%; Score 661.8; DB 4; Length 805;
 Best Local Similarity 98.1%; Pred. No. 8e-159;
 RESULT 96
 ID AAH05206 standard; cDNA; 855 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:2041.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 25.6%; Score 583.6; DB 4; Length 855;
 Best Local Similarity 83.7%; Pred. No. 8.8e-139;
 RESULT 97
 ID AEF89594 standard; cDNA; 560 BP.
 DE Human cDNA down-regulated in melanoma samples, SEQ ID NO:946.
 PN WO2006002433-A2.
 PD 05-JAN-2006.
 PA (VERI-) VERIDEX LLC.
 Query Match 24.4%; Score 558.4; DB 15; Length 560;
 Best Local Similarity 99.8%; Pred. No. 2.1e-132;
 RESULT 98
 ID ACL57227 standard; cDNA; 532 BP.
 DE Human colon cancer differentially expressed polynucleotide, SEQ ID:3362.
 PN WO2005000087-A2.
 PD 06-JAN-2005.
 PA (CHIR-) CHIRON CORP.
 Query Match 23.2%; Score 530.4; DB 14; Length 532;
 Best Local Similarity 99.8%; Pred. No. 3e-125;
 RESULT 99
 ID AAC76591 standard; cDNA; 517 BP.
 DE Human ORFX ORF2146 polynucleotide sequence SEQ ID NO:4291.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 22.4%; Score 511.8; DB 3; Length 517;
 Best Local Similarity 99.8%; Pred. No. 1.7e-120;
 RESULT 100
 ID ABV88065 standard; cDNA; 513 BP.
 DE Human colon cancer related cDNA SEQ ID NO 1376.
 PN WO200258534-A2.
 PD 01-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 22.4%; Score 511.4; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 2.2e-120;
 RESULT 101
 ID ABV87510 standard; cDNA; 513 BP.
 DE Human colon cancer related cDNA SEQ ID NO 821.
 PN WO200258534-A2.
 PD 01-AUG-2002.
 PA (CORI-) CORIXA CORP.

Query Match 22.4%; Score 511; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 2.7e-120;
 RESULT 102
 ID AAV87407 standard; cDNA; 548 BP.
 DE EST clone CF85.
 PN WO9845435-A2.
 PD 15-OCT-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 21.9%; Score 499.6; DB 2; Length 548;
 Best Local Similarity 98.0%; Pred. No. 2.3e-117;
 RESULT 103
 ID AAH12872 standard; cDNA; 522 BP.
 DE Human cDNA clone (3'-primer) SEQ ID NO:9707.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 20.6%; Score 470.2; DB 4; Length 522;
 Best Local Similarity 94.3%; Pred. No. 7.7e-110;
 RESULT 104
 ID AAV89087 standard; cDNA; 422 BP.
 DE EST clone CC335.
 PN WO9845436-A2.
 PD 15-OCT-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 16.9%; Score 386.8; DB 2; Length 422;
 Best Local Similarity 99.5%; Pred. No. 1.6e-88;
 RESULT 105
 ID AAC05822 standard; cDNA; 295 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 9897.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 11.8%; Score 270.2; DB 3; Length 295;
 Best Local Similarity 94.6%; Pred. No. 1e-58;
 RESULT 106
 ID ABX53012 standard; cDNA; 402 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2941.
 PN US2002137160-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 11.7%; Score 266.2; DB 8; Length 402;
 Best Local Similarity 81.0%; Pred. No. 1.2e-57;
 RESULT 107
 ID AAT24664 standard; cDNA to mRNA; 324 BP.
 DE Human gene signature HUMGS06728.
 PN WO9514772-A1.
 PD 01-JUN-1995.
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 Query Match 10.8%; Score 245.6; DB 2; Length 324;
 Best Local Similarity 92.7%; Pred. No. 2.1e-52;
 RESULT 108
 ID ACH44978 standard; cDNA; 478 BP.
 DE Human foetal brain cDNA #5703.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 10.7%; Score 243.4; DB 9; Length 478;
 Best Local Similarity 85.5%; Pred. No. 9.1e-52;
 RESULT 109
 ID ABQ76673 standard; DNA; 160820 BP.
 DE Androgen receptor signalling pathway-associated DNA AB043547.
 PN WO200282081-A2.
 PD 17-OCT-2002.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.6%; Score 241.6; DB 8; Length 160820;

Best Local Similarity 78.8%; Pred. No. 3.6e-50;
RESULT 110
ID AAK81252 standard; DNA; 7601 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:36064.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 239.8; DB 4; Length 7601;
Best Local Similarity 85.1%; Pred. No. 2.6e-50;
RESULT 111
ID AAK81254 standard; DNA; 31203 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:36066.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 239.8; DB 4; Length 31203;
Best Local Similarity 85.1%; Pred. No. 4.9e-50;
RESULT 112
ID AAK87418 standard; DNA; 4026 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:42230.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 239.2; DB 4; Length 4026;
Best Local Similarity 83.7%; Pred. No. 2.8e-50;
RESULT 113
ID ADQ97804 standard; DNA; 50807 BP.
DE Human Cancer associated sequence HD10-048, SEQ ID 781.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.4%; Score 238.6; DB 12; Length 50807;
Best Local Similarity 82.4%; Pred. No. 1.3e-49;
RESULT 114
ID AAK81253 standard; DNA; 19174 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:36065.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 238.2; DB 4; Length 19174;
Best Local Similarity 84.8%; Pred. No. 1e-49;
RESULT 115
ID AD242280 standard; DNA; 73100 BP.
DE Human endothelin converting-enzyme 1 gene with C776A/ T66564C SNPs Seq 7.
PN JP2005110606-A.
PD 28-APR-2005.
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
Query Match 10.4%; Score 238.2; DB 14; Length 73100;
Best Local Similarity 83.7%; Pred. No. 1.9e-49;
RESULT 116
ID ABK94411 standard; DNA; 109906 BP.
DE DNA encoding endothelin converting enzyme 1 (ECB-1) #1.
PN WO200224747-A2.
PD 28-MAR-2002.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.4%; Score 238.2; DB 6; Length 109906;
Best Local Similarity 83.7%; Pred. No. 2.2e-49;
RESULT 117
ID ADL08112 standard; DNA; 109906 BP.
DE Human gene associated with low HDL-C ECE1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIIVITY INC.
Query Match 10.4%; Score 238.2; DB 12; Length 109906;
Best Local Similarity 83.7%; Pred. No. 2.2e-49;
RESULT 118
ID AAL07322 standard; DNA; 7566 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10010.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 237.6; DB 4; Length 7566;

Best Local Similarity 83.4%; Pred. No. 9.6e-50;
RESULT 119
ID AEF74705 standard; DNA; 152037 BP.
DE Human polynucleotide #219.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADRA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 10.4%; Score 236.8; DB 15; Length 152037;
Best Local Similarity 77.2%; Pred. No. 5.9e-49;
RESULT 120
ID ADZ12943 standard; DNA; 126488 BP.
DE Human cancer-associated genomic DNA #40.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.4%; Score 236.6; DB 14; Length 126488;
Best Local Similarity 76.1%; Pred. No. 6.1e-49;
RESULT 121
ID AAH09234 standard; cDNA; 579 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6069.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.4%; Score 236.4; DB 4; Length 579;
Best Local Similarity 89.0%; Pred. No. 6.1e-50;
RESULT 122
ID AAH15304 standard; cDNA; 1555 BP.
DE Human cDNA sequence SEQ ID NO:13457.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.4%; Score 236.4; DB 4; Length 1555;
Best Local Similarity 89.0%; Pred. No. 9.6e-50;
RESULT 123
ID ABQ88198 standard; cDNA; 154902 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 105.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 10.4%; Score 236.4; DB 6; Length 154902;
Best Local Similarity 89.0%; Pred. No. 7.5e-49;
RESULT 124
ID ABZ73998 standard; DNA; 13186 BP.
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1145.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 236; DB 8; Length 13186;
Best Local Similarity 84.2%; Pred. No. 3.2e-49;
RESULT 125
ID ADC20710 standard; DNA; 13187 BP.
DE Human secreted protein-related DNA sequence #128.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 236; DB 10; Length 13187;
Best Local Similarity 84.2%; Pred. No. 3.2e-49;
RESULT 126
ID ABZ73997 standard; DNA; 13862 BP.
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1144.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 236; DB 8; Length 13862;
Best Local Similarity 84.2%; Pred. No. 3.2e-49;
RESULT 127
ID ADC20709 standard; DNA; 13862 BP.
DE Human secreted protein-related DNA sequence #127.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 236; DB 10; Length 13862;
Best Local Similarity 84.2%; Pred. No. 3.2e-49;
RESULT 128
ID ABT11173 standard; DNA; 168174 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 236; DB 6; Length 168174;
Best Local Similarity 80.1%; Pred. No. 9.9e-49;
RESULT 129
ID ABT11114 standard; DNA; 168273 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 236; DB 6; Length 168273;
Best Local Similarity 80.1%; Pred. No. 9.9e-49;
RESULT 130
ID AAK81392 standard; DNA; 773 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36204.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 235.8; DB 4; Length 773;
Best Local Similarity 76.3%; Pred. No. 9.9e-50;
RESULT 131
ID AAK78813 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 235.8; DB 4; Length 51469;
Best Local Similarity 83.8%; Pred. No. 6.6e-49;
RESULT 132
ID AAK70270 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 235.8; DB 4; Length 51469;
Best Local Similarity 83.8%; Pred. No. 6.6e-49;
RESULT 133
ID AAK69322 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 235.8; DB 4; Length 51469;
Best Local Similarity 83.8%; Pred. No. 6.6e-49;
RESULT 134
ID ADQ97733 standard; DNA; 121167 BP.
DE Human cancer associated sequence HD10-035, SEQ ID 710.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 235.8; DB 12; Length 121167;
Best Local Similarity 63.7%; Pred. No. 9.6e-49;
RESULT 135
ID ADL62089 standard; DNA; 18968 BP.
DE Human ovarian cancer DNA marker #20301.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 235.4; DB 5; Length 18968;
Best Local Similarity 84.0%; Pred. No. 5.3e-49;
RESULT 136
ID ABD32769 standard; DNA; 100608 BP.
DE Human cancer-associated genomic DNA HD16-031.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 235.4; DB 13; Length 100608;

Best Local Similarity 85.1%; Pred. No. 1.1e-48;
RESULT 137
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 235.2; DB 13; Length 238417;
Best Local Similarity 79.5%; Pred. No. 1.9e-48;
RESULT 138
ID ABZ70982 standard; DNA; 11173 BP.
DE Human HKR1 related DNA sequence SEQ ID NO:10.
PN WO2003004513-A1.
PD 16-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.3%; Score 235; DB 9; Length 11173;
Best Local Similarity 76.6%; Pred. No. 5.3e-49;
RESULT 139
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 10; Length 128034;
Best Local Similarity 85.4%; Pred. No. 1.6e-48;
RESULT 140
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 10; Length 128034;
Best Local Similarity 85.4%; Pred. No. 1.6e-48;
RESULT 141
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 12; Length 128034;
Best Local Similarity 85.4%; Pred. No. 1.6e-48;
RESULT 142
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 12; Length 128034;
Best Local Similarity 85.4%; Pred. No. 1.6e-48;
RESULT 143
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 10; Length 202100;
Best Local Similarity 85.4%; Pred. No. 1.9e-48;
RESULT 144
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 10.3%; Score 235; DB 12; Length 202100;
Best Local Similarity 85.4%; Pred. No. 1.9e-48;
RESULT 145
ID ACN44854 standard; DNA; 31277 BP.
DE Human genomic sequence hCG22132.
PN WO2003073826-A2.
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.3%; Score 234.8; DB 11; Length 31277;
 Best Local Similarity 86.1%; Pred. No. 9.5e-49;
 RESULT 146
 ID ABK83462 standard; cDNA; 39801 BP.
 DE Human cDNA differentially expressed in granulocytic cells #33.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.3%; Score 234.8; DB 6; Length 39801;
 Best Local Similarity 87.3%; Pred. No. 1.1e-48;
 RESULT 147
 Query Match 10.3%; Score 234.4; DB 10; Length 110000;
 Best Local Similarity 70.4%; Pred. No. 2.1e-48;
 RESULT 148
 ID ACN44006 standard; DNA; 127369 BP.
 DE Human genomic sequence hCG1810774.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.3%; Score 234.2; DB 11; Length 127369;
 Best Local Similarity 84.6%; Pred. No. 2.5e-48;
 RESULT 149
 ID ABK83459 standard; cDNA; 128978 BP.
 DE Human cDNA differentially expressed in granulocytic cells #30.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.3%; Score 234.2; DB 6; Length 128978;
 Best Local Similarity 85.8%; Pred. No. 2.5e-48;
 RESULT 150
 ID AAD54587 standard; DNA; 128978 BP.
 DE Human LIM kinase (LINK) DNA #6.
 PN WO200299048-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 10.3%; Score 234.2; DB 8; Length 128978;
 Best Local Similarity 85.8%; Pred. No. 2.5e-48;
 RESULT 151
 ID ADR52994 standard; DNA; 128978 BP.
 DE Drug therapy altered expressed gene #345.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC/) BURCZYNSKI M.
 PA (TWIN/) TWINE N.
 PA (DORN/) DORNER A. J.
 PA (TREP/) TREPICCHIO W. L.
 Query Match 10.3%; Score 234.2; DB 13; Length 128978;
 Best Local Similarity 85.8%; Pred. No. 2.5e-48;
 RESULT 152
 ID ADX07226 standard; DNA; 128978 BP.
 DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1791.
 PN WO2005012875-A2.
 PD 10-FEB-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 10.3%; Score 234.2; DB 14; Length 128978;
 Best Local Similarity 85.8%; Pred. No. 2.5e-48;
 RESULT 153
 ID ABK42516 standard; DNA; 31871 BP.
 DE Genomic sequence #415 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 234; DB 4; Length 31871;
 Best Local Similarity 80.8%; Pred. No. 1.5e-48;
 RESULT 154
 ID ADB60672 standard; DNA; 31871 BP.
 DE Connective tissue related genomic DNA #415.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 234; DB 9; Length 31871;

Best Local Similarity 80.8%; Pred. No. 1.5e-48;
 RESULT 155
 ID AAK68089 standard; DNA; 40742 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22901.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 234; DB 4; Length 40742;
 Best Local Similarity 80.8%; Pred. No. 1.7e-48;
 RESULT 156
 ID AAK79886 standard; DNA; 40742 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34698.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 234; DB 4; Length 40742;
 Best Local Similarity 80.8%; Pred. No. 1.7e-48;
 RESULT 157
 ID AED89390 standard; DNA; 143389 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 30.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 10.2%; Score 234; DB 14; Length 143389;
 Best Local Similarity 89.2%; Pred. No. 3e-48;
 RESULT 158
 ID AED89384 standard; DNA; 150314 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 24.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 10.2%; Score 234; DB 14; Length 150314;
 Best Local Similarity 89.2%; Pred. No. 3.1e-48;
 RESULT 159
 ID ABK84798 standard; cDNA; 220895 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1369.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.2%; Score 234; DB 6; Length 220895;
 Best Local Similarity 80.8%; Pred. No. 3.6e-48;
 RESULT 160
 ID ADR52737 standard; DNA; 220895 BP.
 DE Drug therapy altered expressed gene #88.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC/) BURCZYNSKI M.
 PA (TWIN/) TWINE N.
 PA (DORN/) DORNER A. J.
 PA (TREP/) TREPICCHIO W. L.
 Query Match 10.2%; Score 234; DB 13; Length 220895;
 Best Local Similarity 80.8%; Pred. No. 3.6e-48;
 RESULT 161
 ID ADN30029 standard; DNA; 7001 BP.
 DE Human cytokine-inducible kinase associated DNA #5.
 PN US2004101857-A1.
 PD 27-MAY-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 10.2%; Score 233.8; DB 12; Length 7001;
 Best Local Similarity 87.3%; Pred. No. 8.7e-49;
 RESULT 162
 ID ADQ97703 standard; DNA; 103665 BP.
 DE Human cancer associated sequence HD10-031, SEQ ID 680.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 10.2%; Score 233.8; DB 12; Length 103665;
 Best Local Similarity 83.6%; Pred. No. 2.9e-48;
 RESULT 163
 ID AED18064 standard; DNA; 107603 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 315.
 PN WO2005098041-A2.

PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 10.2%; Score 233.8; DB 14; Length 107603;
Best Local Similarity 83.7%; Pred. No. 3e-48;
RESULT 164
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 10.2%; Score 233.6; DB 4; Length 160552;
Best Local Similarity 86.8%; Pred. No. 4e-48;
RESULT 165
ID AAV83945 standard; DNA; 1701 BP.
DE Bacterial artificial chromosome (BAC)-F2 contig 5.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 10.2%; Score 233.2; DB 2; Length 1701;
Best Local Similarity 82.4%; Pred. No. 6.6e-49;
RESULT 166
ID ABQ80846 standard; cDNA; 2195 BP.
DE Tyrosine specific protein phosphatase 23.87 coding sequence.
PN CN1352275-A.
PD 05-JUN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 10.2%; Score 233.2; DB 6; Length 2195;
Best Local Similarity 88.3%; Pred. No. 7.4e-49;
RESULT 167
ID ADK43203 standard; DNA; 176001 BP.
DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA 2.
PN WO2004011623-A2.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.2%; Score 233.2; DB 12; Length 176001;
Best Local Similarity 82.4%; Pred. No. 5.3e-48;
RESULT 168
ID ABT10147 standard; cDNA; 185035 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 281.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.2%; Score 233.2; DB 6; Length 185035;
Best Local Similarity 88.3%; Pred. No. 5.4e-48;
RESULT 169
ID ACA44951 standard; DNA; 185035 BP.
DE Human FEN1 DNA corresponding to AC004770.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHORRAY GMBH.
Query Match 10.2%; Score 233.2; DB 8; Length 185035;
Best Local Similarity 88.3%; Pred. No. 5.4e-48;
RESULT 170
ID ADQ20284 standard; DNA; 185035 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.2%; Score 233.2; DB 12; Length 185035;
Best Local Similarity 88.3%; Pred. No. 5.4e-48;
RESULT 171
ID ADK43195 standard; DNA; 186739 BP.
DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA.
PN WO2004011623-A2.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.2%; Score 233.2; DB 12; Length 186739;
Best Local Similarity 82.4%; Pred. No. 5.4e-48;
RESULT 172
ID ACN44514 standard; DNA; 256493 BP.
DE Human genomic sequence hCG17361.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.2%; Score 233; DB 11; Length 256493;
Best Local Similarity 76.8%; Pred. No. 7e-48;
RESULT 173
ID ADQ97870 standard; DNA; 121160 BP.
DE Human cancer associated sequence HD11-015, SEQ ID 847.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 232.8; DB 12; Length 121160;
Best Local Similarity 88.6%; Pred. No. 5.6e-48;
RESULT 174
ID ADQ97183 standard; DNA; 138627 BP.
DE Human cancer associated sequence HD08-011, SEQ ID 159.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 232.8; DB 12; Length 138627;
Best Local Similarity 87.3%; Pred. No. 6e-48;
RESULT 175
ID ABEV49209 standard; cDNA; 461 BP.
DE Human prostate expression marker cDNA 49200.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.2%; Score 232.6; DB 5; Length 461;
Best Local Similarity 83.2%; Pred. No. 5.2e-49;
RESULT 176
ID ABQ88176 standard; cDNA; 100301 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 83.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 10.2%; Score 232.6; DB 6; Length 100301;
Best Local Similarity 85.5%; Pred. No. 5.8e-48;
RESULT 177
ID ADQ20754 standard; DNA; 100301 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3574.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.2%; Score 232.6; DB 12; Length 100301;
Best Local Similarity 85.5%; Pred. No. 5.8e-48;
RESULT 178
ID ADL13684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.2%; Score 232.6; DB 10; Length 247509;
Best Local Similarity 84.3%; Pred. No. 8.8e-48;
RESULT 179
Query Match 10.2%; Score 232.4; DB 9; Length 102457;
Best Local Similarity 85.0%; Pred. No. 6.6e-48;
RESULT 180
Query Match 10.2%; Score 232.4; DB 9; Length 110000;
Best Local Similarity 82.7%; Pred. No. 6.8e-48;
RESULT 181
Query Match 10.2%; Score 232.4; DB 12; Length 110000;
Best Local Similarity 82.7%; Pred. No. 6.8e-48;
RESULT 182
Query Match 10.2%; Score 232.4; DB 14; Length 110000;
Best Local Similarity 82.7%; Pred. No. 6.8e-48;
RESULT 183
ID AED34666 standard; DNA; 458207 BP.
DE ABL1 genomic DNA SEQ ID NO 2.
PN WO2005094291-A2.
PD 13-OCT-2005.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 10.2%; Score 232.4; DB 14; Length 110000;
Best Local Similarity 88.9%; Pred. No. 6.8e-48;
RESULT 184

ID AED89420 standard; DNA; 171427 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 10.2%; Score 232.4; DB 14; Length 171427;
 Best Local Similarity 83.8%; Pred. No. 8.4e-48;
 RESULT 185
 ID AED18538 standard; DNA; 184666 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 10.2%; Score 232.4; DB 14; Length 184666;
 Best Local Similarity 88.9%; Pred. No. 8.6e-48;
 RESULT 186
 ID AAK85311 standard; DNA; 19497 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40123.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232.2; DB 4; Length 19497;
 Best Local Similarity 84.5%; Pred. No. 3.5e-48;
 RESULT 187
 ID AAK82215 standard; DNA; 31934 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37027.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232.2; DB 4; Length 31934;
 Best Local Similarity 80.3%; Pred. No. 4.4e-48;
 RESULT 188
 ID ABA19342 standard; DNA; 13102 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11673.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232; DB 5; Length 13102;
 Best Local Similarity 79.0%; Pred. No. 3.3e-48;
 RESULT 189
 ID AAS28623 standard; DNA; 15366 BP.
 DE Genomic sequence #463 encoding for novel human respiratory antigen.
 PN WO200155448-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232; DB 4; Length 15366;
 Best Local Similarity 84.0%; Pred. No. 3.6e-48;
 RESULT 190
 ID ADG41819 standard; DNA; 15366 BP.
 DE Human respiratory system associated genomic DNA seq id 1057.
 PN US2003215893-A1.
 PD 20-NOV-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232; DB 10; Length 15366;
 Best Local Similarity 84.0%; Pred. No. 3.6e-48;
 RESULT 191
 ID ADI97593 standard; DNA; 15366 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqId1057.
 PN US200307704-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.2%; Score 232; DB 11; Length 15366;
 Best Local Similarity 84.0%; Pred. No. 3.6e-48;
 RESULT 192
 ID ADP13586 standard; DNA; 170245 BP.
 DE Renal cell carcinoma differentially expressed gene #322.
 PN WO2004048933-A2.
 PD 10-JUN-2004.
 PA (AMHP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BURC/) BURCZYNSKI M E.
 PA (TREP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.
 PA (SLOW/) SLOMI D K.
 Query Match 10.2%; Score 232; DB 12; Length 170245;
 Best Local Similarity 79.0%; Pred. No. 1.1e-47;
 RESULT 193
 ID ABS56564 standard; DNA; 260209 BP.
 DE Human SULF2 genomic DNA sequence.
 PN WO200259327-A2.
 PD 01-AUG-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 10.2%; Score 232; DB 6; Length 260209;
 Best Local Similarity 85.2%; Pred. No. 1.3e-47;
 RESULT 194
 ID ADN16204 standard; DNA; 260209 BP.
 DE Human sulfatase SULF1 gene.
 PN WO2004031365-A2.
 PD 15-APR-2004.
 PA (REGC) UNIV CALIFORNIA.
 PA (THIO-) THIOS PHARM INC.
 Query Match 10.2%; Score 232; DB 12; Length 260209;
 Best Local Similarity 85.2%; Pred. No. 1.3e-47;
 RESULT 195
 ID ADD72080 standard; cDNA; 1434 BP.
 DE Human urinary specific nucleic acid sequence SEQ ID NO:364.
 PN WO2003060146-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 10.1%; Score 231.8; DB 10; Length 1434;
 Best Local Similarity 78.6%; Pred. No. 1.4e-48;
 RESULT 196
 ID ABA07182 standard; DNA; 4748 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 501.
 PN WO200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.8; DB 4; Length 4748;
 Best Local Similarity 81.4%; Pred. No. 2.4e-48;
 RESULT 197
 ID AAK89814 standard; DNA; 4748 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3390.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.8; DB 4; Length 4748;
 Best Local Similarity 81.4%; Pred. No. 2.4e-48;
 RESULT 198
 ID AAK80364 standard; DNA; 18544 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35176.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.8; DB 4; Length 18544;
 Best Local Similarity 83.6%; Pred. No. 4.4e-48;
 RESULT 199
 ID ADP65343 standard; DNA; 57038 BP.
 DE Human sequence from clone RP5-1009E24 on chromosome 20 Contains DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 10.1%; Score 231.8; DB 11; Length 57038;
 Best Local Similarity 63.2%; Pred. No. 7.3e-48;
 RESULT 200
 ID ADP65471 standard; DNA; 92794 BP.
 DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 10.1%; Score 231.8; DB 11; Length 92794;
 Best Local Similarity 63.2%; Pred. No. 9e-48;
 RESULT 201
 ID ADP65471 standard; DNA; 92794 BP.
 DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 10.1%; Score 231.8; DB 10; Length 110000;
 Best Local Similarity 87.2%; Pred. No. 9.8e-48;
 RESULT 202

ID ABZ72040 standard; DNA; 207433 BP.
 DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.
 PN WO200178894-A2.
 PD 25-OCT-2001.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 10.1%; Score 231.8; DB 5; Length 207433;
 Best Local Similarity 63.2%; Pred. No. 1.3e-47;
 RESULT 203
 ID ABX74891 standard; DNA; 207433 BP.
 DE BAC1098L22 DNA sequence.
 PN WO200283077-A2.
 PD 24-OCT-2002.
 PA (SCHE-) SCHERING CORP.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 10.1%; Score 231.8; DB 8; Length 207433;
 Best Local Similarity 63.2%; Pred. No. 1.3e-47;
 RESULT 204
 ID ADJ36614 standard; DNA; 207433 BP.
 DE Bacterial artificial chromosome RPC1-11.
 PN US2004002470-A1.
 PD 01-JAN-2004.
 PA (KEIT-) KEITH T.
 PA (LITT-) LITTLE R. D.
 PA (VEER-) VAN ERDEWEGH P.
 PA (DUPU-) DUPUIS J.
 PA (DMAS-) DEL MASTRO R. G.
 PA (SIMO-) SIMON J.
 PA (ALLE-) ALLEN K.
 PA (PAND-) PANDIT S.
 Query Match 10.1%; Score 231.8; DB 12; Length 207433;
 Best Local Similarity 63.2%; Pred. No. 1.3e-47;
 RESULT 205
 ID ADL81193 standard; DNA; 207433 BP.
 DE BAC1098L22 DNA sequence.
 PN US2004023215-A1.
 PD 05-FEB-2004.
 PA (KEIT-) KEITH T.
 PA (LITT-) LITTLE R. D.
 PA (EERD-) EERDEWEGH P. V.
 PA (DUPU-) DUPUIS J.
 PA (DMAS-) DEL MASTRO R. G.
 PA (SIMO-) SIMON J.
 PA (ALLE-) ALLEN K.
 PA (PAND-) PANDIT S.
 Query Match 10.1%; Score 231.8; DB 12; Length 207433;
 Best Local Similarity 63.2%; Pred. No. 1.3e-47;
 RESULT 206
 ID ABV19436 standard; cDNA; 461 BP.
 DE Human prostate expression marker cDNA 19427.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 10.1%; Score 231.6; DB 5; Length 461;
 Best Local Similarity 82.9%; Pred. No. 9.4e-49;
 RESULT 207
 ID AAL05229 standard; DNA; 23748 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7917.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.6; DB 4; Length 23748;
 Best Local Similarity 84.3%; Pred. No. 5.5e-48;
 RESULT 208
 ID ABL98112 standard; DNA; 23748 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2764.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.6; DB 4; Length 23748;
 Best Local Similarity 84.3%; Pred. No. 5.5e-48;
 RESULT 209
 ID ACF62730 standard; DNA; 164702 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.
 PN WO2003013534-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
 Query Match 10.1%; Score 231.6; DB 8; Length 164702;
 Best Local Similarity 85.4%; Pred. No. 1.3e-47;
 RESULT 210
 ID ADB20845 standard; DNA; 164702 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:658.
 PN WO2003013533-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
 Query Match 10.1%; Score 231.6; DB 8; Length 164702;
 Best Local Similarity 85.4%; Pred. No. 1.3e-47;
 RESULT 211
 ID ADB87934 standard; DNA; 164702 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:658.
 PN WO2003013536-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
 Query Match 10.1%; Score 231.6; DB 10; Length 164702;
 Best Local Similarity 85.4%; Pred. No. 1.3e-47;
 RESULT 212
 ID ADB96917 standard; DNA; 164702 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:658.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
 Query Match 10.1%; Score 231.6; DB 10; Length 164702;
 Best Local Similarity 85.4%; Pred. No. 1.3e-47;
 RESULT 213
 ID ADB92108 standard; DNA; 164702 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:658.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
 Query Match 10.1%; Score 231.6; DB 10; Length 164702;
 Best Local Similarity 85.4%; Pred. No. 1.3e-47;
 RESULT 214
 ID ADL13638 standard; DNA; 186528 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #170.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 10.1%; Score 231.6; DB 10; Length 186528;
 Best Local Similarity 82.1%; Pred. No. 1.4e-47;
 RESULT 215
 ID ABA14926 standard; DNA; 840 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7257.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.4; DB 5; Length 840;
 Best Local Similarity 85.0%; Pred. No. 1.4e-48;
 RESULT 216
 ID ABA14923 standard; DNA; 3765 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7254.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.4; DB 5; Length 3765;
 Best Local Similarity 85.0%; Pred. No. 2.7e-48;
 RESULT 217
 ID ABA14921 standard; DNA; 6867 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7252.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231.4; DB 5; Length 6867;
 Best Local Similarity 85.0%; Pred. No. 3.6e-48;
 RESULT 218
 ID ABA14924 standard; DNA; 7270 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7255.
 PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 231.4; DB 5; Length 7270;
Best Local Similarity 85.0%; Pred. No. 3.6e-48;
RESULT 219
ID AAK67891 standard; DNA; 8515 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22703.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 231.4; DB 4; Length 8515;
Best Local Similarity 74.7%; Pred. No. 3.9e-48;
RESULT 220
ID ABD33424 standard; DNA; 39451 BP.
DE Human cancer-associated (CA) gene HD07-079.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.1%; Score 231.4; DB 13; Length 39451;
Best Local Similarity 85.0%; Pred. No. 7.8e-48;
RESULT 221
ID AEJ13546 standard; DNA; 39451 BP.
DE Cancer-associated gene sequence - SEQ ID 554.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 10.1%; Score 231.4; DB 15; Length 39451;
Best Local Similarity 85.0%; Pred. No. 7.8e-48;
RESULT 222
ID ADG86768 standard; DNA; 104245 BP.
DE Human clone RP1-109F14 from chromosome 6p21.2-21.3.
PN US2003224514-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.1%; Score 231.4; DB 12; Length 104245;
Best Local Similarity 85.0%; Pred. No. 1.2e-47;
RESULT 223
ID ADL34706 standard; DNA; 104245-BP.
DE Human PPAR-delta DNA fragment SEQ ID 4.
PN US2004063129-A1.
PD 01-APR-2004.
PA (GAAR/) GAARDE W.
PA (FREI/) FREIER S M.
PA (WATT/) WATT A T.
Query Match 10.1%; Score 231.4; DB 12; Length 104245;
Best Local Similarity 85.0%; Pred. No. 1.2e-47;
RESULT 224
Query Match 10.1%; Score 231.4; DB 12; Length 110000;
Best Local Similarity 82.7%; Pred. No. 1.2e-47;
RESULT 225
ID AAD48308 standard; DNA; 114693 BP.
DE Human transporter protein encoding gene.
Query Match 10.1%; Score 231.4; DB 8; Length 114693;
Best Local Similarity 80.6%; Pred. No. 1.3e-47;
RESULT 226
ID AEF75216 standard; DNA; 135928 BP.
DE Human polynucleotide #730.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 10.1%; Score 231.4; DB 15; Length 135928;
Best Local Similarity 86.2%; Pred. No. 1.4e-47;
RESULT 227
ID ADP45593 standard; DNA; 147300 BP.
DE Human Rho family guanine-nucleotide exchange factor KIAA0861 gDNA.
PN WO2004047623-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.1%; Score 231.4; DB 12; Length 147300;
Best Local Similarity 86.2%; Pred. No. 1.4e-47;
RESULT 228

ID ADX98570 standard; DNA; 147700 BP.
DE Human guanine-nucleotide exchange factor KIAA0861 genomic DNA.
Query Match 10.1%; Score 231.4; DB 14; Length 147700;
Best Local Similarity 86.2%; Pred. No. 1.4e-47;
RESULT 229
ID AEE96613 standard; DNA; 147700 BP.
DE KIAA0861 genomic DNA sequence, SEQ ID NO:1.
PN WO2005118856-A1.
PD 15-DEC-2005.
PA (SEQU-) SEQUENOM INC.
Query Match 10.1%; Score 231.4; DB 15; Length 147700;
Best Local Similarity 86.2%; Pred. No. 1.4e-47;
RESULT 230
ID ADP13586 standard; DNA; 170245 BP.
DE Renal cell carcinoma differentially expressed gene #322.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M B.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 10.1%; Score 231.4; DB 12; Length 170245;
Best Local Similarity 85.0%; Pred. No. 1.5e-47;
RESULT 231
ID AED89398 standard; DNA; 171162 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 38.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 10.1%; Score 231.4; DB 14; Length 171162;
Best Local Similarity 87.5%; Pred. No. 1.5e-47;
RESULT 232
ID AEE06394 standard; DNA; 267966 BP.
DE Glycogen synthase kinase-3beta (GSK-3beta) gene.
PN WO2005108582-A1.
PD 17-NOV-2005.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.1%; Score 231.4; DB 14; Length 267966;
Best Local Similarity 80.8%; Pred. No. 1.8e-47;
RESULT 233
ID ACN44570 standard; DNA; 19640 BP.
DE Human genomic sequence hCG38237.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 231.2; DB 11; Length 19640;
Best Local Similarity 85.7%; Pred. No. 6.4e-48;
RESULT 234
ID AEE04781 standard; DNA; 112679 BP.
DE Cancer-associated gene SEQ ID NO:99.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.1%; Score 231.2; DB 14; Length 112679;
Best Local Similarity 84.5%; Pred. No. 1.4e-47;
RESULT 235
ID ABD33075 standard; DNA; 152759 BP.
DE Human cancer-associated (CA) gene HD07-002.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.1%; Score 231.2; DB 13; Length 152759;
Best Local Similarity 83.3%; Pred. No. 1.6e-47;
RESULT 236
ID AEJ13002 standard; DNA; 152759 BP.
DE Cancer-associated gene sequence - SEQ ID 10.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.

Query Match 10.1%; Score 231.2; DB 15; Length 152759;
 Best Local Similarity 83.3%; Pred. No. 1.6e-47;
 RESULT 237
 ID AAL03321 standard; DNA; 292 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6009.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 231; DB 4; Length 292;
 Best Local Similarity 89.1%; Pred. No. 1.1e-48;
 RESULT 238
 ID ACN44490 standard; DNA; 32865 BP.
 DE Human genomic sequence HCG25375.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.1%; Score 231; DB 11; Length 32865;
 Best Local Similarity 85.2%; Pred. No. 9.1e-48;
 RESULT 239
 ID ABD333436 standard; DNA; 52710 BP.
 DE Human cancer-associated (CA) gene HD07-082.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 10.1%; Score 231; DB 13; Length 52710;
 Best Local Similarity 85.2%; Pred. No. 1.1e-47;
 RESULT 240
 ID AEJ13564 standard; DNA; 52710 BP.
 DE Cancer-associated gene sequence - SEQ ID 572.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match 10.1%; Score 231; DB 15; Length 52710;
 Best Local Similarity 85.2%; Pred. No. 1.1e-47;
 RESULT 241
 ID ADH7123 standard; DNA; 126001 BP.
 DE Human PAZ/PIWI domain-containing protein polynucleotide #3.
 PN US2003232442-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 10.1%; Score 231; DB 12; Length 126001;
 Best Local Similarity 85.2%; Pred. No. 1.7e-47;
 RESULT 242
 ID ADD71332 standard; DNA; 720 BP.
 DE Glutamine:fructose-6-phosphate amide transferase 1 gene intron 13.
 PN WO2003023063-A1.
 PD 20-MAR-2003.
 PA (SANY) SANKYO CO LTD.
 Query Match 10.1%; Score 230.8; DB 10; Length 720;
 Best Local Similarity 81.4%; Pred. No. 1.8e-48;
 RESULT 243
 ID ADA02576 standard; DNA; 87878 BP.
 DE Human FRBP5 carcinoma associated gene, SEQ ID NO:1094.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.1%; Score 230.8; DB 9; Length 87878;
 Best Local Similarity 79.4%; Pred. No. 1.6e-47;
 RESULT 244
 ID ADH72314 standard; DNA; 87878 BP.
 DE Human FRBP5 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.1%; Score 230.8; DB 10; Length 87878;
 Best Local Similarity 79.4%; Pred. No. 1.6e-47;
 RESULT 245
 ID ADE95824 standard; DNA; 87878 BP.
 DE Human FRBP5 gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 10.1%; Score 230.8; DB 10; Length 87878;
 Best Local Similarity 79.4%; Pred. No. 1.6e-47;
 RESULT 246
 ID AEK60095 standard; DNA; 87878 BP.
 DE Human FRBP5 genomic sequence, SEQ ID NO: 82.
 PN US2006204982-A1.
 PD 14-SEP-2006.
 PA (MORR/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Query Match 10.1%; Score 230.8; DB 15; Length 87878;
 Best Local Similarity 79.4%; Pred. No. 1.6e-47;
 RESULT 247
 ID ADD71350 standard; DNA; 93390 BP.
 DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.
 PN WO2003023063-A1.
 PD 20-MAR-2003.
 PA (SANY) SANKYO CO LTD.
 Query Match 10.1%; Score 230.8; DB 10; Length 93390;
 Best Local Similarity 81.4%; Pred. No. 1.6e-47;
 RESULT 248
 ID AAK67371 standard; DNA; 13496 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22183.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 230.6; DB 4; Length 13496;
 Best Local Similarity 85.4%; Pred. No. 7.7e-48;
 RESULT 249
 ID AAS28364 standard; DNA; 17498 BP.
 DE Genomic sequence #204 encoding for novel human respiratory antigen.
 PN WO200155448-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 230.6; DB 4; Length 17498;
 Best Local Similarity 81.8%; Pred. No. 8.7e-48;
 RESULT 250
 ID ADG41560 standard; DNA; 17498 BP.
 DE Human respiratory system associated genomic DNA seq id 798.
 PN US2003215893-A1.
 PD 20-NOV-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 230.6; DB 10; Length 17498;
 Best Local Similarity 81.8%; Pred. No. 8.7e-48;
 RESULT 251
 ID ADI97334 standard; DNA; 17498 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID798.
 PN US2003077704-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 230.6; DB 11; Length 17498;
 Best Local Similarity 81.8%; Pred. No. 8.7e-48;
 RESULT 252
 ID AEC74895 standard; DNA; 69914 BP.
 DE Human tyrosine phosphatase PTPN22 genomic DNA.
 Query Match 10.1%; Score 230.6; DB 14; Length 69914;
 Best Local Similarity 72.7%; Pred. No. 1.6e-47;
 RESULT 253
 ID ABD33104 standard; DNA; 130877 BP.
 DE Human cancer-associated (CA) gene HD07-009.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 10.1%; Score 230.6; DB 13; Length 130877;
 Best Local Similarity 80.0%; Pred. No. 2.1e-47;
 RESULT 254
 ID AEJ13046 standard; DNA; 130877 BP.
 DE Cancer-associated gene sequence - SEQ ID 54.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match 10.1%; Score 230.6; DB 15; Length 130877;
 Best Local Similarity 80.0%; Pred. No. 2.1e-47;

RESULT 255
ID ADL13962 standard; DNA; 160198 BP.
DE Osteoarthritis-associated polymorphic nucleotide #494.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCV-) INCYTE GENOMICS INC.
Query Match 10.1%; Score 230.6; DB 10; Length 160198;
Best Local Similarity 82.0%; Pred. No. 2.3e-47;
RESULT 256
ID ACF62732 standard; DNA; 177531 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 230.6; DB 8; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 257
ID ADB20847 standard; DNA; 177531 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 230.6; DB 8; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 258
ID ADB87936 standard; DNA; 177531 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:660.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 230.6; DB 10; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 259
ID ADB96919 standard; DNA; 177531 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:660.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 230.6; DB 10; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 260
ID ADB92110 standard; DNA; 177531 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:660.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 230.6; DB 10; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 261
ID ADH74617 standard; DNA; 177531 BP.
DE Human BAC clone GS1-259H13 CYP3A5 genomic DNA.
PN US2003143537-A1.
PD 31-JUL-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 10.1%; Score 230.6; DB 10; Length 177531;
Best Local Similarity 82.0%; Pred. No. 2.5e-47;
RESULT 262
ID AAK67462 standard; DNA; 24268 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22274.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230.4; DB 4; Length 24268;
Best Local Similarity 86.1%; Pred. No. 1.1e-47;
RESULT 263
ID ABT44359 standard; DNA; 6777 BP.
DE Concatenated exons of the human oestrogen receptor beta DNA.
PN WO2003050133-A1.
PD 19-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.1%; Score 230.2; DB 9; Length 6777;
Best Local Similarity 86.9%; Pred. No. 7.2e-48;
RESULT 264

ID ADS89097 standard; DNA; 13286 BP.
DE Human ESR2 gene SEQ ID NO:113.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 230.2; DB 13; Length 13286;
Best Local Similarity 86.9%; Pred. No. 9.7e-48;
RESULT 265
ID AAK69104 standard; DNA; 26059 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23916.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230.2; DB 4; Length 26059;
Best Local Similarity 75.1%; Pred. No. 1.3e-47;
RESULT 266
ID ABT44365 standard; DNA; 113000 BP.
DE Partial genomic sequence of human oestrogen receptor beta DNA.
PN WO2003050133-A1.
PD 19-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.1%; Score 230.2; DB 9; Length 113000;
Best Local Similarity 86.9%; Pred. No. 2.5e-47;
RESULT 267
ID AEF19127 standard; DNA; 188056 BP.
DE Human NIPBL genomic sequence.
PN US2006003354-A1.
PD 05-JAN-2006.
PA (KRAN/) KRANTZ I D.
PA (JACK/) JACKSON L G.
Query Match 10.1%; Score 230.2; DB 15; Length 188056;
Best Local Similarity 85.6%; Pred. No. 3.2e-47;
RESULT 268
ID ADV16961 standard; DNA; 290040 BP.
DE Human protein associated with myc (PAM) genomic DNA.
PN EP1481685-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 10.1%; Score 230.2; DB 14; Length 290040;
Best Local Similarity 75.1%; Pred. No. 3.9e-47;
RESULT 269
ID ADU92049 standard; DNA; 290040 BP.
DE Human PAM (protein associated with myc) genomic DNA.
PN EP1481680-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 10.1%; Score 230.2; DB 14; Length 290040;
Best Local Similarity 75.1%; Pred. No. 3.9e-47;
RESULT 270
ID AAS43104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PEKE) PE CORP NY.
Query Match 10.1%; Score 230.2; DB 4; Length 325791;
Best Local Similarity 86.9%; Pred. No. 4.1e-47;
RESULT 271
ID RAI58350 standard; cDNA; 955 BP.
DE Human polynucleotide SEQ ID NO 553.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 230; DB 4; Length 955;
Best Local Similarity 87.7%; Pred. No. 3.3e-48;
RESULT 272
ID ADQ98558 standard; cDNA; 955 BP.
DE DNA encoding human GPCR-like protein segid 228.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 230; DB 5; Length 955;
Best Local Similarity 87.7%; Pred. No. 3.3e-48;
RESULT 273

ID ADB48318 standard; cDNA; 955 BP.
DE Novel human cDNA SEQ ID NO 228.
PN US2003104529-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 229.8; DB 4; Length 24884;
Best Local Similarity 74.4%; Pred. No. 1.6e-47;
RESULT 282
ID ACN44218 standard; DNA; 66972 BP.
DE Human genomic sequence hCG15409.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 229.8; DB 11; Length 66972;
Best Local Similarity 79.2%; Pred. No. 2.5e-47;
RESULT 283
ID AAD53223 standard; DNA; 487980 BP.
DE Human chromosome 3 p-arm breakpoint region.
PN WO200290541-A1.
PD 14-NOV-2002.
PA (MURD-) MURDOCH CHILDRENS RES INST.
PA (DELA/) DELATYCKI M.
Query Match 10.1%; Score 229.8; DB 8; Length 110000;
Best Local Similarity 83.5%; Pred. No. 3.2e-47;
RESULT 284
ID AED18452 standard; DNA; 180283 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 10.1%; Score 229.8; DB 14; Length 180283;
Best Local Similarity 78.5%; Pred. No. 4e-47;
RESULT 285
ID AAH15562 standard; cDNA; 1645 BP.
DE Human cDNA sequence SEQ ID NO:13851.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.1%; Score 229.6; DB 4; Length 1645;
Best Local Similarity 83.0%; Pred. No. 5.4e-48;
RESULT 286
ID ASK72689 standard; DNA; 17800 BP.
DE Human potassium channel interacting protein (PCIP) genomic DNA #3.
PN WO200226984-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 229.6; DB 6; Length 17800;
Best Local Similarity 85.4%; Pred. No. 1.6e-47;
RESULT 287
ID ADQ97497 standard; DNA; 21850 BP.
DE Human cancer associated sequence HD09-005, SEQ ID 474.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.1%; Score 229.6; DB 12; Length 21850;
Best Local Similarity 86.6%; Pred. No. 1.7e-47;
RESULT 288
ID AAK76168 standard; DNA; 25541 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30980.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 229.6; DB 4; Length 25541;
Best Local Similarity 82.9%; Pred. No. 1.9e-47;
RESULT 289
ID AAS28368 standard; DNA; 32248 BP.
DE Genomic sequence #208 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 229.6; DB 4; Length 32248;
Best Local Similarity 82.9%; Pred. No. 2.1e-47;
RESULT 290
ID ADG41564 standard; DNA; 32248 BP.

ID ADB48318 standard; cDNA; 955 BP.
DE Novel human cDNA SEQ ID NO 228.
PN US2003104529-A1.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 10.1%; Score 230; DB 9; Length 955;
Best Local Similarity 87.7%; Pred. No. 3.3e-48;
RESULT 274
ID AAL37485 standard; DNA; 17146 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3850.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230; DB 4; Length 17146;
Best Local Similarity 87.7%; Pred. No. 1.2e-47;
RESULT 275
ID ABX60473 standard; cDNA; 17146 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2817.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.1%; Score 230; DB 8; Length 17146;
Best Local Similarity 87.7%; Pred. No. 1.2e-47;
RESULT 276
ID ADJ31223 standard; DNA; 17146 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3850.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230; DB 12; Length 17146;
Best Local Similarity 87.7%; Pred. No. 1.2e-47;
RESULT 277
ID AAL37486 standard; DNA; 30568 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3851.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230; DB 4; Length 30568;
Best Local Similarity 87.7%; Pred. No. 1.6e-47;
RESULT 278
ID ABX60474 standard; cDNA; 30568 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2818.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.1%; Score 230; DB 8; Length 30568;
Best Local Similarity 87.7%; Pred. No. 1.6e-47;
RESULT 279
ID ADJ31224 standard; DNA; 30568 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3851.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 230; DB 12; Length 30568;
Best Local Similarity 87.7%; Pred. No. 1.6e-47;
RESULT 280
ID ABA14925 standard; DNA; 7872 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7256.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 229.8; DB 5; Length 7872;
Best Local Similarity 84.6%; Pred. No. 9.7e-48;
RESULT 281
ID AAK67892 standard; DNA; 24884 BP.

DE Human respiratory system associated genomic DNA seq id 802.
 PN US2003215893-A1.
 PD 20-NOV-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 229.6; DB 10; Length 32248;
 Best Local Similarity 82.9%; Pred. No. 2.1e-47;
 RESULT 291
 ID AD197338 standard; DNA; 32248 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID802.
 PN US200307704-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 229.6; DB 11; Length 32248;
 Best Local Similarity 82.9%; Pred. No. 2.1e-47;
 RESULT 292
 ID AAK76172 standard; DNA; 34435 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30984.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.1%; Score 229.6; DB 4; Length 34435;
 Best Local Similarity 82.9%; Pred. No. 2.1e-47;
 RESULT 293
 ID AEA61148 standard; DNA; 79977 BP.
 DE Human SCNN1B gene genomic sequence SEQ ID NO:58.
 PN US2005130172-A1.
 PD 16-JUN-2005.
 PA (FARB) BAYER CORP.
 Query Match 10.1%; Score 229.6; DB 8; Length 67571;
 Best Local Similarity 77.2%; Pred. No. 2.9e-47;
 RESULT 294
 ID AEA61148 standard; DNA; 79977 BP.
 DE Human SCNN1B gene genomic sequence SEQ ID NO:58.
 PN US2005130172-A1.
 PD 16-JUN-2005.
 PA (FARB) BAYER CORP.
 Query Match 10.1%; Score 229.6; DB 14; Length 79977;
 Best Local Similarity 77.6%; Pred. No. 3.1e-47;
 RESULT 295
 ID ADL13556 standard; DNA; 95240 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #89.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 10.1%; Score 229.6; DB 10; Length 95240;
 Best Local Similarity 84.2%; Pred. No. 3.3e-47;
 RESULT 296
 ID AEI93839 standard; DNA; 97650 BP.
 DE Human glutamate receptor, ionotropic, delta 2 (GRID2) genomic sequence.
 PN WO2006074061-A2.
 PD 13-JUL-2006.
 PA (SEQU-) SEQUENOM INC.
 Query Match 10.1%; Score 229.6; DB 15; Length 97650;
 Best Local Similarity 71.5%; Pred. No. 3.4e-47;
 RESULT 297
 ID AED18395 standard; DNA; 128117 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 646.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 10.1%; Score 229.6; DB 14; Length 128117;
 Best Local Similarity 87.9%; Pred. No. 3.8e-47;
 RESULT 298
 ID ACN45054 standard; DNA; 133632 BP.
 DE Human genomic sequence hCG28560.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.1%; Score 229.6; DB 11; Length 133632;
 Best Local Similarity 87.9%; Pred. No. 3.9e-47;
 RESULT 299
 ID ADZ13285 standard; DNA; 133642 BP.
 DE Human cancer-associated genomic DNA #66.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 10.1%; Score 229.6; DB 14; Length 133642;
 Best Local Similarity 87.9%; Pred. No. 3.9e-47;

RESULT 300
 ID AED18452 standard; DNA; 180283 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 10.1%; Score 229.6; DB 14; Length 180283;
 Best Local Similarity 83.0%; Pred. No. 4.5e-47;
 RESULT 301
 ID ACN44010 standard; DNA; 198522 BP.
 DE Human genomic sequence hCG1643869.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.1%; Score 229.6; DB 11; Length 198522;
 Best Local Similarity 83.0%; Pred. No. 4.7e-47;
 RESULT 302
 ID ADP75180 standard; DNA; 304905 BP.
 DE Human Endophilin 2 gene.
 PN WO2003031594-A2.
 PD 17-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 10.1%; Score 229.6; DB 11; Length 304905;
 Best Local Similarity 87.9%; Pred. No. 5.6e-47;
 RESULT 303
 ID ABD32620 standard; DNA; 27499 BP.
 DE Human cancer-associated genomic DNA HD13-010.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 10.0%; Score 229.4; DB 13; Length 27499;
 Best Local Similarity 83.7%; Pred. No. 2.2e-47;
 RESULT 304
 ID ACN45006 standard; DNA; 67810 BP.
 DE Human genomic sequence hCG32956.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.0%; Score 229.4; DB 11; Length 67810;
 Best Local Similarity 82.6%; Pred. No. 3.2e-47;
 RESULT 305
 ID AED55989 standard; DNA; 95900 BP.
 DE Human WASPIP DNA.
 PN WO2005100604-A2.
 PD 24-NOV-2004.
 PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
 Query Match 10.0%; Score 229.4; DB 14; Length 95900;
 Best Local Similarity 86.1%; Pred. No. 3.8e-47;
 RESULT 306
 ID ADY70791 standard; DNA; 104424 BP.
 DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.
 PN CN1548557-A.
 PD 24-NOV-2004.
 PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
 Query Match 10.0%; Score 229.4; DB 14; Length 104424;
 Best Local Similarity 84.9%; Pred. No. 3.9e-47;
 RESULT 307
 ID ADZ46659 standard; DNA; 104424 BP.
 DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.
 PN CN1548553-A.
 PD 24-NOV-2004.
 PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
 Query Match 10.0%; Score 229.4; DB 14; Length 104424;
 Best Local Similarity 84.9%; Pred. No. 3.9e-47;
 RESULT 308
 ID ADZ46659 standard; DNA; 128668 BP.
 DE Human genomic sequence hCG40471.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.0%; Score 229.4; DB 11; Length 128668;
 Best Local Similarity 82.7%; Pred. No. 4.3e-47;

RESULT 310
ID ACN44674 standard; DNA; 129042 BP.
DE Human genomic sequence HCG27276.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 229.4; DB 11; Length 129042;
Best Local Similarity 83.7%; Pred. No. 4.3e-47;
RESULT 311
ID AAD28763 standard; DNA; 154465 BP.
DE Human AKAP allelic variant (AKAP10-1) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 6; Length 154465;
Best Local Similarity 74.9%; Pred. No. 4.7e-47;
RESULT 312
ID AAD28762 standard; DNA; 158245 BP.
DE Human AKAP allelic variant (AKAP10) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 6; Length 158245;
Best Local Similarity 74.9%; Pred. No. 4.7e-47;
RESULT 313
ID AAH02340 standard; DNA; 161425 BP.
DE Human AKAP10 gene SEQ ID NO: 36.
PN WO200127857-A2.
PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 4; Length 161425;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 314
ID RAH02339 standard; DNA; 162025 BP.
DE Human AKAP10 gene SEQ ID NO: 35.
PN WO200127857-A2.
PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 4; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 315
ID AAD28758 standard; DNA; 162025 BP.
DE Human AKAP allelic variant (AKAP10-6) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 6; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 316
ID AAD28759 standard; DNA; 162025 BP.
DE Human AKAP allelic variant (AKAP10-7) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 6; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 317
ID ADS75958 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-6 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 13; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 318
ID ADS75959 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-7 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 13; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 319
ID ADB72194 standard; DNA; 31670 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-1 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 13; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 320
ID ADS75962 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 wild type genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 229.4; DB 13; Length 162025;
Best Local Similarity 74.9%; Pred. No. 4.8e-47;
RESULT 321
ID ACN43938 standard; DNA; 186391 BP.
DE Human genomic sequence HCG40117.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 229.4; DB 11; Length 186391;
Best Local Similarity 85.4%; Pred. No. 5.1e-47;
RESULT 322
ID AEE04958 standard; DNA; 212235 BP.
DE Cancer-associated gene SEQ ID NO:276.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.0%; Score 229.4; DB 14; Length 212235;
Best Local Similarity 84.9%; Pred. No. 5.4e-47;
RESULT 323
ID ADQ97397 standard; DNA; 225587 BP.
DE Human cancer associated sequence HD08-043, SEQ ID 374.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 229.4; DB 12; Length 225587;
Best Local Similarity 82.6%; Pred. No. 5.5e-47;
RESULT 324
ID ADL13693 standard; DNA; 231222 BP.
DE Osteoarthritis-associated polymorphic nucleotide #225.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 229.4; DB 10; Length 231222;
Best Local Similarity 82.9%; Pred. No. 5.6e-47;
RESULT 325
ID ABV50077 standard; cDNA; 454 BP.
DE Human prostate expression marker cDNA 50068.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.0%; Score 229.2; DB 5; Length 454;
Best Local Similarity 86.8%; Pred. No. 3.8e-48;
RESULT 326
ID AAD56093 standard; DNA; 31670 BP.
DE Human CCR7 carcinoma associated (CA) gene.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 229.2; DB 8; Length 31670;
Best Local Similarity 83.3%; Pred. No. 2.6e-47;
RESULT 327
ID ADA02455 standard; DNA; 31670 BP.
DE Human CCR7 carcinoma associated gene, SEQ ID NO:974.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 229.2; DB 9; Length 31670;
Best Local Similarity 83.3%; Pred. No. 2.6e-47;
RESULT 328
ID ADB72194 standard; DNA; 31670 BP.

DE Human CCR7 gene.
PD WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 229.2; DB 10; Length 31670;
Best Local Similarity 83.3%; Pred. No. 2.6e-47;
RESULT 329
ID ADR6958 standard; DNA; 31670 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:4.
PD WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 229.2; DB 13; Length 31670;
Best Local Similarity 83.3%; Pred. No. 2.6e-47;
RESULT 330
ID ADZ12484 standard; DNA; 31704 BP.
DE Human cancer-associated genomic DNA #1.
PD WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.0%; Score 229.2; DB 14; Length 31704;
Best Local Similarity 83.3%; Pred. No. 2.6e-47;
RESULT 331
ID ADO85988 standard; cDNA; 2373 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2860.
PD WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD) WU T D.
PA (ZHOU) ZHOU Y.
Query Match 10.0%; Score 229; DB 13; Length 2373;
Best Local Similarity 86.3%; Pred. No. 9.1e-48;
RESULT 332
ID APT06537 standard; DNA; 2495 BP.
DE Human oestrogen receptor beta gene fragment.
PD WO200259347-A2.
PD 01-AUG-2002.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 10.0%; Score 229; DB 6; Length 2495;
Best Local Similarity 85.1%; Pred. No. 9.3e-48;
RESULT 333
ID ADM83714 standard; DNA; 2495 BP.
DE Human oestrogen receptor beta gene promoter and partial CDS.
PD US2003138783-A1.
PD 24-JUL-2003.
PA (SUKU) SUKUMAR S.
PA (EVRO) EVRON E.
PA (DOOL) DOOLEY W C.
PA (SACC) SACCHI N.
PA (DAVI) DAVIDSON N.
PA (PACK) FACKLER M J.
Query Match 10.0%; Score 229; DB 11; Length 2495;
Best Local Similarity 85.1%; Pred. No. 9.3e-48;
RESULT 334
ID ABC22598 standard; DNA; 2495 BP.
DE Human estrogen receptor beta gene promoter and partial CDS SEQ ID NO:104.
PD US2005191640-A1.
PD 01-SEP-2005.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 10.0%; Score 229; DB 14; Length 2495;
Best Local Similarity 85.1%; Pred. No. 9.3e-48;
RESULT 335
ID AAL03517 standard; DNA; 3961 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6205.
PD WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 4; Length 3961;
Best Local Similarity 86.3%; Pred. No. 1.1e-47;
RESULT 336
ID AAL03518 standard; DNA; 3961 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6206.
PD WO200155320-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 4; Length 3961;
Best Local Similarity 86.3%; Pred. No. 1.1e-47;
RESULT 337
ID AAS36147 standard; DNA; 10758 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1647.
PD WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 4; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 338
ID AAS36150 standard; DNA; 10758 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1650.
PD WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 4; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 339
ID ADE46841 standard; DNA; 10758 BP.
DE Human cardiovascular system related genomic DNA #407.
PD US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 10; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 340
ID ADE46844 standard; DNA; 10758 BP.
DE Human cardiovascular system related genomic DNA #410.
PD US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 10; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 341
ID ADJ08259 standard; DNA; 10758 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1647.
PD US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 13; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 342
ID ADJ08262 standard; DNA; 10758 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1650.
PD US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 13; Length 10758;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 343
ID AAS36149 standard; DNA; 10759 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1649.
PD WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 4; Length 10759;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 344
ID ADE46843 standard; DNA; 10759 BP.
DE Human cardiovascular system related genomic DNA #409.
PD US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 10; Length 10759;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 345
ID ADJ08261 standard; DNA; 10759 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1649.
PD US2004005575-A1.
PD 08-JAN-2004.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 229; DB 13; Length 10759;
Best Local Similarity 86.3%; Pred. No. 1.8e-47;
RESULT 346
ID AD242279 standard; DNA; 14501 BP.
DE Human uroresensin II gene with G7032A SNP Seq 6.
PN JP2005110606-A.
PD 28-APR-2005.
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
PA (DOKU-) DOKURITSU GYOSEI HOJIN IVAKUHIN IRYO KIK.
Query Match 10.0%; Score 229; DB 14; Length 14501;
Best Local Similarity 85.1%; Pred. No. 2e-47;
RESULT 347
ID AD959374 standard; DNA; 25899 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:10.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 229; DB 12; Length 25899;
Best Local Similarity 85.1%; Pred. No. 2.7e-47;
RESULT 348
ID ADT92806 standard; DNA; 50977 BP.
DE Human DGC88 gene sequence - SEQ ID 1.
PN JP2004290022-A.
PD 21-OCT-2004.
PA (KEIO-) GH KEIO GIJUKU.
Query Match 10.0%; Score 229; DB 13; Length 50977;
Best Local Similarity 86.3%; Pred. No. 3.6e-47;
RESULT 349
ID ADZ13418 standard; DNA; 85920 BP.
DE Human cancer-associated genomic DNA #80.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 10.0%; Score 229; DB 14; Length 85920;
Best Local Similarity 85.1%; Pred. No. 4.6e-47;
RESULT 350
ID ABK83568 standard; DNA; 201143 BP.
DE Human DNA differentially expressed in granulocytic cells #139.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 229; DB 6; Length 201143;
Best Local Similarity 82.8%; Pred. No. 6.7e-47;
RESULT 351
ID ADC87068 standard; DNA; 11995 BP.
DE Human GPCR gene SEQ ID NO:1521.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.0%; Score 228.8; DB 10; Length 11995;
Best Local Similarity 88.4%; Pred. No. 2.1e-47;
RESULT 352
ID AAS27823 standard; DNA; 16489 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1483.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.8; DB 4; Length 16489;
Best Local Similarity 81.3%; Pred. No. 2.4e-47;
RESULT 353
ID ADB94626 standard; DNA; 16489 BP.
DE Novel human protein DNA #235.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) ROSEN S M.
PA (BARA/) BARASH S C.
Query Match 10.0%; Score 228.8; DB 10; Length 16489;
Best Local Similarity 81.3%; Pred. No. 2.4e-47;
RESULT 354
ID ADH56913 standard; DNA; 68571 BP.

DE Human CARD4 genomic DNA sequence SeqID 1.
PN US2003219810-A1.
PD 27-NOV-2003.
PA (BARN/) BARNES G.
PA (BERT/) BERTIN J.
Query Match 10.0%; Score 228.8; DB 12; Length 68571;
Best Local Similarity 65.5%; Pred. No. 4.6e-47;
RESULT 355
ID ADQ59506 standard; DNA; 81968 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:142.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 228.8; DB 12; Length 81968;
Best Local Similarity 82.3%; Pred. No. 5e-47;
RESULT 356
ID ADZ13883 standard; DNA; 84105 BP.
DE Human cancer-associated genomic DNA #120.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 10.0%; Score 228.8; DB 14; Length 84105;
Best Local Similarity 82.3%; Pred. No. 5.1e-47;
RESULT 357
Query Match 10.0%; Score 228.8; DB 12; Length 98800;
Best Local Similarity 87.3%; Pred. No. 5.5e-47;
RESULT 358
Query Match 10.0%; Score 228.8; DB 13; Length 98800;
Best Local Similarity 87.3%; Pred. No. 5.5e-47;
RESULT 359
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence HCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228.8; DB 11; Length 175077;
Best Local Similarity 72.3%; Pred. No. 7.1e-47;
RESULT 360
ID ABA18609 standard; DNA; 538 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10940.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 5; Length 538;
Best Local Similarity 86.6%; Pred. No. 5.9e-48;
RESULT 361
ID AAS35890 standard; DNA; 10093 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1390.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 4; Length 10093;
Best Local Similarity 79.9%; Pred. No. 2.2e-47;
RESULT 362
ID ABA07184 standard; DNA; 10093 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 4; Length 10093;
Best Local Similarity 79.9%; Pred. No. 2.2e-47;
RESULT 363
ID AAK89816 standard; DNA; 10093 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 4; Length 10093;
Best Local Similarity 79.9%; Pred. No. 2.2e-47;
RESULT 364
ID ADE46584 standard; DNA; 10093 BP.
DE Human cardiovascular system related genomic DNA #150.
PN US2003059908-A1.

PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 10; Length 10093;
Best Local Similarity 79.9%; Pred. No. 2.2e-47;
RESULT 365
ID ADJ08002 standard; DNA; 10093 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1390.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.6; DB 13; Length 10093;
Best Local Similarity 79.9%; Pred. No. 2.2e-47;
RESULT 366
ID AED89407 standard; DNA; 166111 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 47.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 10.0%; Score 228.6; DB 14; Length 166111;
Best Local Similarity 83.0%; Pred. No. 7.7e-47;
RESULT 367
ID ACN44846 standard; DNA; 330973 BP.
DE Human genomic sequence hCG22679.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228.6; DB 11; Length 330973;
Best Local Similarity 72.7%; Pred. No. 1.1e-46;
RESULT 368
ID ADH19017 standard; DNA; 15657 BP.
DE Human heparin cofactor II (HCF2) gDNA.
PN WO2003091453-A1.
PD 06-NOV-2003.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 10.0%; Score 228.4; DB 10; Length 15657;
Best Local Similarity 81.5%; Pred. No. 3e-47;
RESULT 369
ID AA232190 standard; DNA; 15848 BP.
DE Human heparin cofactor II exon 1 to 5 nucleotide sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 10.0%; Score 228.4; DB 2; Length 15848;
Best Local Similarity 81.5%; Pred. No. 3e-47;
RESULT 370
ID ABN95864 standard; DNA; 15849 BP.
DE Gene #2362 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 228.4; DB 6; Length 15849;
Best Local Similarity 81.5%; Pred. No. 3e-47;
RESULT 371
ID ACN44482 standard; DNA; 34096 BP.
DE Human genomic sequence hCG26017.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228.4; DB 11; Length 34096;
Best Local Similarity 83.6%; Pred. No. 4.3e-47;
RESULT 372
ID ACN45006 standard; DNA; 67810 BP.
DE Human genomic sequence hCG32956.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228.4; DB 11; Length 67810;
Best Local Similarity 87.3%; Pred. No. 5.8e-47;
RESULT 373
Query Match 10.0%; Score 228.4; DB 9; Length 110000;
Best Local Similarity 84.8%; Pred. No. 7.2e-47;
RESULT 374
ID ADH76849 standard; DNA; 122557 BP.

DE Melanin-concentrating hormone receptor 1 locus clone.
PN WO2003104489-A2.
PD 18-DEC-2003.
PA (UYPH-) UNIV PHILIPPS MARBURG.
Query Match 10.0%; Score 228.4; DB 12; Length 122557;
Best Local Similarity 83.7%; Pred. No. 7.6e-47;
RESULT 375
ID AEA61155 standard; DNA; 127602 BP.
DE Human GLUC gene genomic sequence SEQ ID NO:65.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 10.0%; Score 228.4; DB 14; Length 127602;
Best Local Similarity 83.8%; Pred. No. 7.7e-47;
RESULT 376
ID AAS38473 standard; cDNA; 407 BP.
DE Novel human diagnostic and therapeutic gene #1531.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 228.2; DB 4; Length 407;
Best Local Similarity 77.9%; Pred. No. 6.6e-48;
RESULT 377
ID AED14353 standard; DNA; 3208 BP.
DE Human cumulus cell differentially expressed gene.
PN WO2005094306-A2.
PD 13-OCT-2005.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 10.0%; Score 228.2; DB 14; Length 3208;
Best Local Similarity 84.1%; Pred. No. 1.7e-47;
RESULT 378
ID AAK68430 standard; DNA; 6007 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23242.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228.2; DB 4; Length 6007;
Best Local Similarity 78.2%; Pred. No. 2.2e-47;
RESULT 379
ID AED17756 standard; DNA; 34200 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 7.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 10.0%; Score 228.2; DB 14; Length 34200;
Best Local Similarity 82.1%; Pred. No. 4.8e-47;
RESULT 380
ID ABS57150 standard; DNA; 63588 BP.
DE Human gene encoding a serine/threonine kinase.
Query Match 10.0%; Score 228.2; DB 8; Length 63588;
Best Local Similarity 82.1%; Pred. No. 6.4e-47;
RESULT 381
ID ADQ59187 standard; DNA; 73583 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:24.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 10.0%; Score 228.2; DB 12; Length 73583;
Best Local Similarity 83.3%; Pred. No. 6.8e-47;
RESULT 382
ID AEC82893 standard; cDNA; 156321 BP.
DE Breast cancer associated cDNA SEQ ID NO 461.
PN WO2005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 10.0%; Score 228.2; DB 14; Length 156321;
Best Local Similarity 79.5%; Pred. No. 9.5e-47;
RESULT 383
ID AEG92892 standard; cDNA; 156321 BP.

DE Human tumor cell cDNA SEQ ID NO:388.
PN WO2006036025-A1.
PA (EISA) EISAI CO LTD.
Query Match 10.0%; Score 228.2; DB 15; Length 156321;
Best Local Similarity 79.5%; Pred. No. 9.5e-47;
RESULT 384
ID AEG71009 standard; cDNA; 156321 BP.
DE Human p53 mutational status predicting gene SEQ ID NO:483.
PN US2006074565-A1.
PD 06-APR-2006.
PA (MILL/) MILLER L D.
PA (GEOR/) GEORGE J.
PA (VEGA/) VEGA V B.
Query Match 10.0%; Score 228.2; DB 15; Length 156321;
Best Local Similarity 79.5%; Pred. No. 9.5e-47;
RESULT 385
ID ACN44958 standard; DNA; 285020 BP.
DE Human genomic sequence HCG37193.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228.2; DB 11; Length 285020;
Best Local Similarity 86.8%; Pred. No. 1.3e-46;
RESULT 386
ID ADR07732 standard; cDNA; 2941 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1238.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.0%; Score 228; DB 13; Length 2941;
Best Local Similarity 76.2%; Pred. No. 1.8e-47;
RESULT 387
ID AAK94548 standard; DNA; 8387 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39360.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 4; Length 8387;
Best Local Similarity 87.6%; Pred. No. 2.9e-47;
RESULT 388
ID ABA14892 standard; DNA; 8387 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7223.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 5; Length 8387;
Best Local Similarity 87.8%; Pred. No. 2.9e-47;
RESULT 389
ID AAK91515 standard; DNA; 13526 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5091.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 4; Length 13526;
Best Local Similarity 83.9%; Pred. No. 3.6e-47;
RESULT 390
ID AAS32169 standard; DNA; 13526 BP.
DE Human liver associated genomic DNA #343.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 5; Length 13526;
Best Local Similarity 83.9%; Pred. No. 3.6e-47;
RESULT 391
ID AEN90524 standard; DNA; 13526 BP.
DE Human liver antigen HALSD51 genomic sequence, SEQ ID NO:645.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.0%; Score 228; DB 6; Length 13526;

Best Local Similarity 83.9%; Pred. No. 3.6e-47;
RESULT 392
ID ADJ15437 standard; DNA; 13526 BP.
DE Human liver-related genomic DNA - SEQ ID 645.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 11; Length 13526;
Best Local Similarity 83.9%; Pred. No. 3.6e-47;
RESULT 393
ID AAK91514 standard; DNA; 14337 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5090.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 4; Length 14337;
Best Local Similarity 83.9%; Pred. No. 3.7e-47;
RESULT 394
ID AAS32168 standard; DNA; 14337 BP.
DE Human liver associated genomic DNA #342.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 5; Length 14337;
Best Local Similarity 83.9%; Pred. No. 3.7e-47;
RESULT 395
ID AEN90523 standard; DNA; 14337 BP.
DE Human liver antigen HALSD51 genomic sequence, SEQ ID NO:644.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.0%; Score 228; DB 6; Length 14337;
Best Local Similarity 83.9%; Pred. No. 3.7e-47;
RESULT 396
ID ADJ15436 standard; DNA; 14337 BP.
DE Human liver-related genomic DNA - SEQ ID 644.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 11; Length 14337;
Best Local Similarity 83.9%; Pred. No. 3.7e-47;
RESULT 397
ID AAL04340 standard; DNA; 32194 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7028.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 228; DB 4; Length 32194;
Best Local Similarity 85.0%; Pred. No. 5.3e-47;
RESULT 398
ID ACN43918 standard; DNA; 32607 BP.
DE Human genomic sequence hCG1644496.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 228; DB 11; Length 32607;
Best Local Similarity 85.0%; Pred. No. 5.3e-47;
RESULT 399
ID ADZ59528 standard; DNA; 37442 BP.
DE Secondary hyperparathyroidism detection polymorphic gene IL12RB1, SEQ 22.
PN JP2005102601-A.
PD 21-APR-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (JIKE-) UNIV JIKEI.
Query Match 10.0%; Score 228; DB 14; Length 37442;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
RESULT 400
ID ADZ59517 standard; DNA; 37442 BP.
DE Secondary hyperparathyroidism detection polymorphic gene IL12RB1, SEQ 11.
PN JP2005102601-A.
PD 21-APR-2005.

PA (HYUB-) HYUBITTO GENOMICS KK.
PA (JIKR-) UNIV JIKRI.
Query Match 10.0%; Score 228; DB 14; Length 37442;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
RESULT 401
ID AEB96540 standard; DNA; 37442 BP.
DE Human IL128B1 gene, SEQ ID 24.
Query Match 10.0%; Score 228; DB 14; Length 37442;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
RESULT 402
ID ABD32754 standard; DNA; 62124 BP.
DE Human cancer-associated genomic DNA HD16-028.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 228; DB 13; Length 62124;
Best Local Similarity 85.0%; Pred. No. 7.1e-47;
RESULT 403
ID ADQ9518 standard; DNA; 100762 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 228; DB 12; Length 100762;
Best Local Similarity 79.1%; Pred. No. 8.8e-47;
RESULT 404
ID ADZ13899 standard; DNA; 100822 BP.
DE Human cancer-associated genomic DNA #122.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.0%; Score 228; DB 14; Length 100822;
Best Local Similarity 79.1%; Pred. No. 8.8e-47;
RESULT 405
ID ADF13116 standard; DNA; 128779 BP.
DE Hypermethylation site in human breast cancer CpG island locus HBC-45.
PN US2003129602-A1.
PD 10-JUL-2003.
PA (HUAN/) HUANG T H.
Query Match 10.0%; Score 228; DB 12; Length 128779;
Best Local Similarity 83.9%; Pred. No. 9.8e-47;
RESULT 406
ID ADI37262 standard; DNA; 128779 BP.
DE Hypermethylation in cancer (HBC) locus-45.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR) UNIV MISSOURI.
Query Match 10.0%; Score 228; DB 12; Length 128779;
Best Local Similarity 83.9%; Pred. No. 9.8e-47;
RESULT 407
ID AAK75933 standard; DNA; 9039 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30745.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.8; DB 4; Length 9039;
Best Local Similarity 85.8%; Pred. No. 3.4e-47;
RESULT 408
ID AAK85246 standard; DNA; 9039 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40058.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.8; DB 4; Length 9039;
Best Local Similarity 85.8%; Pred. No. 3.4e-47;
RESULT 409
ID AAK84138 standard; DNA; 17758 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.8; DB 4; Length 17758;
Best Local Similarity 83.4%; Pred. No. 4.5e-47;

RESULT 410
ID AAD00147 standard; DNA; 35414 BP.
DE TR12 related DNA-11.
PN WO200023572-A1.
PD 27-APR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.8; DB 3; Length 35414;
Best Local Similarity 85.8%; Pred. No. 6.2e-47;
RESULT 411
ID ABL91800 standard; DNA; 39328 BP.
DE Human lipase endothelial (LIPG) isogene genomic DNA sequence.
PN WO200216397-A2.
PD 28-FEB-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 10.0%; Score 227.8; DB 6; Length 39328;
Best Local Similarity 81.2%; Pred. No. 6.5e-47;
RESULT 412
ID AAZ23902 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 4.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Query Match 10.0%; Score 227.8; DB 2; Length 49999;
Best Local Similarity 83.4%; Pred. No. 7.2e-47;
RESULT 413
ID AAX23517 standard; DNA; 50000 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 1.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 10.0%; Score 227.8; DB 2; Length 50000;
Best Local Similarity 80.2%; Pred. No. 7.2e-47;
RESULT 414
ID ACN43882 standard; DNA; 60815 BP.
DE Human genomic sequence hCG1777139.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.8; DB 11; Length 60815;
Best Local Similarity 84.6%; Pred. No. 7.9e-47;
RESULT 415
ID ADP66763 standard; DNA; 75033 BP.
DE Human endothelial lipase polynucleotide seqid 18.
PN US2004115653-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.0%; Score 227.8; DB 12; Length 75033;
Best Local Similarity 81.2%; Pred. No. 8.7e-47;
RESULT 416
ID ADL27146 standard; DNA; 96593 BP.
DE Human genomic sequence for PPP3CC.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 10.0%; Score 227.8; DB 11; Length 96593;
Best Local Similarity 76.6%; Pred. No. 9.7e-47;
RESULT 417
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.8; DB 9; Length 96595;
Best Local Similarity 76.6%; Pred. No. 9.7e-47;
RESULT 418
ID ADB72806 standard; DNA; 96595 BP.
DE Human PPP3CC gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.8; DB 10; Length 96595;
Best Local Similarity 76.6%; Pred. No. 9.7e-47;

RESULT 419
ID ADM6352 standard; DNA; 96596 BP.
DE Human PPP3CC gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.8; DB 9; Length 96596;
Best Local Similarity 76.6%; Pred. No. 9.7e-47;
RESULT 420
ID ADR52892 standard; DNA; 151152 BP.
DE Drug therapy altered expressed gene #243.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TREP/) TREPICCHIO W. L.
Query Match 10.0%; Score 227.8; DB 13; Length 151152;
Best Local Similarity 80.2%; Pred. No. 1.2e-46;
RESULT 421
ID ACN44046 standard; DNA; 260027 BP.
DE Human genomic sequence HCG1735292.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.8; DB 11; Length 260027;
Best Local Similarity 83.4%; Pred. No. 1.5e-46;
RESULT 422
ID ABD33509 standard; cDNA; 5115 BP.
DE Human cancer-associated (CA) cDNA HR07-099.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 227.6; DB 13; Length 5115;
Best Local Similarity 84.1%; Pred. No. 2.9e-47;
RESULT 423
ID AEJ13675 standard; DNA; 5115 BP.
DE Cancer-associated protein coding sequence - SEQ ID 683.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D. W.
PA (MALA/) MALANDRO M. S.
Query Match 10.0%; Score 227.6; DB 15; Length 5115;
Best Local Similarity 84.1%; Pred. No. 2.9e-47;
RESULT 424
ID ABD33508 standard; DNA; 36871 BP.
DE Human cancer-associated (CA) gene HD07-099.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.0%; Score 227.6; DB 13; Length 36871;
Best Local Similarity 84.1%; Pred. No. 7.1e-47;
RESULT 425
ID AEJ13674 standard; DNA; 36871 BP.
DE Cancer-associated gene sequence - SEQ ID 682.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D. W.
PA (MALA/) MALANDRO M. S.
Query Match 10.0%; Score 227.6; DB 15; Length 36871;
Best Local Similarity 84.1%; Pred. No. 7.1e-47;
RESULT 426
ID AAZ35351 standard; DNA; 41599 BP.
DE Cosmid including sequence spanning human chromosome 9p21.
PN WO9967634-A1.
PD 29-DEC-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 10.0%; Score 227.6; DB 3; Length 41599;
Best Local Similarity 78.0%; Pred. No. 7.5e-47;
RESULT 427
ID ACN44766 standard; DNA; 77478 BP.
DE Human genomic sequence HCG32368.

PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.6; DB 11; Length 77478;
Best Local Similarity 82.9%; Pred. No. 9.9e-47;
RESULT 428
ID ABN96931 standard; DNA; 99014 BP.
DE Gene #3429 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 227.6; DB 6; Length 99014;
Best Local Similarity 85.3%; Pred. No. 1.1e-46;
RESULT 429
ID ACN44602 standard; DNA; 126266 BP.
DE Human genomic sequence HCG1781402.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.6; DB 11; Length 126266;
Best Local Similarity 81.8%; Pred. No. 1.2e-46;
RESULT 430
ID ADH63063 standard; DNA; 132762 BP.
DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
PN WO2003024987-A1.
PD 27-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.0%; Score 227.6; DB 10; Length 132762;
Best Local Similarity 81.8%; Pred. No. 1.3e-46;
RESULT 431
ID ADZ12560 standard; DNA; 136489 BP.
DE Human cancer-associated genomic DNA #9.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.0%; Score 227.6; DB 14; Length 136489;
Best Local Similarity 86.5%; Pred. No. 1.3e-46;
RESULT 432
ID AED89420 standard; DNA; 171427 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 10.0%; Score 227.6; DB 14; Length 171427;
Best Local Similarity 89.2%; Pred. No. 1.4e-46;
RESULT 433
ID AED89401 standard; DNA; 177623 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 41.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 10.0%; Score 227.6; DB 14; Length 177623;
Best Local Similarity 82.9%; Pred. No. 1.4e-46;
RESULT 434
ID AAF92831 standard; DNA; 183999 BP.
DE Human ABC1 genomic DNA.
PN WO200115676-A2.
PD 08-MAR-2001.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
Query Match 10.0%; Score 227.6; DB 4; Length 183999;
Best Local Similarity 81.6%; Pred. No. 1.5e-46;
RESULT 435
ID ADU76470 standard; DNA; 183999 BP.
DE Human ABC1 genomic sequence.
PN US2004229275-A1.
PD 18-NOV-2004.
PA (HAYD/) HAYDEN M. R.
PA (BROO/) BROOKS-WILSON A. R.
PA (FIMS/) FIMSTONE S. N.
PA (CLEE/) CLEE S. M.
Query Match 10.0%; Score 227.6; DB 13; Length 183999;
Best Local Similarity 81.6%; Pred. No. 1.5e-46;

RESULT 436
ID AD213735 standard; DNA; 187851 BP.
DE Human cancer-associated genomic DNA #108.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 10.0%; Score 227.6; DB 14; Length 187851;
Best Local Similarity 82.9%; Pred. No. 1.5e-46;
RESULT 437
ID ADBG2937 standard; cDNA; 1988 BP.
DE Human cDNA encoding clone PLAC60120280.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 227.4; DB 10; Length 1988;
Best Local Similarity 86.0%; Pred. No. 2.2e-47;
RESULT 438
ID ABA14762 standard; DNA; 3283 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7093.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.4; DB 5; Length 3283;
Best Local Similarity 83.6%; Pred. No. 2.7e-47;
RESULT 439
ID ABA14761 standard; DNA; 3283 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7092.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 227.4; DB 5; Length 3283;
Best Local Similarity 83.6%; Pred. No. 2.7e-47;
RESULT 440
ID ACN43926 standard; DNA; 53242 BP.
DE Human genomic sequence HCG1782215.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.4; DB 11; Length 53242;
Best Local Similarity 83.6%; Pred. No. 9.4e-47;
RESULT 441
ID ABLG2910 standard; DNA; 65608 BP.
DE Breast cancer related gene sequence SEQ ID NO:1247.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 227.4; DB 6; Length 65608;
Best Local Similarity 81.4%; Pred. No. 1e-46;
RESULT 442
ID ABL64414 standard; DNA; 65608 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2751.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 227.4; DB 6; Length 65608;
Best Local Similarity 81.4%; Pred. No. 1e-46;
RESULT 443
ID ABL67668 standard; DNA; 65608 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6005.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 227.4; DB 6; Length 65608;
Best Local Similarity 81.4%; Pred. No. 1e-46;
RESULT 444
ID ACN44066 standard; DNA; 99886 BP.
DE Human genomic sequence HCG15674.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.0%; Score 227.4; DB 11; Length 99886;
Best Local Similarity 86.0%; Pred. No. 1.3e-46;

RESULT 445
ID ADQ17329 standard; DNA; 101685 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 227.4; DB 12; Length 101685;
Best Local Similarity 86.0%; Pred. No. 1.3e-46;
RESULT 446
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 227.4; DB 6; Length 172570;
Best Local Similarity 83.6%; Pred. No. 1.6e-46;
RESULT 447
ID AAK76049 standard; DNA; 2610 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30861.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 227.2; DB 4; Length 2610;
Best Local Similarity 85.5%; Pred. No. 2.7e-47;
RESULT 448
ID AEE05157 standard; DNA; 49617 BP.
DE Cancer-associated cDNA SEQ ID NO:475.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 227.2; DB 14; Length 49617;
Best Local Similarity 85.5%; Pred. No. 1e-46;
RESULT 449
ID ADZ12791 standard; DNA; 64700 BP.
DE Human cancer-associated genomic DNA #27.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 227.2; DB 14; Length 64700;
Best Local Similarity 77.3%; Pred. No. 1.2e-46;
RESULT 450
ID ABK90695 standard; DNA; 73467 BP.
DE DNA encoding human transporter protein.
Query Match 9.9%; Score 227.2; DB 6; Length 73467;
Best Local Similarity 81.0%; Pred. No. 1.2e-46;
RESULT 451
ID ABX93843 standard; DNA; 73467 BP.
DE Genomic DNA encoding novel human transporter protein.
Query Match 9.9%; Score 227.2; DB 8; Length 73467;
Best Local Similarity 81.0%; Pred. No. 1.2e-46;
RESULT 452
ID ABC00670 standard; DNA; 73467 BP.
DE Human sodium/glucose cotransporter related genomic DNA, SEQ ID NO: 3.
Query Match 9.9%; Score 227.2; DB 14; Length 73467;
Best Local Similarity 81.0%; Pred. No. 1.2e-46;
RESULT 453
ID ADD71350 standard; DNA; 93390 BP.
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.
PN WO2003023063-A1.
PD 20-MAR-2003.
PA (SANY) SANKYO CO LTD.
Query Match 9.9%; Score 227.2; DB 10; Length 93390;
Best Local Similarity 77.3%; Pred. No. 1.4e-46;
RESULT 454
ID AED55991 standard; DNA; 98100 BP.
DE Human BVES DNA.
Query Match 9.9%; Score 227.2; DB 14; Length 98100;
Best Local Similarity 82.6%; Pred. No. 1.4e-46;
RESULT 455
ID ADP03055 standard; cDNA; 124987 BP.
DE Human housekeeping gene cDNA #96.
PN JP2004135552-A.

PD 13-MAY-2004.
 PA (NIGA) NGK INSULATORS LTD.
 Query Match 9.9%; Score 227.2; DB 12; Length 124987;
 Best Local Similarity 86.8%; Pred. No. 1.6e-46;
 RESULT 456
 ID ADS88553 standard; cDNA; 124990 BP.
 DE Human housekeeping gene cDNA sequence SEQ ID NO:96.
 PN W02004035785-A1.
 PD 29-APR-2004.
 PA (NIGA) NGK INSULATORS LTD.
 Query Match 9.9%; Score 227.2; DB 13; Length 124990;
 Best Local Similarity 86.8%; Pred. No. 1.6e-46;
 RESULT 457
 ID ADU60195 standard; cDNA; 124990 BP.
 DE Housekeeping gene cDNA, SEQ ID 156.
 PN US2004229233-A1.
 PD 18-NOV-2004.
 PA (NIGA) NGK INSULATORS LTD.
 Query Match 9.9%; Score 227.2; DB 13; Length 124990;
 Best Local Similarity 86.8%; Pred. No. 1.6e-46;
 RESULT 458
 ID ADQ59197 standard; DNA; 155225 BP.
 DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.
 PN XZ2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G.
 PA (KIMN/) KIM N G.
 PA (LEEJ/) LEE J S.
 PA (RHEE/) RHEE H S.
 Query Match 9.9%; Score 227.2; DB 12; Length 155225;
 Best Local Similarity 85.5%; Pred. No. 1.7e-46;
 RESULT 459
 ID ADL13748 standard; DNA; 169144 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #280.
 PN W02003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.9%; Score 227.2; DB 10; Length 169144;
 Best Local Similarity 85.5%; Pred. No. 1.8e-46;
 RESULT 460
 ID ADL13719 standard; DNA; 199878 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #251.
 PN W02003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.9%; Score 227.2; DB 10; Length 199878;
 Best Local Similarity 82.0%; Pred. No. 1.9e-46;
 RESULT 461
 ID ADA52974 standard; cDNA; 1960 BP.
 DE Human coding sequence, SEQ ID 542.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.9%; Score 227; DB 10; Length 1960;
 Best Local Similarity 86.2%; Pred. No. 2.7e-47;
 RESULT 462
 ID ADJ96582 standard; DNA; 7364 BP.
 DE Human Nim-A related protein kinase SK516 DNA SeqID 39.
 PN W02004006838-A2.
 PD 22-JAN-2004.
 PA (SUGE-) SUGEN INC.
 Query Match 9.9%; Score 227; DB 12; Length 7364;
 Best Local Similarity 81.0%; Pred. No. 4.9e-47;
 RESULT 463
 ID ABA08132 standard; DNA; 32152 BP.
 DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.
 PN W0200155325-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 227; DB 4; Length 32152;
 Best Local Similarity 86.2%; Pred. No. 9.5e-47;
 RESULT 464

ID ABA17155 standard; DNA; 32249 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9486.
 PN W0200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 227; DB 5; Length 32249;
 Best Local Similarity 87.5%; Pred. No. 9.5e-47;
 RESULT 465
 ID ABK52612 standard; DNA; 58837 BP.
 DE Human Claspin genomic sequence.
 PN W0200233115-A2.
 PD 25-APR-2002.
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 Query Match 9.9%; Score 227; DB 6; Length 58837;
 Best Local Similarity 71.8%; Pred. No. 1.2e-46;
 RESULT 466
 ID AEG34296 standard; DNA; 67787 BP.
 DE DNA including human hypoxia-inducible factor 1-beta encoding DNA.
 PN W02006026485-A2.
 PD 09-MAR-2006.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.9%; Score 227; DB 15; Length 67787;
 Best Local Similarity 85.0%; Pred. No. 1.3e-46;
 RESULT 467
 ID ACN44742 standard; DNA; 87731 BP.
 DE Human genomic sequence hCG1738334.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.9%; Score 227; DB 11; Length 87731;
 Best Local Similarity 85.0%; Pred. No. 1.5e-46;
 RESULT 468
 ID ADQ18615 standard; DNA; 104729 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1434.
 PN W02004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.9%; Score 227; DB 12; Length 104729;
 Best Local Similarity 83.8%; Pred. No. 1.6e-46;
 RESULT 469
 ID ACN44210 standard; DNA; 238484 BP.
 DE Human genomic sequence hCG28803.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.9%; Score 227; DB 11; Length 238484;
 Best Local Similarity 86.2%; Pred. No. 2.3e-46;
 RESULT 470
 ID AEL18970 standard; DNA; 325775 BP.
 DE Human acetyl-CoA carboxylase-alpha (ACCI) gene SEQ ID NO:7.
 PN W02006110775-A2.
 PD 19-OCT-2006.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.9%; Score 227; DB 15; Length 325775;
 Best Local Similarity 83.8%; Pred. No. 2.7e-46;
 RESULT 471
 ID AAK83997 standard; DNA; 603 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38809.
 PN W0200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 226.8; DB 4; Length 603;
 Best Local Similarity 85.7%; Pred. No. 1.8e-47;
 RESULT 472
 ID ADB63769 standard; cDNA; 2643 BP.
 DE Human cDNA encoding clone UTERU20040390.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.9%; Score 226.8; DB 10; Length 2643;
 Best Local Similarity 84.5%; Pred. No. 3.5e-47;
 RESULT 473

PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 9.9%; Score 226.8; DB 6; Length 178896;
Best Local Similarity 85.7%; Pred. No. 2.3e-46;
RESULT 483
ID ADQ97687 standard; DNA; 179487 BP.
DE Human cancer associated sequence HD10-028, SEQ ID 664.
PN WO2004060304-A2.
PD 22-JUL-2004.
Query Match 9.9%; Score 226.8; DB 12; Length 179487;
Best Local Similarity 80.2%; Pred. No. 2.3e-46;
RESULT 484
ID ACN4374 standard; DNA; 181684 BP.
DE Human genomic sequence hCG16651.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.8; DB 11; Length 181684;
Best Local Similarity 85.7%; Pred. No. 2.3e-46;
RESULT 485
ID AEN65477 standard; CDNA; 620 BP.
DE Human cancer related polynucleotide SEQ ID NO 5444.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 226.6; DB 6; Length 620;
Best Local Similarity 81.8%; Pred. No. 2e-47;
RESULT 486
ID AAH04714 standard; CDNA; 772 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:1549.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.9%; Score 226.6; DB 4; Length 772;
Best Local Similarity 84.0%; Pred. No. 2.3e-47;
RESULT 487
ID AAH18426 standard; CDNA; 1656 BP.
DE Human cDNA sequence SEQ ID NO:18505.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.9%; Score 226.6; DB 4; Length 1656;
Best Local Similarity 84.0%; Pred. No. 3.2e-47;
RESULT 488
ID AC82887 standard; DNA; 7001 BP.
DE Human thyroid hormone receptor interactor 6 (TRIP6) gene fragment.
PN WO2003040328-A2.
PD 15-MAY-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.9%; Score 226.6; DB 10; Length 7001;
Best Local Similarity 81.8%; Pred. No. 6.1e-47;
RESULT 489
ID AED13475 standard; DNA; 7001 BP.
DE Human hormone receptor interactor 6 gene region Seqid10.
PN US2005222073-A1.
PD 06-OCT-2005.
PA (BENN/) BENNETT C F.
PA (MONI/) MONIA B P.
PA (CROO/) CROOKE R M.
PA (GRAH/) GRAHAM M J.
PA (FREI/) FREIER S M.
PA (NERO/) NERO P S.
PA (WANC/) WANCIEWICZ E.
PA (DEAN/) DEAN N M.
PA (COWS/) COWSERT L M.
PA (DOBI/) DOBIE K W.
Query Match 9.9%; Score 226.6; DB 14; Length 7001;
Best Local Similarity 81.8%; Pred. No. 6.1e-47;
RESULT 490
ID AD212506 standard; DNA; 24244 BP.
DE Human cancer-associated genomic DNA #4.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.8; DB 4; Length 13934;
Best Local Similarity 87.0%; Pred. No. 7.4e-47;
RESULT 475
ID AAK81690 standard; DNA; 21302 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36502.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.8; DB 4; Length 13934;
Best Local Similarity 82.2%; Pred. No. 8.9e-47;
RESULT 476
ID ADT77137 standard; DNA; 24475 BP.
DE Type II diabetes gene SEQ ID NO 14.
PN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM/) DAIMON M.
PA (KATO/) KATO T.
Query Match 9.9%; Score 226.8; DB 13; Length 24475;
Best Local Similarity 82.2%; Pred. No. 9.5e-47;
RESULT 477
ID AAK78746 standard; DNA; 33513 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33558.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.8; DB 4; Length 33513;
Best Local Similarity 83.3%; Pred. No. 1.1e-46;
RESULT 478
ID ACN44314 standard; DNA; 60057 BP.
DE Human genomic sequence hCG19476.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.8; DB 11; Length 60057;
Best Local Similarity 83.3%; Pred. No. 1.4e-46;
RESULT 479
Query Match 9.9%; Score 226.8; DB 14; Length 110000;
Best Local Similarity 80.2%; Pred. No. 1.9e-46;
RESULT 480
ID ACN43914 standard; DNA; 160482 BP.
DE Human genomic sequence hCG26773.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.8; DB 11; Length 160482;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 481
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.9%; Score 226.8; DB 12; Length 178024;
Best Local Similarity 85.7%; Pred. No. 2.3e-46;
RESULT 482
ID ABQ88146 standard; CDNA; 178896 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 53.
PN WO200250301-A2.
PD 27-JUN-2002.

PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 226.6; DB 14; Length 24244;
Best Local Similarity 85.2%; Pred. No. 1.1e-46;
RESULT 491
ID AEB96546 standard; DNA; 32704 BP.
DE Human FGL1 gene, SEQ ID 30.
Query Match 9.9%; Score 226.6; DB 14; Length 32704;
Best Local Similarity 84.0%; Pred. No. 1.2e-46;
RESULT 492
ID AAK77216 standard; DNA; 43938 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32028.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.6; DB 4; Length 43938;
Best Local Similarity 79.8%; Pred. No. 1.4e-46;
RESULT 493
ID AAK77217 standard; DNA; 45017 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32029.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.6; DB 4; Length 45017;
Best Local Similarity 79.8%; Pred. No. 1.4e-46;
RESULT 494
ID ABL68647 standard; DNA; 49634 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6984.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.9%; Score 226.6; DB 6; Length 49634;
Best Local Similarity 84.0%; Pred. No. 1.5e-46;
RESULT 495
ID AEF74987 standard; DNA; 49634 BP.
DE Human polynucleotide #501.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 9.9%; Score 226.6; DB 15; Length 49634;
Best Local Similarity 84.0%; Pred. No. 1.5e-46;
RESULT 496
ID AEA61178 standard; DNA; 67253 BP.
DE Human GPR105 gene genomic sequence SEQ ID NO:88.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 9.9%; Score 226.6; DB 14; Length 67253;
Best Local Similarity 84.0%; Pred. No. 1.7e-46;
RESULT 497
ID ACN44438 standard; DNA; 73967 BP.
DE Human genomic sequence hCG27607.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.6; DB 11; Length 73967;
Best Local Similarity 83.9%; Pred. No. 1.8e-46;
RESULT 498
ID AEB96528 standard; DNA; 87495 BP.
DE Human APlB1 gene, SEQ ID 12.
Query Match 9.9%; Score 226.6; DB 14; Length 87495;
Best Local Similarity 86.5%; Pred. No. 1.9e-46;
RESULT 499
ID ACN44746 standard; DNA; 92117 BP.
DE Human genomic sequence hCG29513.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.6; DB 11; Length 92117;
Best Local Similarity 82.9%; Pred. No. 1.9e-46;
RESULT 500

ID ADQ18808 standard; DNA; 111084 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1627.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.9%; Score 226.6; DB 12; Length 111084;
Best Local Similarity 84.0%; Pred. No. 2.1e-46;
RESULT 501
ID AAD54480 standard; DNA; 117962 BP.
DE Human CIP DNA #1.
PN WO200299055-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 9.9%; Score 226.6; DB 8; Length 117962;
Best Local Similarity 81.8%; Pred. No. 2.2e-46;
RESULT 502
ID ASI21870 standard; DNA; 181150 BP.
DE Human repetitive element associated DNA SEQ ID NO 47.
PN WO2006060308-A2.
PD 08-JUN-2006.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
Query Match 9.9%; Score 226.6; DB 15; Length 181150;
Best Local Similarity 79.8%; Pred. No. 2.6e-46;
RESULT 503
ID AAR51258 standard; DNA; 2387 BP.
DE Human AD4 gene genomic sequence stm.genB.
PN WO9703192-A2..
PD 30-JAN-1997.
PA (DARW-) DARWIN MOLECULAR CORP.
PA (VAME-) VA MEDICAL CENT.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.9%; Score 226.4; DB 2; Length 2387;
Best Local Similarity 83.5%; Pred. No. 4.2e-47;
RESULT 504
ID ABA18607 standard; DNA; 2854 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10938.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.4; DB 5; Length 2854;
Best Local Similarity 87.2%; Pred. No. 4.6e-47;
RESULT 505
ID AAS32249 standard; DNA; 32187 BP.
DE Human DNA repair and processing genomic DNA #35.
PN WO200155204-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.4; DB 5; Length 32187;
Best Local Similarity 85.9%; Pred. No. 1.4e-46;
RESULT 506
ID ABS67552 standard; DNA; 32187 BP.
DE Novel human DNA repair protein, genomic sequence #35.
PN US2002086353-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 226.4; DB 6; Length 32187;
Best Local Similarity 85.9%; Pred. No. 1.4e-46;
RESULT 507
ID ADJ12398 standard; DNA; 43991 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq252.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.

PA (FLOR/) FLORENCE C.
PA (EBNE/) ERNER R.
PA (OLSE/) OLSEN H.
Query Match 9.9%; Score 226.4; DB 12; Length 43991;
Best Local Similarity 85.9%; Pred. No. 1.6e-46;
RESULT 508
ID ADO97623 standard; DNA; 86764 BP.
DE Human cancer associated sequence HD10-016, SEQ ID 600.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.9%; Score 226.4; DB 12; Length 86764;
Best Local Similarity 87.2%; Pred. No. 2.1e-46;
RESULT 509
ID ACN44286 standard; DNA; 105219 BP.
DE Human genomic sequence HCG36856.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.4; DB 11; Length 105219;
Best Local Similarity 80.3%; Pred. No. 2.3e-46;
RESULT 510
ID AEA61160 standard; DNA; 354592 BP.
DE Human NEDD4L gene genomic sequence SEQ ID NO:70.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 9.9%; Score 226.4; DB 14; Length 110000;
Best Local Similarity 79.4%; Pred. No. 2.4e-46;
RESULT 511
ID AED34666 standard; DNA; 458207 BP.
DE ABL1 genomic DNA SEQ ID NO 2.
PN WO2005094291-A2.
PD 13-OCT-2005.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 9.9%; Score 226.4; DB 14; Length 110000;
Best Local Similarity 81.4%; Pred. No. 2.4e-46;
RESULT 512
ID AEF9730 standard; DNA; 163218 BP.
DE Human chromosome 17 sequence, clone hRPK.318_A_15.
PN WO2006020269-A2.
PD 23-FEB-2006.
PA (UYRP) UNIV ROCHESTER.
Query Match 9.9%; Score 226.4; DB 15; Length 163218;
Best Local Similarity 85.9%; Pred. No. 2.8e-46;
RESULT 513
ID ABA18608 standard; DNA; 546 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10939.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.2; DB 5; Length 546;
Best Local Similarity 85.4%; Pred. No. 2.4e-47;
RESULT 514
ID ABN84129 standard; cDNA; 1615 BP.
DE Human cytokine receptor 16.5 coding sequence.
PN CN1331154-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 9.9%; Score 226.2; DB 6; Length 1615;
Best Local Similarity 84.2%; Pred. No. 4e-47;
RESULT 515
ID AAS26795 standard; DNA; 32248 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1769.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.2; DB 4; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 516
ID AAL37122 standard; DNA; 32248 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3487.
PN WO200155367-A1.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.2; DB 4; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 517
ID ABA204112 standard; DNA; 32248 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12743.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.2; DB 5; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 518
ID ABX74144 standard; DNA; 32248 BP.
DE Human novel polynucleotide #972.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 226.2; DB 8; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 519
ID ABX60110 standard; cDNA; 32248 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2454.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 226.2; DB 8; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 520
ID ADJ30860 standard; DNA; 32248 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3487.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 226.2; DB 12; Length 32248;
Best Local Similarity 86.7%; Pred. No. 1.5e-46;
RESULT 521
ID AAD56075 standard; DNA; 32767 BP.
DE Human SNL carcinoma associated (CA) gene.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.2; DB 8; Length 32767;
Best Local Similarity 78.1%; Pred. No. 1.5e-46;
RESULT 522
ID ADA02437 standard; DNA; 32767 BP.
DE Human SNL carcinoma associated gene, SEQ ID NO:956.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.2; DB 9; Length 32767;
Best Local Similarity 78.1%; Pred. No. 1.5e-46;
RESULT 523
ID ADB72176 standard; DNA; 32767 BP.
DE Human SNL gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.2; DB 10; Length 32767;
Best Local Similarity 78.1%; Pred. No. 1.5e-46;
RESULT 524
ID ADE82920 standard; DNA; 32767 BP.
DE Human SNL genomic DNA sequence.
PN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 226.2; DB 10; Length 32767;
Best Local Similarity 78.1%; Pred. No. 1.5e-46;
RESULT 525

ID ABD33436 standard; DNA; 52710 BP.
 DE Human cancer-associated (CA) gene HD07-082.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.9%; Score 226.2; DB 13; Length 52710;
 Best Local Similarity 83.1%; Pred. No. 1.9e-46;
 RESULT 526
 ID AEJ13564 standard; DNA; 52710 BP.
 DE Cancer-associated gene sequence - SEQ ID 572.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match 9.9%; Score 226.2; DB 15; Length 52710;
 Best Local Similarity 83.1%; Pred. No. 1.9e-46;
 RESULT 527
 ID AAD15256 standard; DNA; 74962 BP.
 DE Human phosphatase gene.
 PN WO200160992-A2.
 PD 23-AUG-2001.
 PA (PEKE) PE CORP NV.
 Query Match 9.9%; Score 226.2; DB 4; Length 74962;
 Best Local Similarity 84.3%; Pred. No. 2.2e-46;
 RESULT 528
 ID AEF92655 standard; cDNA; 174318 BP.
 DE Human Ras effector protein Rin3, cDNA.
 PN WO2006020269-A2.
 PD 23-FEB-2006.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 9.9%; Score 226.2; DB 15; Length 174318;
 Best Local Similarity 85.4%; Pred. No. 3.3e-46;
 RESULT 529
 ID ABQ75562 standard; DNA; 188888 BP.
 DE Human related CYP 27C1 clone RP11-30F3 SEQ ID NO:21.
 PN WO200264765-A2.
 PD 22-AUG-2002.
 PA (CYTO-) CYTOCHROMA INC.
 Query Match 9.9%; Score 226.2; DB 6; Length 188888;
 Best Local Similarity 73.5%; Pred. No. 3.4e-46;
 RESULT 530
 ID AAS27712 standard; DNA; 4087 BP.
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1372.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 226; DB 4; Length 4087;
 Best Local Similarity 84.9%; Pred. No. 6.8e-47;
 RESULT 531
 ID ADB94515 standard; DNA; 4087 BP.
 DE Novel human protein DNA #124.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.9%; Score 226; DB 10; Length 4087;
 Best Local Similarity 84.9%; Pred. No. 6.8e-47;
 RESULT 532
 ID ABK83562 standard; cDNA; 139904 BP.
 DE Human cDNA differentially expressed in granulocytic cells #133.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.9%; Score 226; DB 6; Length 139904;
 Best Local Similarity 82.4%; Pred. No. 3.3e-46;
 RESULT 533
 ID AAD54634 standard; DNA; 142519 BP.
 DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
 PN WO200298899-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 9.9%; Score 226; DB 10; Length 142519;

Best Local Similarity 84.9%; Pred. No. 3.4e-46;
 RESULT 534
 ID AEN83124 standard; DNA; 172637 BP.
 DE Human voltage-activated ion channel transporter protein gene.
 Query Match 9.9%; Score 226; DB 6; Length 172637;
 Best Local Similarity 78.6%; Pred. No. 3.7e-46;
 RESULT 535
 ID AEB80195 standard; DNA; 172637 BP.
 DE Human transporter genomic DNA.
 Query Match 9.9%; Score 226; DB 14; Length 172637;
 Best Local Similarity 78.6%; Pred. No. 3.7e-46;
 RESULT 536
 ID ACF62736 standard; DNA; 183610 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.
 PN WO2003013534-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.9%; Score 226; DB 8; Length 183610;
 Best Local Similarity 77.7%; Pred. No. 3.8e-46;
 RESULT 537
 ID ADB20851 standard; DNA; 183610 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:664.
 PN WO2003013533-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.9%; Score 226; DB 8; Length 183610;
 Best Local Similarity 77.7%; Pred. No. 3.8e-46;
 RESULT 538
 ID ADB87940 standard; DNA; 183610 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:664.
 PN WO2003013536-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.9%; Score 226; DB 10; Length 183610;
 Best Local Similarity 77.7%; Pred. No. 3.8e-46;
 RESULT 539
 ID ADB96923 standard; DNA; 183610 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:664.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.9%; Score 226; DB 10; Length 183610;
 Best Local Similarity 77.7%; Pred. No. 3.8e-46;
 RESULT 540
 ID ADB92114 standard; DNA; 183610 BP.
 DE Human-MDR1 related DNA sequence SEQ ID NO:664.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.9%; Score 226; DB 10; Length 183610;
 Best Local Similarity 77.7%; Pred. No. 3.8e-46;
 RESULT 541
 ID ABQ80552 standard; DNA; 237961 BP.
 DE Human Canion gene fragment #2.
 PN WO200246404-A2.
 PD 13-JUN-2002.
 PA (GSET) GENSET.
 Query Match 9.9%; Score 226; DB 6; Length 237961;
 Best Local Similarity 78.6%; Pred. No. 4.2e-46;
 RESULT 542
 ID AED76155 standard; DNA; 261108 BP.
 DE Human CA genomic DNA sequence-ID hd25-006.
 PN WO2005104810-A2.
 PD 10-NOV-2005.
 PA (SAGR-) SAGRES DISCOVERY INC.
 PA (LAIA/) LAI A.
 PA (FATT/) FATTAEY A.
 Query Match 9.9%; Score 226; DB 14; Length 261108;
 Best Local Similarity 88.9%; Pred. No. 4.4e-46;
 RESULT 543
 ID AAK67132 standard; DNA; 310 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21944.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 310;
 Best Local Similarity 87.0%; Pred. No. 2.4e-47;
 RESULT 544
 ID AAK67294 standard; DNA; 699 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22106.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 699;
 Best Local Similarity 81.1%; Pred. No. 3.5e-47;
 RESULT 545
 ID AAS22674 standard; cDNA; 4385 BP.
 DE Human cDNA encoding a novel human protein #240.
 PN WO200155437-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 4385;
 Best Local Similarity 84.4%; Pred. No. 7.9e-47;
 RESULT 546
 ID ABE23807 standard; DNA; 4385 BP.
 DE Novel human protein coding sequence (contig) - SEQ ID 476.
 PN US2005266423-A1.
 PD 01-DEC-2005.
 PA (NUVE-) NUVELO INC.
 Query Match 9.9%; Score 225.8; DB 15; Length 4385;
 Best Local Similarity 84.4%; Pred. No. 7.9e-47;
 RESULT 547
 ID AAS30660 standard; DNA; 5530 BP.
 DE DNA encoding novel lung cancer antigen, Seq ID No 112.
 PN WO200155300-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 548
 ID AAK66712 standard; DNA; 5530 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21524.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 549
 ID AAS28733 standard; DNA; 5530 BP.
 DE Genomic sequence #573 encoding for novel human respiratory antigen.
 PN WO200155448-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 550
 ID ACA03423 standard; DNA; 5530 BP.
 DE DNA encoding human lung cancer antigen HCLBW86.
 PN US2002173454-A1.
 PD 21-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.9%; Score 225.8; DB 8; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 551
 ID ADB96771 standard; DNA; 5530 BP.
 DE Novel lung cancer antigen genomic DNA #42.
 PN US2003049703-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 9; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 552
 ID ADG41929 standard; DNA; 5530 BP.
 DE Human respiratory system associated genomic DNA seq id 1167.

PN US2003215893-A1.
 PD 20-NOV-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 10; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 553
 ID ADI97703 standard; DNA; 5530 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID1167.
 PN US2003077704-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 11; Length 5530;
 Best Local Similarity 87.0%; Pred. No. 8.8e-47;
 RESULT 554
 ID ACC50871 standard; cDNA; 28215 BP.
 DE Human secreted protein HAC clone SEQ ID NO 1051.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 8; Length 28215;
 Best Local Similarity 83.3%; Pred. No. 1.8e-46;
 RESULT 555
 ID ABZ71493 standard; DNA; 28215 BP.
 DE Secreted protein gene 24 genomic fragment HCND847, SEQ ID NO:603.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 8; Length 28215;
 Best Local Similarity 83.3%; Pred. No. 1.8e-46;
 RESULT 556
 ID ADB91849 standard; DNA; 28215 BP.
 DE Human secreted protein related DNA #SEQ ID 795.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 9; Length 28215;
 Best Local Similarity 83.3%; Pred. No. 1.8e-46;
 RESULT 557
 ID ADC74632 standard; DNA; 28215 BP.
 DE Human secreted protein-related DNA - SEQ ID 1365.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 10; Length 28215;
 Best Local Similarity 83.3%; Pred. No. 1.8e-46;
 RESULT 558
 ID AEL94875 standard; DNA; 28215 BP.
 DE Human secreted protein-related DNA sequence - SEQ ID 1057.
 PN US2006246483-A1.
 PD 02-NOV-2006.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 15; Length 28215;
 Best Local Similarity 83.3%; Pred. No. 1.8e-46;
 RESULT 559
 ID AAL35901 standard; DNA; 28818 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2266.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.8; DB 4; Length 28818;
 Best Local Similarity 81.1%; Pred. No. 1.8e-46;
 RESULT 560
 ID ABX58889 standard; cDNA; 28818 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1233.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.9%; Score 225.8; DB 8; Length 28818;
 Best Local Similarity 81.1%; Pred. No. 1.8e-46;
 RESULT 561
 ID ADJ29639 standard; DNA; 28818 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2266.

PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.8; DB 12; Length 28818;
Best Local Similarity 81.1%; Pred. No. 1.8e-46;
RESULT 562
ID AAF54723 standard; DNA; 35465 BP.
DE Nucleotide sequence of a human polynucleotide sequence.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR) BIOMERIEUX STELHVS.
Query Match 9.9%; Score 225.8; DB 4; Length 35465;
Best Local Similarity 83.3%; Pred. No. 2e-46;
RESULT 563
ID ABT17380 standard; DNA; 35465 BP.
DE Human IG gene related nucleic acid SEQ ID No 6.
PN WO20029040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 9.9%; Score 225.8; DB 8; Length 35465;
Best Local Similarity 83.3%; Pred. No. 2e-46;
RESULT 564
ID ABT17382 standard; DNA; 36991 BP.
DE Human IG gene related nucleic acid SEQ ID No 8.
PN WO20029040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 9.9%; Score 225.8; DB 8; Length 36991;
Best Local Similarity 83.3%; Pred. No. 2.1e-46;
RESULT 565
ID AED18110 standard; DNA; 36991 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 361.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.9%; Score 225.8; DB 14; Length 36991;
Best Local Similarity 83.3%; Pred. No. 2.1e-46;
RESULT 566
ID AEF75130 standard; DNA; 36991 BP.
DE Human polynucleotide #644.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 9.9%; Score 225.8; DB 15; Length 36991;
Best Local Similarity 83.3%; Pred. No. 2.1e-46;
RESULT 567
ID ACN44494 standard; DNA; 60381 BP.
DE Human genomic sequence hCG27935.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225.8; DB 11; Length 60381;
Best Local Similarity 76.5%; Pred. No. 2.6e-46;
RESULT 568
ID AD032260 standard; DNA; 106707 BP.
DE Human chromosome 20 region containing type 2 diabetes mellitus genes.
PN WO2004039554-A2.
PD 13-MAY-2004.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 9.9%; Score 225.8; DB 12; Length 106707;
Best Local Similarity 85.7%; Pred. No. 3.3e-46;
RESULT 569
ID AEH93956 standard; DNA; 118899 BP.
DE DNMT31 variant full length coding sequence.
PN US2006115829-A1.
PD 01-JUN-2006.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 9.9%; Score 225.8; DB 15; Length 118899;
Best Local Similarity 87.1%; Pred. No. 3.5e-46;
RESULT 570
ID ADZ13043 standard; DNA; 140342 BP.
DE Human cancer-associated genomic DNA #52.

PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 225.8; DB 14; Length 140342;
Best Local Similarity 82.2%; Pred. No. 3.7e-46;
RESULT 571
ID ASF80130 standard; DNA; 162302 BP.
DE Cancer-associated polypeptide genomic DNA sequence hb27-009 SEQ ID NO:26.
PN US2006024677-A1.
PD 02-FEB-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
PA (LALA/) LAI A.
PA (TSEC/) TSE C.
PA (FATT/) FATTAEY A.
Query Match 9.9%; Score 225.8; DB 15; Length 162302;
Best Local Similarity 79.2%; Pred. No. 4e-46;
RESULT 572
ID ADZ13735 standard; DNA; 187851 BP.
DE Human cancer-associated genomic DNA #108.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 225.8; DB 14; Length 187851;
Best Local Similarity 84.4%; Pred. No. 4.3e-46;
RESULT 573
ID ADB62640 standard; cDNA; 2946 BP.
DE Human cDNA encoding clone KIDNE20150730.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.9%; Score 225.6; DB 10; Length 2946;
Best Local Similarity 85.2%; Pred. No. 7.4e-47;
RESULT 574
ID AAL07337 standard; DNA; 4059 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10025.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.6; DB 4; Length 4059;
Best Local Similarity 85.2%; Pred. No. 8.6e-47;
RESULT 575
ID AAZ50904 standard; DNA; 17590 BP.
DE Human TBC-1 partial genomic DNA comprising 5' end sequence.
PN WO200008209-A2.
PD 17-FEB-2000.
PA (GEST) GENSET.
Query Match 9.9%; Score 225.6; DB 3; Length 17590;
Best Local Similarity 86.4%; Pred. No. 1.7e-46;
RESULT 576
ID AEJ63934 standard; DNA; 17590 BP.
DE Human TBC-1 genomic SEQ ID NO 1.
PN US2006084073-A1.
PD 20-APR-2006.
PA (GEST) GENSET SA.
Query Match 9.9%; Score 225.6; DB 15; Length 17590;
Best Local Similarity 86.4%; Pred. No. 1.7e-46;
RESULT 577
ID ADU12398 standard; DNA; 43991 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq252.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.

PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 9.9%; Score 225.6; DB 12; Length 43991;
 Best Local Similarity 84.2%; Pred. No. 2.5e-46;
 RESULT 578
 Query Match 9.9%; Score 225.6; DB 14; Length 110000;
 Best Local Similarity 82.8%; Pred. No. 3.8e-46;
 RESULT 579
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVT1 genomic DNA sequence.
 PN WO2003080808-A2.
 PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.9%; Score 225.6; DB 10; Length 167163;
 Best Local Similarity 82.8%; Pred. No. 4.6e-46;
 RESULT 580
 ID APT10147 standard; cDNA; 185035 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 281.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.9%; Score 225.6; DB 6; Length 185035;
 Best Local Similarity 87.8%; Pred. No. 4.8e-46;
 RESULT 581
 ID ACA64951 standard; DNA; 185035 BP.
 DE Human FEN1 DNA corresponding to AC004770.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHARRAY GMBH.
 Query Match 9.9%; Score 225.6; DB 8; Length 185035;
 Best Local Similarity 87.8%; Pred. No. 4.8e-46;
 RESULT 582
 ID ADQ20284 standard; DNA; 185035 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.9%; Score 225.6; DB 12; Length 185035;
 Best Local Similarity 87.8%; Pred. No. 4.8e-46;
 RESULT 583
 ID AAK83109 standard; DNA; 2816 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37921.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.4; DB 4; Length 2816;
 Best Local Similarity 85.9%; Pred. No. 8.2e-47;
 RESULT 584
 ID ADR07011 standard; cDNA; 3847 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 517.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.9%; Score 225.4; DB 13; Length 3847;
 Best Local Similarity 81.7%; Pred. No. 9.4e-47;
 RESULT 585
 ID AAK79618 standard; DNA; 9510 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34430.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.4; DB 4; Length 9510;
 Best Local Similarity 82.7%; Pred. No. 1.4e-46;
 RESULT 586
 ID ABX13167 standard; DNA; 19650 BP.
 DE Human gene encoding a zinc metalloprotease.
 PN US6482629-B1.
 PD 19-NOV-2002.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 8; Length 19650;
 Best Local Similarity 84.9%; Pred. No. 2e-46;
 RESULT 587
 ID AAD62720 standard; DNA; 19650 BP.

DE Human zinc metalloprotease genomic DNA.
 PN US2003129700-A1.
 PD 10-JUL-2003.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 10; Length 19650;
 Best Local Similarity 84.9%; Pred. No. 2e-46;
 RESULT 588
 ID ADQ88304 standard; DNA; 19650 BP.
 DE Human zinc metalloprotease genomic DNA.
 PN US2004142439-A1.
 PD 22-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 13; Length 19650;
 Best Local Similarity 84.9%; Pred. No. 2e-46;
 RESULT 589
 ID ADY74758 standard; DNA; 19650 BP.
 DE Human zinc metalloprotease genomic DNA.
 PN US2005059075-A1.
 PD 17-MAR-2005.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 14; Length 19650;
 Best Local Similarity 84.9%; Pred. No. 2e-46;
 RESULT 590
 ID AAK65309 standard; DNA; 19969 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20121.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.4; DB 4; Length 19969;
 Best Local Similarity 74.8%; Pred. No. 2e-46;
 RESULT 591
 ID AAF24851 standard; DNA; 20598 BP.
 DE Nucleotide sequence of a human helical cytokine designated Zalpha33.
 PN WO200077209-A1.
 PD 21-DEC-2000.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 9.9%; Score 225.4; DB 4; Length 20598;
 Best Local Similarity 74.8%; Pred. No. 2e-46;
 RESULT 592
 ID AAD42515 standard; DNA; 20598 BP.
 DE Human zalpha33 gene.
 PN US6406888-B1.
 PD 18-JUN-2002.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 9.9%; Score 225.4; DB 6; Length 20598;
 Best Local Similarity 74.8%; Pred. No. 2e-46;
 RESULT 593
 ID ACH00110 standard; DNA; 20598 BP.
 DE Human zalpha33 genomic DNA.
 PN US2003064479-A1.
 PD 03-APR-2003.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 9.9%; Score 225.4; DB 9; Length 20598;
 Best Local Similarity 74.8%; Pred. No. 2e-46;
 RESULT 594
 ID ABA20763 standard; DNA; 26427 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13094.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.4; DB 5; Length 26427;
 Best Local Similarity 85.9%; Pred. No. 2.2e-46;
 RESULT 595
 ID ABA20762 standard; DNA; 26427 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13093.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.4; DB 5; Length 26427;
 Best Local Similarity 85.9%; Pred. No. 2.2e-46;
 RESULT 596
 ID ADQ97657 standard; DNA; 32787 BP.
 DE Human cancer associated sequence HD10-022, SEQ ID 634.

PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.9%; Score 225.4; DB 12; Length 32787;
 Best Local Similarity 73.6%; Pred. No. 2.5e-46;
 RESULT 597
 ID ACN44490 standard; DNA; 32865 BP.
 DE Human genomic sequence HCG25375.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.9%; Score 225.4; DB 11; Length 32865;
 Best Local Similarity 70.4%; Pred. No. 2.5e-46;
 RESULT 598
 ID ADJ10262 standard; DNA; 51001 BP.
 DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
 PN US2004005570-A1.
 PD 08-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 12; Length 51001;
 Best Local Similarity 86.1%; Pred. No. 3e-46;
 RESULT 599
 ID ADQ97249 standard; DNA; 59575 BP.
 DE Human cancer associated sequence HD08-021, SEQ ID 225.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.9%; Score 225.4; DB 12; Length 59575;
 Best Local Similarity 81.5%; Pred. No. 3.2e-46;
 RESULT 600
 ID ABS52847 standard; DNA; 90541 BP.
 DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.
 PN US2002094560-A1.
 PD 18-JUL-2002.
 PA (ABUT/) ABU-THREIDEH J.
 PA (GONG/) GONG F.
 PA (KERC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 9.9%; Score 225.4; DB 6; Length 90541;
 Best Local Similarity 85.9%; Pred. No. 3.9e-46;
 RESULT 601
 ID ADJ37690 standard; DNA; 90541 BP.
 DE Human kinase genomic DNA.
 PN US2003175927-A1.
 PD 18-SEP-2003.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 10; Length 90541;
 Best Local Similarity 85.9%; Pred. No. 3.9e-46;
 RESULT 602
 ID ADR31219 standard; DNA; 90541 BP.
 DE Human SRPK2 kinase protein alternative splice form genomic DNA.
 PN US2004157297-A1.
 PD 12-AUG-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 13; Length 90541;
 Best Local Similarity 85.9%; Pred. No. 3.9e-46;
 RESULT 603
 ID ACC45150 standard; DNA; 96649 BP.
 DE Human NAC nucleotide sequence SEQ ID NO:10.
 PN WO2003024988-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 8; Length 96649;
 Best Local Similarity 83.5%; Pred. No. 4e-46;
 RESULT 604
 ID ADQ19183 standard; DNA; 110665 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2002.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.9%; Score 225.4; DB 12; Length 110665;
 Best Local Similarity 81.5%; Pred. No. 4.3e-46;
 RESULT 606
 ID AAL54213 standard; DNA; 113033 BP.
 DE SR protein-specific kinase-1 DNA, SEQ ID No 5.
 PN WO200299427-A1.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 9.9%; Score 225.4; DB 8; Length 113033;
 Best Local Similarity 85.9%; Pred. No. 4.3e-46;
 RESULT 607
 ID ADQ21090 standard; DNA; 114411 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3910.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.9%; Score 225.4; DB 12; Length 114411;
 Best Local Similarity 81.3%; Pred. No. 4.3e-46;
 RESULT 608
 ID AAA34791 standard; DNA; 138169 BP.
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2480.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 9.9%; Score 225.4; DB 3; Length 138169;
 Best Local Similarity 82.7%; Pred. No. 4.7e-46;
 RESULT 609
 ID ABD20695 standard; DNA; 141589 BP.
 DE Human pulmonary and inflammatory target DNA #306.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 11; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 610
 ID AAA35005 standard; DNA; 141589 BP.
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2694.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 9.9%; Score 225.4; DB 3; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 611
 ID AAA35030 standard; DNA; 141589 BP.
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2719.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 9.9%; Score 225.4; DB 3; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 612
 ID AAF21152 standard; DNA; 141589 BP.
 DE Human low adenosine anticense oligonucleotide related sequence #2719.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match 9.9%; Score 225.4; DB 3; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 613
 ID AAF20913 standard; DNA; 141589 BP.
 DE Human ELAM-1 polynucleotide fragment #2480.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match 9.9%; Score 225.4; DB 3; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 614
 ID AAF21127 standard; DNA; 141589 BP.
 DE Human low adenosine anticense oligonucleotide related sequence #2694.
 PN WO200062736-A2.

PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match 9.9%; Score 225.4; DB 3; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 615
 ID ABZ96821 standard; DNA; 141589 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 616
 ID ABZ96607 standard; DNA; 141589 BP.
 DE Human ELAM-1 nucleic acid.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 617
 ID ABZ96846 standard; DNA; 141589 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 618
 ID ABD20670 standard; DNA; 141589 BP.
 DE Human pulmonary and inflammatory target DNA #281.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 11; Length 141589;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 619
 ID ABD19162 standard; DNA; 141601 BP.
 DE Human ELAM-1 DNA fragment #2.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 11; Length 141601;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 620
 ID AAF21442 standard; DNA; 146981 BP.
 DE Human ELAM-1 polynucleotide fragment #3009.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match 9.9%; Score 225.4; DB 3; Length 146981;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 621
 ID ABZ97136 standard; DNA; 146982 BP.
 DE Human ELAM-1 antisense fragment no.1738.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 146982;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 622
 ID ABD19160 standard; DNA; 146984 BP.
 DE Human ELAM-1 DNA fragment 1738.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 11; Length 146984;
 Best Local Similarity 82.7%; Pred. No. 4.8e-46;
 RESULT 623
 ID ADS36467 standard; DNA; 154799 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1681.

PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 9.9%; Score 225.4; DB 13; Length 154799;
 Best Local Similarity 82.4%; Pred. No. 5e-46;
 RESULT 624
 ID AEF92730 standard; DNA; 163218 BP.
 DE Human chromosome 17 sequence, clone hRPK.318_A_15.
 PN WO2006020269-A2.
 PD 23-FEB-2006.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 9.9%; Score 225.4; DB 15; Length 163218;
 Best Local Similarity 81.3%; Pred. No. 5.1e-46;
 RESULT 625
 ID ADL13501 standard; DNA; 167932 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #33.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 167932;
 Best Local Similarity 85.9%; Pred. No. 5.1e-46;
 RESULT 626
 ID ADL13752 standard; DNA; 190000 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #284.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 190000;
 Best Local Similarity 81.3%; Pred. No. 5.4e-46;
 RESULT 627
 ID AAF21437 standard; DNA; 209273 BP.
 DE Human factor-related antisense polynucleotide #3004.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match 9.9%; Score 225.4; DB 3; Length 209273;
 Best Local Similarity 82.7%; Pred. No. 5.7e-46;
 RESULT 628
 ID ABZ97131 standard; DNA; 209274 BP.
 DE Human enzyme-related antisense polynucleotide.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 9.9%; Score 225.4; DB 10; Length 209274;
 Best Local Similarity 82.7%; Pred. No. 5.7e-46;
 RESULT 629
 ID AAK67291 standard; DNA; 681 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22103.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 225.2; DB 4; Length 681;
 Best Local Similarity 81.9%; Pred. No. 4.9e-47;
 RESULT 630
 ID AAI96126 standard; cDNA; 811 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2201.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match 9.9%; Score 225.2; DB 4; Length 811;
 Best Local Similarity 84.2%; Pred. No. 5.3e-47;
 RESULT 631
 ID ABT42918 standard; DNA; 811 BP.
 DE Human neuroblastoma-related DNA sequence, SEQ ID NO:199.
 PN WO2002103017-A1.
 PD 27-DEC-2002.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match 9.9%; Score 225.2; DB 8; Length 811;
 Best Local Similarity 84.2%; Pred. No. 5.3e-47;
 RESULT 632

ID ADK67850 standard; cDNA; 1370 BP.
DE Phosphoadenosine-phosphosulfate synthetase, modifier of AXIN pathway.
PN WO2004013309-A2.
PD 12-FEB-2004.
PA (EXEL-) EXELIXIS INC. 9.9%; Score 225.2; DB 12; Length 1370;
Query Match 86.7%; Pred. No. 6.7e-47;
Best Local Similarity 86.7%; Pred. No. 6.7e-47;
RESULT 633
ID AAL35996 standard; DNA; 1655 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2361.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.2; DB 4; Length 1655;
Best Local Similarity 81.9%; Pred. No. 7.3e-47;
RESULT 634
ID ABX58984 standard; cDNA; 1655 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1328.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 225.2; DB 8; Length 1655;
Best Local Similarity 81.9%; Pred. No. 7.3e-47;
RESULT 635
ID ADJ29734 standard; DNA; 1655 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2361.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.2; DB 12; Length 1655;
Best Local Similarity 81.9%; Pred. No. 7.3e-47;
RESULT 636
ID AEI44902 standard; DNA; 2177 BP.
DE Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 DNA SEQ ID: 1.
PN US7067311-B1.
PD 27-JUN-2006.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 9.9%; Score 225.2; DB 15; Length 2177;
Best Local Similarity 86.7%; Pred. No. 8.2e-47;
RESULT 637
ID AEJ92460 standard; DNA; 2177 BP.
DE Human 3'-phosphoadenosine-5'-phosphosulfate synthetase 1 exon 1 DNA.
PN US2006188973-A1.
PD 24-AUG-2006.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 9.9%; Score 225.2; DB 15; Length 2177;
Best Local Similarity 86.7%; Pred. No. 8.2e-47;
RESULT 638
ID AAH17855 standard; cDNA; 2706 BP.
DE Human cDNA sequence SEQ ID NO:17555.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.9%; Score 225.2; DB 4; Length 2706;
Best Local Similarity 84.2%; Pred. No. 9.1e-47;
RESULT 639
ID ADR07592 standard; cDNA; 3877 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1098.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.9%; Score 225.2; DB 13; Length 3877;
Best Local Similarity 83.0%; Pred. No. 1.1e-46;
RESULT 640
ID AAK74563 standard; DNA; 5283 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29375.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.2; DB 4; Length 5283;
Best Local Similarity 85.4%; Pred. No. 1.2e-46;

RESULT 641
ID AAS42014 standard; DNA; 6437 BP.
DE Genomic sequence #330 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.2; DB 4; Length 6437;
Best Local Similarity 80.9%; Pred. No. 1.3e-46;
RESULT 642
ID AAS42015 standard; DNA; 9742 BP.
DE Genomic sequence #331 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225.2; DB 4; Length 9742;
Best Local Similarity 80.9%; Pred. No. 1.6e-46;
RESULT 643
ID AEB96529 standard; DNA; 20001 BP.
DE Human SULT2B1 gene, SEQ ID 13.
PN JP2005204549-A.
PD 04-AUG-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (KAWA/) KAWADA Y.
Query Match 9.9%; Score 225.2; DB 14; Length 20001;
Best Local Similarity 84.2%; Pred. No. 2.2e-46;
RESULT 644
ID ADZ13548 standard; DNA; 38636 BP.
DE Human cancer-associated genomic DNA #91.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 225.2; DB 14; Length 38636;
Best Local Similarity 75.1%; Pred. No. 3e-46;
RESULT 645
ID ADZ13582 standard; DNA; 73702 BP.
DE Human cancer-associated genomic DNA #94.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.9%; Score 225.2; DB 14; Length 73702;
Best Local Similarity 83.0%; Pred. No. 4e-46;
RESULT 646
ID AHD33145 standard; DNA; 73723 BP.
DE Human cancer-associated (CA) gene HD07-018.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.9%; Score 225.2; DB 13; Length 73723;
Best Local Similarity 83.0%; Pred. No. 4e-46;
RESULT 647
ID AEJ13110 standard; DNA; 73723 BP.
DE Cancer-associated gene sequence - SEQ ID 118.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.9%; Score 225.2; DB 15; Length 73723;
Best Local Similarity 83.0%; Pred. No. 4e-46;
RESULT 648
ID ADC85284 standard; DNA; 92562 BP.
DE Human itk genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225.2; DB 10; Length 92562;
Best Local Similarity 71.0%; Pred. No. 4.4e-46;
RESULT 649
ID ADA02804 standard; DNA; 92563 BP.
DE Human ITK carcinoma associated gene, SEQ ID NO:1322.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225.2; DB 9; Length 92563;

Best Local Similarity 71.0%; Pred. No. 4.4e-46;
RESULT 650
ID ADB72542 standard; DNA; 92563 BP.
DE Human ITK gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225.2; DB 10; Length 92563;
Best Local Similarity 71.0%; Pred. No. 4.4e-46;
RESULT 651
ID ADM74399 standard; DNA; 92563 BP.
DE Human carcinoma associated (CA) nucleic acid #34.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.9%; Score 225.2; DB 12; Length 92563;
Best Local Similarity 71.0%; Pred. No. 4.4e-46;
RESULT 652
Query Match 9.9%; Score 225.2; DB 6; Length 110000;
Best Local Similarity 82.3%; Pred. No. 4.8e-46;
RESULT 653
Query Match 9.9%; Score 225.2; DB 6; Length 110000;
Best Local Similarity 82.3%; Pred. No. 4.8e-46;
RESULT 654
Query Match 9.9%; Score 225.2; DB 8; Length 110000;
Best Local Similarity 82.3%; Pred. No. 4.8e-46;
RESULT 655
Query Match 9.9%; Score 225.2; DB 10; Length 110000;
Best Local Similarity 82.3%; Pred. No. 4.8e-46;
RESULT 656
Query Match 9.9%; Score 225.2; DB 12; Length 110000;
Best Local Similarity 81.9%; Pred. No. 4.8e-46;
RESULT 657
ID ADC89520 standard; DNA; 139257 BP.
DE Human COREST genomic DNA #SEQ ID 11.
PN WO2003011890-A1.
PD 13-FEB-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.9%; Score 225.2; DB 10; Length 139257;
Best Local Similarity 83.0%; Pred. No. 5.3e-46;
RESULT 658
ID AAL35995 standard; DNA; 1647 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2360.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225; DB 4; Length 1647;
Best Local Similarity 81.5%; Pred. No. 8.1e-47;
RESULT 659
ID ABX58983 standard; cDNA; 1647 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1327.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 225; DB 8; Length 1647;
Best Local Similarity 81.5%; Pred. No. 8.1e-47;
RESULT 660
ID ADJ29733 standard; DNA; 1647 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2360.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225; DB 12; Length 1647;
Best Local Similarity 81.5%; Pred. No. 8.1e-47;
RESULT 661
ID AAK70585 standard; DNA; 5086 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25397.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.9%; Score 225; DB 4; Length 5086;
Best Local Similarity 78.6%; Pred. No. 1.4e-46;
RESULT 662
ID AAK70584 standard; DNA; 5093 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25396.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225; DB 4; Length 5093;
Best Local Similarity 78.6%; Pred. No. 1.4e-46;
RESULT 663
ID AAK70338 standard; DNA; 9481 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25150.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225; DB 4; Length 9481;
Best Local Similarity 82.8%; Pred. No. 1.8e-46;
RESULT 664
ID ABD32562 standard; DNA; 21478 BP.
DE Human cancer-associated genomic DNA HD14-034.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.9%; Score 225; DB 13; Length 21478;
Best Local Similarity 81.3%; Pred. No. 2.6e-46;
RESULT 665
ID ADA02702 standard; DNA; 21666 BP.
DE Human Nuprl carcinoma associated gene, SEQ ID NO:1220.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225; DB 9; Length 21666;
Best Local Similarity 83.7%; Pred. No. 2.6e-46;
RESULT 666
ID ADB72440 standard; DNA; 21666 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225; DB 10; Length 21666;
Best Local Similarity 83.7%; Pred. No. 2.6e-46;
RESULT 667
ID ADE95950 standard; DNA; 21666 BP.
DE Human hCG1745228 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.9%; Score 225; DB 10; Length 21666;
Best Local Similarity 83.7%; Pred. No. 2.6e-46;
RESULT 668
ID AEK60221 standard; DNA; 21666 BP.
DE Human NUPRI genomic sequence, SEQ ID NO: 208.
PN US2006204982-A1.
PD 14-SEP-2006.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.9%; Score 225; DB 15; Length 21666;
Best Local Similarity 83.7%; Pred. No. 2.6e-46;
RESULT 669
ID AAK86932 standard; DNA; 22465 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41744.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 225; DB 4; Length 22465;
Best Local Similarity 82.6%; Pred. No. 2.6e-46;
RESULT 670
ID ACN45138 standard; DNA; 23694 BP.
DE Human genomic sequence hCG17175.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match
 Best Local Similarity 9.9%; Score 225; DB 11; Length 23694;
 RESULT 671
 ID ABD33540 standard; DNA; 25428 BP.
 DE Human cancer-associated (CA) gene HD07-107.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 13; Length 25428;
 RESULT 672
 ID AEJ13722 standard; DNA; 25428 BP.
 DE Cancer-associated gene sequence - SEQ ID 730.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 15; Length 25428;
 RESULT 673
 ID ABD33544 standard; DNA; 25899 BP.
 DE Human cancer-associated (CA) gene HD07-108.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 13; Length 25899;
 RESULT 674
 ID AEJ13728 standard; DNA; 25899 BP.
 DE Cancer-associated gene sequence - SEQ ID 736.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 15; Length 25899;
 RESULT 675
 ID ADS36474 standard; DNA; 40947 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 13; Length 40947;
 RESULT 676
 ID ABD33453 standard; DNA; 51837 BP.
 DE Human cancer-associated (CA) gene HD07-086.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 13; Length 51837;
 RESULT 677
 ID AEJ13590 standard; DNA; 51837 BP.
 DE Cancer-associated gene sequence - SEQ ID 598.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 15; Length 51837;
 RESULT 678
 ID ABD32769 standard; DNA; 100608 BP.
 DE Human cancer-associated genomic DNA HD16-031.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 13; Length 100608;
 RESULT 679
 ID AED89397 standard; DNA; 150481 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 37.
 PN WO2005106044-A1.

PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 14; Length 150481;
 RESULT 680
 ID ADQ20461 standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 12; Length 166181;
 RESULT 681
 ID ADQ18633 standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 12; Length 166181;
 RESULT 682
 ID AED89398 standard; DNA; 171162 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 38.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 14; Length 171162;
 RESULT 683
 ID ACN44626 standard; DNA; 175077 BP.
 DE Human genomic sequence hCG19724.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match
 Best Local Similarity 9.9%; Score 225; DB 11; Length 175077;
 RESULT 684
 ID ADQ22654 standard; DNA; 3820 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5474.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 9.8%; Score 224.8; DB 12; Length 3820;
 RESULT 685
 ID ADP13403 standard; DNA; 16689 BP.
 DE Renal cell carcinoma differentially expressed gene #139.
 PN WO2004048933-A2.
 PD 10-JUN-2004.
 PA (AMHP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BURC/) BURCZYNSKI M E.
 PA (TREP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J A.
 PA (SLON/) SLONI D K.
 Query Match
 Best Local Similarity 9.8%; Score 224.8; DB 12; Length 16689;
 RESULT 686
 ID ABA36261 standard; DNA; 16689 BP.
 DE Human nucleic acid sequence #193.
 PN WO2005054507-A2.
 PD 16-JUN-2005.
 PA (UYSH-) UNIV SHEFFIELD.
 Query Match
 Best Local Similarity 9.8%; Score 224.8; DB 14; Length 16689;
 RESULT 687
 ID AEG93507 standard; cDNA; 16689 BP.
 DE Human tumor cell cDNA SEQ ID NO:1003.
 PN WO2006036025-A1.
 PD 06-APR-2006.
 PA (EISA) EISAI CO LTD.
 Query Match
 Best Local Similarity 9.8%; Score 224.8; DB 15; Length 16689;

Best Local Similarity 85.6%; Pred. No. 2.6e-46;
 RESULT 688
 ID ADO43240 standard; DNA; 37620 BP.
 DE Vacuolar protein sorting factor Vps4B gene, involved in HIV-1 budding.
 PN WO2004039311-A2.
 PD 13-MAY-2004.
 PA (UTAH) UNIV UTAH RES FOUND.
 Query Match 9.8%; Score 224.8; DB 12; Length 37620;
 Best Local Similarity 85.8%; Pred. No. 3.7e-46;
 RESULT 689
 ID AEA61175 standard; DNA; 53779 BP.
 DE Human ENT5D5 gene genomic sequence SEQ ID NO:85.
 PN US2005130172-A1.
 PD 16-JUN-2005.
 PA (FARB) BAYER CORP.
 Query Match 9.8%; Score 224.8; DB 14; Length 53779;
 Best Local Similarity 81.1%; Pred. No. 4.4e-46;
 RESULT 690
 ID ADL13866 standard; DNA; 79597 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #398.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.8%; Score 224.8; DB 10; Length 79597;
 Best Local Similarity 85.8%; Pred. No. 5.2e-46;
 RESULT 691
 ID ABX14763 standard; DNA; 88191 BP.
 DE Genomic DNA encoding novel human ras-like protein.
 PN US2002132291-A1.
 PD 19-SEP-2002.
 PA (YEJU/) YE J.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 9.8%; Score 224.8; DB 8; Length 88191;
 Best Local Similarity 81.1%; Pred. No. 5.5e-46;
 RESULT 692
 ID AEG303293 standard; DNA; 94000 BP.
 DE Human genomic nucleotide region of an ADCYAP1R1 region.
 PN WO2006022638-A1.
 PD 02-MAR-2006.
 PA (SEQU-) SEQUENOM INC.
 Query Match 9.8%; Score 224.8; DB 15; Length 94000;
 Best Local Similarity 84.4%; Pred. No. 5.6e-46;
 RESULT 693
 ID ABD33009 standard; DNA; 99918 BP.
 DE Human cancer-associated genomic DNA HD21-032.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.8%; Score 224.8; DB 13; Length 99918;
 Best Local Similarity 84.4%; Pred. No. 5.8e-46;
 RESULT 694
 ID ADQ17641 standard; DNA; 114771 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 458.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.8%; Score 224.8; DB 12; Length 114771;
 Best Local Similarity 71.4%; Pred. No. 6.2e-46;
 RESULT 695
 ID AAX90201 standard; DNA; 119950 BP.
 DE Human ves1 gene.
 PN WO9935290-A1.
 PD 15-JUL-1999.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 9.8%; Score 224.8; DB 2; Length 119950;
 Best Local Similarity 81.6%; Pred. No. 6.3e-46;
 RESULT 696
 ID AEB71426 standard; cDNA; 177556 BP.
 DE Human sGC alpha1 and beta1 subunit containing cDNA clone SEQ ID NO:6.
 PN US2005176043-A1.
 PD 11-AUG-2005.

PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match 9.8%; Score 224.8; DB 14; Length 177556;
 Best Local Similarity 83.2%; Pred. No. 7.5e-46;
 RESULT 697
 ID ACD28257 standard; DNA; 177563 BP.
 DE Mouse soluble guanylyl cyclase sGC associated DNA #4.
 PN US2003096240-A1.
 PD 22-MAY-2003.
 PA (MURA/) MURAD F.
 PA (SHAR/) SHARINA I G.
 PA (KRUM/) KRUMENACKER J S.
 PA (MART/) MARTIN E.
 Query Match 9.8%; Score 224.8; DB 9; Length 177563;
 Best Local Similarity 83.2%; Pred. No. 7.5e-46;
 RESULT 698
 ID AEN64959 standard; cDNA; 525 BP.
 DE Human cancer related polynucleotide SEQ ID NO 4926.
 PN WO200214500-A2.
 PD 21-FEB-2002.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.8%; Score 224.6; DB 6; Length 525;
 Best Local Similarity 86.4%; Pred. No. 6.2e-47;
 RESULT 699
 ID AED34711 standard; DNA; 1920 BP.
 DE ABL1 probe SEQ ID NO 47.
 PN WO2005094291-A2.
 PD 13-OCT-2005.
 PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
 Query Match 9.8%; Score 224.6; DB 14; Length 1920;
 Best Local Similarity 83.8%; Pred. No. 1.1e-46;
 RESULT 700
 ID ABK88737 standard; cDNA; 3053 BP.
 DE cDNA encoding methionyl tRNA synthetase 35.09.
 PN CN1341727-A.
 PD 27-MAR-2002.
 PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
 Query Match 9.8%; Score 224.6; DB 6; Length 3053;
 Best Local Similarity 81.7%; Pred. No. 1.4e-46;
 RESULT 701
 ID ADR07960 standard; cDNA; 4056 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1466.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.8%; Score 224.6; DB 13; Length 4056;
 Best Local Similarity 83.9%; Pred. No. 1.5e-46;
 RESULT 702
 ID ABA19375 standard; DNA; 25525 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11706.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 5; Length 25525;
 Best Local Similarity 83.9%; Pred. No. 3.5e-46;
 RESULT 703
 ID AAK89019 standard; DNA; 32204 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 2595.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 4; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 704
 ID AAK91533 standard; DNA; 32204 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 5109.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 4; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 705
 ID AAI57790 standard; DNA; 32204 BP.

DE Human colorectal cancer antigen coding sequence SEQ ID NO: 327.
 PN W0200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 4; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 706
 ID AAS39620 standard; DNA; 32204 BP.
 DE Genomic sequence #39 encoding human colon associated polypeptide.
 PN W0200155302-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 5; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 707
 ID ABS9967 standard; DNA; 32204 BP.
 DE Genomic DNA #171 encoding human colorectal cancer related protein.
 PN US2002119919-A1.
 PD 29-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.8%; Score 224.6; DB 6; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 708
 ID ADB32580 standard; DNA; 32204 BP.
 DE Human novel colon related polypeptide DNA SEQ ID NO 517.
 PN US2003050231-A1.
 PD 13-MAR-2003.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.8%; Score 224.6; DB 9; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 709
 ID ADB93120 standard; DNA; 32204 BP.
 DE Human colorectal cancer related polypeptide DNA #171.
 PN US2003054420-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 10; Length 32204;
 Best Local Similarity 82.8%; Pred. No. 3.9e-46;
 RESULT 710
 ID AAK71358 standard; DNA; 37314 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26170.
 PN W0200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.6; DB 4; Length 37314;
 Best Local Similarity 82.8%; Pred. No. 4.2e-46;
 RESULT 711
 ID ABL64158 standard; DNA; 84539 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2495.
 PN W0200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 9.8%; Score 224.6; DB 6; Length 84539;
 Best Local Similarity 83.8%; Pred. No. 6.1e-46;
 RESULT 712
 ID ADL13479 standard; DNA; 84539 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #11.
 PN W02003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.8%; Score 224.6; DB 10; Length 84539;
 Best Local Similarity 83.8%; Pred. No. 6.1e-46;
 RESULT 713
 ID ASF73876 standard; DNA; 84539 BP.
 DE Human protein tyrosine kinase ABL-1 gene.
 PN W02006015084-A2.
 PD 09-FEB-2006.
 PA (INVI-) INVITROGEN CORP.
 Query Match 9.8%; Score 224.6; DB 15; Length 84539;

Best Local Similarity 83.8%; Pred. No. 6.1e-46;
 RESULT 714
 ID AEF74626 standard; DNA; 84539 BP.
 DE Human polynucleotide #140.
 PN W02006013561-A2.
 PD 03-FEB-2006.
 PA (YISS-) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 9.8%; Score 224.6; DB 15; Length 84539;
 Best Local Similarity 83.8%; Pred. No. 6.1e-46;
 RESULT 715
 ID ACN44154 standard; DNA; 101209 BP.
 DE Human genomic sequence hCG28567.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 224.6; DB 11; Length 101209;
 Best Local Similarity 81.8%; Pred. No. 6.6e-46;
 RESULT 716
 Query Match 9.8%; Score 224.6; DB 11; Length 110000;
 Best Local Similarity 83.9%; Pred. No. 6.8e-46;
 RESULT 717
 Query Match 9.8%; Score 224.6; DB 14; Length 110000;
 Best Local Similarity 83.8%; Pred. No. 6.8e-46;
 RESULT 718
 ID ACN44262 standard; DNA; 168821 BP.
 DE Human genomic sequence hCG18035.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 224.6; DB 11; Length 168821;
 Best Local Similarity 82.9%; Pred. No. 8.3e-46;
 RESULT 719
 ID AAD62832 standard; DNA; 180216 BP.
 DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.
 PN US2003170683-A1.
 PD 11-SEP-2003.
 PA (LEDE/) LEIDER P.
 PA (LEAD/) LEADER B.
 Query Match 9.8%; Score 224.6; DB 10; Length 180216;
 Best Local Similarity 80.6%; Pred. No. 8.5e-46;
 RESULT 720
 ID AAL54074 standard; DNA; 197997 BP.
 DE Human transporter protein encoding genomic DNA.
 Query Match 9.8%; Score 224.6; DB 10; Length 197997;
 Best Local Similarity 76.1%; Pred. No. 8.9e-46;
 RESULT 721
 ID ADL08109 standard; DNA; 247682 BP.
 DE Human gene associated with low HDL-C AT3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VTI-) VITIVITY INC.
 Query Match 9.8%; Score 224.6; DB 12; Length 247682;
 Best Local Similarity 84.0%; Pred. No. 9.8e-46;
 RESULT 722
 ID ADQ97433 standard; DNA; 295772 BP.
 DE Human cancer associated sequence HD08-047, SEQ ID 410.
 PN W02004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.8%; Score 224.6; DB 12; Length 295772;
 Best Local Similarity 87.7%; Pred. No. 1.1e-45;
 RESULT 723
 ID AAH09299 standard; cDNA; 572 BP.
 DE Human cDNA clone (3'-primer) SEQ ID NO:6134.
 PN EPI074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 9.8%; Score 224.4; DB 4; Length 572;
 Best Local Similarity 82.3%; Pred. No. 7.2e-47;
 RESULT 724
 ID AAH15337 standard; cDNA; 1380 BP.
 DE Human cDNA sequence SEQ ID NO:13505.

PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 9.8%; Score 224.4; DB 4; Length 1380;
 Best Local Similarity 82.3%; Pred. No. 1.1e-46;
 RESULT 725
 ID AAK68489 standard; DNA; 1958 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23301.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 4; Length 1958;
 Best Local Similarity 84.6%; Pred. No. 1.3e-46;
 RESULT 726
 ID ADJ94116 standard; DNA; 3577 BP.
 DE DLBCL tumour-associated antigen OX-TES-2 DNA.
 PN WO2003082916-A2.
 PD 09-OCT-2003.
 PA (ISIS-) ISIS INNOVATION LTD.
 Query Match 9.8%; Score 224.4; DB 10; Length 3577;
 Best Local Similarity 82.3%; Pred. No. 1.6e-46;
 RESULT 727
 ID AAK81191 standard; DNA; 5987 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36003.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 4; Length 5987;
 Best Local Similarity 85.9%; Pred. No. 2.1e-46;
 RESULT 728
 ID AEE83905 standard; cDNA; 7224 BP.
 DE Human cDNA differentially expressed in asthma, SEQ ID NO:313.
 PN WO2005118403-A2.
 PD 15-DEC-2005.
 PA (LINK-) LINKAGENE LTD.
 Query Match 9.8%; Score 224.4; DB 15; Length 7224;
 Best Local Similarity 71.5%; Pred. No. 2.3e-46;
 RESULT 729
 ID AAS34684 standard; DNA; 9054 BP.
 DE Human DNA for a novel foetal antigen, SEQ ID NO 2108.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 5; Length 9054;
 Best Local Similarity 83.3%; Pred. No. 2.5e-46;
 RESULT 730
 ID AAI93973 standard; DNA; 9439 BP.
 DE Human excretory related polynucleotide SEQ ID NO 1137.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 4; Length 9439;
 Best Local Similarity 82.3%; Pred. No. 2.5e-46;
 RESULT 731
 ID AAL35859 standard; DNA; 9439 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2224.
 PN WO200155317-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 4; Length 9439;
 Best Local Similarity 82.3%; Pred. No. 2.5e-46;
 RESULT 732
 ID AAI63723 standard; DNA; 9439 BP.
 DE Human kidney related polynucleotide SEQ ID NO 1038.
 PN WO200155323-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 5; Length 9439;
 Best Local Similarity 82.3%; Pred. No. 2.5e-46;
 RESULT 733
 ID ABX58847 standard; cDNA; 9439 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1191.
 PN US2002147140-A1.

PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.8%; Score 224.4; DB 8; Length 9439;
 Best Local Similarity 82.3%; Pred. No. 2.5e-46;
 RESULT 734
 ID ADJ29597 standard; DNA; 9439 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2224.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 12; Length 9439;
 Best Local Similarity 82.3%; Pred. No. 2.5e-46;
 RESULT 735
 ID ABA20516 standard; DNA; 14006 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 12847.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 224.4; DB 5; Length 14006;
 Best Local Similarity 83.4%; Pred. No. 3e-46;
 RESULT 736
 ID ADA2966 standard; DNA; 31842 BP.
 DE Human LCK carcinoma associated gene, SEQ ID NO:1484.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 224.4; DB 9; Length 31842;
 Best Local Similarity 82.3%; Pred. No. 4.4e-46;
 RESULT 737
 ID ADB72704 standard; DNA; 31842 BP.
 DE Human LCK gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 224.4; DB 10; Length 31842;
 Best Local Similarity 82.3%; Pred. No. 4.4e-46;
 RESULT 738
 ID ADC85446 standard; DNA; 31842 BP.
 DE Human Lck genomic sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 224.4; DB 10; Length 31842;
 Best Local Similarity 82.3%; Pred. No. 4.4e-46;
 RESULT 739
 ID ADM74561 standard; DNA; 31842 BP.
 DE Human carcinoma associated (CA) nucleic acid #115.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORE/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Query Match 9.8%; Score 224.4; DB 12; Length 31842;
 Best Local Similarity 82.3%; Pred. No. 4.4e-46;
 RESULT 740
 ID AEF80111 standard; DNA; 36911 BP.
 DE Cancer-associated polypeptide genomic DNA sequence hd22-022 SEQ ID NO:6.
 PN US2006024677-A1.
 PD 02-FEB-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 PA (LAIA/) LAI A.
 PA (TSEC/) TSE C.
 PA (FATT/) FATTAEY A.
 Query Match 9.8%; Score 224.4; DB 15; Length 36911;
 Best Local Similarity 85.9%; Pred. No. 4.7e-46;
 RESULT 741
 ID ADA02840 standard; DNA; 47573 BP.
 DE Human MAP3K8 carcinoma associated gene, SEQ ID NO:1358.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 9.8%; Score 224.4; DB 9; Length 47573;
Best Local Similarity 84.6%; Pred. No. 5.3e-46;
RESULT 742
ID ADB72578 standard; DNA; 47573 BP.
DE Human MAP3K8 gene.
PN WO2003008593-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.4; DB 10; Length 47573;
Best Local Similarity 84.6%; Pred. No. 5.3e-46;
RESULT 743
ID ADC85319 standard; DNA; 47573 BP.
DE Mouse Map3K8 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.4; DB 10; Length 47573;
Best Local Similarity 84.6%; Pred. No. 5.3e-46;
RESULT 744
ID ADM74435 standard; DNA; 47573 BP.
DE Human carcinoma associated (CA) nucleic acid #52.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.8%; Score 224.4; DB 12; Length 47573;
Best Local Similarity 84.6%; Pred. No. 5.3e-46;
RESULT 745
ID ABE04835 standard; DNA; 70803 BP.
DE Cancer-associated gene SEQ ID NO:153.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.8%; Score 224.4; DB 14; Length 70803;
Best Local Similarity 85.9%; Pred. No. 6.3e-46;
RESULT 746
ID ACN43958 standard; DNA; 75839 BP.
DE Human genomic sequence hCG1640505.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.4; DB 11; Length 75839;
Best Local Similarity 82.3%; Pred. No. 6.5e-46;
RESULT 747
ID ABE32806 standard; DNA; 653458 BP.
DE Human cancer-associated genomic DNA HD16-059.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224.4; DB 13; Length 110000;
Best Local Similarity 84.6%; Pred. No. 7.7e-46;
RESULT 748
ID ADL13931 standard; DNA; 180385 BP.
DE Osteoarthritis-associated polymorphic nucleotide #463.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.8%; Score 224.4; DB 10; Length 180385;
Best Local Similarity 80.4%; Pred. No. 9.6e-46;
RESULT 749
ID ADL13850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.8%; Score 224.4; DB 10; Length 180550;
Best Local Similarity 79.3%; Pred. No. 9.6e-46;
RESULT 750
ID ADQ20606 standard; DNA; 195917 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 9.8%; Score 224.4; DB 12; Length 195917;
Best Local Similarity 82.3%; Pred. No. 9.9e-46;
RESULT 751
ID AEE05008 standard; DNA; 246386 BP.
DE Cancer-associated gene SEQ ID NO:326.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.8%; Score 224.4; DB 14; Length 246386;
Best Local Similarity 84.6%; Pred. No. 1.1e-45;
RESULT 752
ID AAK78073 standard; DNA; 1071 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32885.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 1071;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 753
ID AAK78077 standard; DNA; 1071 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32889.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 1071;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 754
ID AAK78075 standard; DNA; 1071 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32887.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 1071;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 755
ID ACN37326 standard; cDNA; 1810 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323793, SEQ ID NO:133.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 224.2; DB 13; Length 1810;
Best Local Similarity 86.6%; Pred. No. 1.4e-46;
RESULT 756
ID AAS36599 standard; DNA; 2687 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2099.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 2687;
Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 757
ID AAS36600 standard; DNA; 2687 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2100.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 2687;
Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 758
ID ADE47293 standard; DNA; 2687 BP.
DE Human cardiovascular system related genomic DNA #859.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 10; Length 2687;
Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 759
ID ADE47294 standard; DNA; 2687 BP.
DE Human cardiovascular system related genomic DNA #860.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 10; Length 2687;

Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 760
ID ADJ08712 standard; DNA; 2687 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2100.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 13; Length 2687;
Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 761
ID ADJ08711 standard; DNA; 2687 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2099.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 13; Length 2687;
Best Local Similarity 83.0%; Pred. No. 1.6e-46;
RESULT 762
ID ADA53076 standard; cDNA; 2850 BP.
DE Human coding sequence, SEQ ID 644.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.8%; Score 224.2; DB 10; Length 2850;
Best Local Similarity 85.3%; Pred. No. 1.7e-46;
RESULT 763
ID ABZ57227 standard; cDNA; 2981 BP.
DE Human ATP dependent serine protein hydrolase 47.19-encoding cDNA.
PN CN1364900-A.
PD 21-AUG-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 9.8%; Score 224.2; DB 8; Length 2981;
Best Local Similarity 85.3%; Pred. No. 1.7e-46;
RESULT 764
ID RAD46552 standard; DNA; 29844 BP.
DE Human cMOAT Gene #2.
PN WO200272888-A2.
PD 19-SEP-2002.
PA (ASTR-) ASTRAZENECA AB.
Query Match 9.8%; Score 224.2; DB 6; Length 29844;
Best Local Similarity 83.3%; Pred. No. 4.8e-46;
RESULT 765
ID AAK89020 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2596.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 766
ID AAK91534 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5110.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 767
ID AAI57791 standard; DNA; 32152 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 328.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 768
ID AAS39621 standard; DNA; 32152 BP.
DE Genomic sequence #40 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.8%; Score 224.2; DB 5; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 769
ID ABS99968 standard; DNA; 32152 BP.
DE Genomic DNA #172 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.8%; Score 224.2; DB 6; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 770
ID ADB32581 standard; DNA; 32152 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 518.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.8%; Score 224.2; DB 9; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 771
ID ADB93121 standard; DNA; 32152 BP.
DE Human colorectal cancer related polypeptide DNA #172.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 10; Length 32152;
Best Local Similarity 81.9%; Pred. No. 5e-46;
RESULT 772
ID AAK67282 standard; DNA; 33147 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 33147;
Best Local Similarity 80.8%; Pred. No. 5e-46;
RESULT 773
ID AAK66362 standard; DNA; 36933 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21174.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224.2; DB 4; Length 36933;
Best Local Similarity 81.9%; Pred. No. 5.3e-46;
RESULT 774
ID ADQ97343 standard; DNA; 61739 BP.
DE Human cancer associated sequence HD08-035, SEQ ID 320.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224.2; DB 12; Length 61739;
Best Local Similarity 84.2%; Pred. No. 6.7e-46;
RESULT 775
ID ADA03032 standard; DNA; 99957 BP.
DE Human MCG10516 homologue carcinoma associated gene, SEQ ID NO:1550.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.2; DB 9; Length 99957;
Best Local Similarity 78.9%; Pred. No. 8.3e-46;
RESULT 776
ID ADB72770 standard; DNA; 99957 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.2; DB 10; Length 99957;
Best Local Similarity 78.9%; Pred. No. 8.3e-46;
RESULT 777
ID ADC85512 standard; DNA; 99957 BP.
DE Human genomic sequence.

PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224.2; DB 10; Length 99957;
Best Local Similarity 78.9%; Pred. No. 8.3e-46;
RESULT 778
ID ADM74627 standard; DNA; 99957 BP.
DE Human carcinoma associated (CA) nucleic acid #148.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.8%; Score 224.2; DB 12; Length 99957;
Best Local Similarity 78.9%; Pred. No. 8.3e-46;
RESULT 779
ID AEO03503 standard; DNA; 100097 BP.
DE Acute myelogenous leukemia prognosis related DNA sequence SEQ ID NO: 165.
PN JP2005333987-A.
PD 08-DEC-2005.
PA (VERI-) VERIDEX LLC.
Query Match 9.8%; Score 224.2; DB 15; Length 100097;
Best Local Similarity 74.5%; Pred. No. 8.3e-46;
RESULT 780
ID AEO03502 standard; DNA; 100097 BP.
DE Acute myelogenous leukemia prognosis related DNA sequence SEQ ID NO: 164.
PN JP2005333987-A.
PD 08-DEC-2005.
PA (VERI-) VERIDEX LLC.
Query Match 9.8%; Score 224.2; DB 15; Length 100097;
Best Local Similarity 74.5%; Pred. No. 8.3e-46;
RESULT 781
ID AEG70729 standard; cDNA; 100097 BP.
DE Human p53 mutational status predicting gene SEQ ID NO: 203.
PN US2006074565-A1.
PD 06-APR-2006.
PA (MILL/) MILLER L D.
PA (GEOR/) GEORGE J.
PA (VEGA/) VEGA V B.
Query Match 9.8%; Score 224.2; DB 15; Length 100097;
Best Local Similarity 74.5%; Pred. No. 8.3e-46;
RESULT 782
ID ABD33179 standard; DNA; 100445 BP.
DE Human cancer-associated (CA) gene HD07-026.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224.2; DB 13; Length 100445;
Best Local Similarity 78.0%; Pred. No. 8.3e-46;
RESULT 783
ID AEJ13162 standard; DNA; 100445 BP.
DE Cancer-associated gene sequence - SEQ ID 170.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.8%; Score 224.2; DB 15; Length 100445;
Best Local Similarity 78.0%; Pred. No. 8.3e-46;
RESULT 784
ID ADQ17729 standard; DNA; 143239 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 546.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.8%; Score 224.2; DB 12; Length 143239;
Best Local Similarity 83.0%; Pred. No. 9.7e-46;
RESULT 785
ID ABL64403 standard; DNA; 167343 BP.
DE Stomach cancer related gene sequence SEQ ID NO: 2740.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.8%; Score 224.2; DB 6; Length 167343;
Best Local Similarity 83.0%; Pred. No. 1e-45;

RESULT 786
ID ABL67239 standard; DNA; 167343 BP.
DE Thyroid cancer related gene sequence SEQ ID NO: 5576.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.8%; Score 224.2; DB 6; Length 167343;
Best Local Similarity 83.0%; Pred. No. 1e-45;
RESULT 787
ID AD209671 standard; DNA; 224931 BP.
DE Human breast cancer marker ZAP3 DNA.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 9.8%; Score 224.2; DB 14; Length 224931;
Best Local Similarity 85.3%; Pred. No. 1.2e-45;
RESULT 788
ID AED76155 standard; DNA; 261108 BP.
DE Human CA genomic DNA sequence-ID HD25-006.
PN WO2005104810-A2.
PD 10-NOV-2005.
PA (SAGR-) SAGRES DISCOVERY INC.
PA (LAIJA/) LAI A.
PA (PATI/) PATTAIEY A.
Query Match 9.8%; Score 224.2; DB 14; Length 261108;
Best Local Similarity 83.0%; Pred. No. 1.3e-45;
RESULT 789
ID AED33362 standard; DNA; 301477 BP.
DE Human cancer-associated (CA) gene HD07-066.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224.2; DB 13; Length 301477;
Best Local Similarity 86.6%; Pred. No. 1.4e-45;
RESULT 790
ID AEJ13448 standard; DNA; 301477 BP.
DE Cancer-associated gene sequence - SEQ ID 456.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.8%; Score 224.2; DB 15; Length 301477;
Best Local Similarity 86.6%; Pred. No. 1.4e-45;
RESULT 791
ID AAS32547 standard; DNA; 2425 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 501.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224; DB 4; Length 2425;
Best Local Similarity 87.4%; Pred. No. 1.7e-46;
RESULT 792
ID AAK65546 standard; DNA; 8223 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 20358.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224; DB 4; Length 8223;
Best Local Similarity 79.4%; Pred. No. 3e-46;
RESULT 793
ID ABT16305 standard; DNA; 22400 BP.
DE Zinc finger protein 9 (ZNF9) DNA SEQ ID No 1.
PN WO200292763-A2.
PD 21-NOV-2002.
PA (MINU) UNIV MINNESOTA.
PA (RANU/) RANUM L P W.
PA (DAYJ/) DAY J W.
PA (LIQU/) LIQUORI C.
Query Match 9.8%; Score 224; DB 8; Length 22400;
Best Local Similarity 82.6%; Pred. No. 4.7e-46;
RESULT 794
ID AAK68575 standard; DNA; 32145 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 23387.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224; DB 4; Length 32145;
Best Local Similarity 83.6%; Pred. No. 5.6e-46;
RESULT 795
ID AAK68491 standard; DNA; 32145 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23303.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 224; DB 4; Length 32145;
Best Local Similarity 83.6%; Pred. No. 5.6e-46;
RESULT 796
ID ADQ97173 standard; DNA; 40783 BP.
DE Human cancer associated sequence HD08-010, SEQ ID 149.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224; DB 12; Length 40783;
Best Local Similarity 80.4%; Pred. No. 6.2e-46;
RESULT 797
Query Match 9.8%; Score 224; DB 14; Length 75899;
Best Local Similarity 84.8%; Pred. No. 8.2e-46;
RESULT 798
ID ADT77142 standard; DNA; 93500 BP.
DE Type II diabetes gene SEQ ID NO 19.
PN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM-) DAIMON M.
PA (KATO/) KATO T.
Query Match 9.8%; Score 224; DB 13; Length 93500;
Best Local Similarity 83.6%; Pred. No. 9e-46;
RESULT 799
ID ADC85367 standard; DNA; 96593 BP.
DE Mouse Bim coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224; DB 10; Length 96593;
Best Local Similarity 81.4%; Pred. No. 9.2e-46;
RESULT 800
ID ADA02888 standard; DNA; 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224; DB 9; Length 96594;
Best Local Similarity 81.4%; Pred. No. 9.2e-46;
RESULT 801
ID ADB72626 standard; DNA; 96594 BP.
DE Human BLM gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224; DB 10; Length 96594;
Best Local Similarity 81.4%; Pred. No. 9.2e-46;
RESULT 802
ID ADM74483 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.8%; Score 224; DB 12; Length 96594;
Best Local Similarity 81.4%; Pred. No. 9.2e-46;
RESULT 803
ID ADA03032 standard; DNA; 99957 BP.
DE Human mCG10516 homologue carcinoma associated gene, SEQ ID NO:1550.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 9.8%; Score 224; DB 9; Length 99957;
Best Local Similarity 80.4%; Pred. No. 9.3e-46;
RESULT 804
ID ADB72770 standard; DNA; 99957 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224; DB 10; Length 99957;
Best Local Similarity 80.4%; Pred. No. 9.3e-46;
RESULT 805
ID ADC85512 standard; DNA; 99957 BP.
DE Human genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 224; DB 10; Length 99957;
Best Local Similarity 80.4%; Pred. No. 9.3e-46;
RESULT 806
ID ADM74627 standard; DNA; 99957 BP.
DE Human carcinoma associated (CA) nucleic acid #148.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 9.8%; Score 224; DB 12; Length 99957;
Best Local Similarity 80.4%; Pred. No. 9.3e-46;
RESULT 807
ID ABD33163 standard; DNA; 138837 BP.
DE Human cancer-associated (CA) gene HD07-022.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224; DB 13; Length 138837;
Best Local Similarity 87.4%; Pred. No. 1.1e-45;
RESULT 808
ID AEJ13138 standard; DNA; 138837 BP.
DE Cancer-associated gene sequence - SEQ ID 146.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.8%; Score 224; DB 15; Length 138837;
Best Local Similarity 87.4%; Pred. No. 1.1e-45;
RESULT 809
ID ABD32694 standard; DNA; 252907 BP.
DE Human cancer-associated genomic DNA HD14-012.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 224; DB 13; Length 252907;
Best Local Similarity 86.1%; Pred. No. 1.4e-45;
RESULT 810
ID ACC46432 standard; cDNA; 608 BP.
DE Human dithp membrane transport protein-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.8%; Score 223.8; DB 8; Length 608;
Best Local Similarity 80.0%; Pred. No. 1.1e-46;
RESULT 811
ID AAK65471 standard; DNA; 1275 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20283.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.8; DB 4; Length 1275;
Best Local Similarity 88.2%; Pred. No. 1.5e-46;
RESULT 812
ID ACC50219 standard; cDNA; 2519 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:281.
PN WO2003004989-A2.
PD 16-JAN-2003.

PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 9.8%; Score 223.8; DB 8; Length 2519;
 Best Local Similarity 85.6%; Pred. No. 2e-46;
 RESULT 813
 ID AEB3862 standard; cDNA; 3088 BP.
 DE Human cDNA differentially expressed in asthma, SEQ ID NO:270.
 PN WO2005118403-A2.
 PD 15-DEC-2005.
 PA (LINK-) LINKAGENE LTD.
 Query Match 9.8%; Score 223.8; DB 15; Length 3088;
 Best Local Similarity 85.6%; Pred. No. 2.2e-46;
 RESULT 814
 ID AAI58419 standard; cDNA; 6799 BP.
 DE Human polynucleotide SEQ ID NO 622.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.8%; Score 223.8; DB 4; Length 6799;
 Best Local Similarity 80.4%; Pred. No. 3.1e-46;
 RESULT 815
 ID ADQ98629 standard; cDNA; 6799 BP.
 DE DNA encoding human GPCR-like protein seqid 299.
 PN US6569662-B1.
 PD 27-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.8%; Score 223.8; DB 5; Length 6799;
 Best Local Similarity 80.4%; Pred. No. 3.1e-46;
 RESULT 816
 ID ADB48389 standard; cDNA; 6799 BP.
 DE Novel human cDNA SEQ ID NO 299.
 PN US2003104529-A1.
 PD 05-JUN-2003.
 PA (ZHOU/) ZHOU P.
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V. T.
 PA (DRWA/) DRWANAC R. T.
 Query Match 9.8%; Score 223.8; DB 9; Length 6799;
 Best Local Similarity 80.4%; Pred. No. 3.1e-46;
 RESULT 817
 ID AAF97856 standard; DNA; 10097 BP.
 DE Human neuroblastoma cell line NB-1 ip36 nucleotide sequence SEQ ID NO:70.
 PN WO200116311-A1.
 PD 08-MAR-2001.
 PA (HISM) HISAMITSU PHARM CO LTD.
 PA (CHIB-) CHIBA PREFECTURE.
 Query Match 9.8%; Score 223.8; DB 5; Length 10097;
 Best Local Similarity 84.3%; Pred. No. 3.7e-46;
 RESULT 818
 ID AAL04059 standard; DNA; 10339 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6747.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.8; DB 4; Length 10339;
 Best Local Similarity 84.3%; Pred. No. 3.8e-46;
 RESULT 819
 ID AAS40445 standard; DNA; 10339 BP.
 DE DNA encoding human prostate cancer antigen, Seq ID No 597.
 PN WO200155316-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.8; DB 5; Length 10339;
 Best Local Similarity 84.3%; Pred. No. 3.8e-46;
 RESULT 820
 ID ADJ09651 standard; DNA; 10339 BP.
 DE Human prostate cancer associated gene-related DNA SeqID597.
 PN US2003054373-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.8; DB 11; Length 10339;
 Best Local Similarity 84.3%; Pred. No. 3.8e-46;
 RESULT 821

ID AAK65305 standard; DNA; 22916 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20117.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.8; DB 4; Length 22916;
 Best Local Similarity 82.1%; Pred. No. 5.4e-46;
 RESULT 822
 ID AEE04693 standard; DNA; 55071 BP.
 DE Cancer-associated gene SEQ ID NO:11.
 PN WO2005107396-A2.
 PD 17-NOV-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.8%; Score 223.8; DB 14; Length 65071;
 Best Local Similarity 79.1%; Pred. No. 8.6e-46;
 RESULT 823
 ID ACN44190 standard; DNA; 74183 BP.
 DE Human genomic sequence hCG27588.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 223.8; DB 11; Length 74183;
 Best Local Similarity 85.6%; Pred. No. 9.1e-46;
 RESULT 824
 ID ADN94799 standard; DNA; 91352 BP.
 DE DNA encoding human nidogen.
 PN US2004097451-A1.
 PD 20-MAY-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.8%; Score 223.8; DB 12; Length 91352;
 Best Local Similarity 81.2%; Pred. No. 1e-45;
 RESULT 825
 Query Match 9.8%; Score 223.8; DB 9; Length 110000;
 Best Local Similarity 85.6%; Pred. No. 1.1e-45;
 RESULT 826
 ID ADE11169 standard; DNA; 394191 BP.
 DE Human transporter protein encoding gene SEQ ID NO:1.
 Query Match 9.8%; Score 223.8; DB 10; Length 110000;
 Best Local Similarity 80.0%; Pred. No. 1.1e-45;
 RESULT 827
 Query Match 9.8%; Score 223.8; DB 12; Length 110000;
 Best Local Similarity 85.6%; Pred. No. 1.1e-45;
 RESULT 828
 Query Match 9.8%; Score 223.8; DB 14; Length 110000;
 Best Local Similarity 85.6%; Pred. No. 1.1e-45;
 RESULT 829
 Query Match 9.8%; Score 223.8; DB 14; Length 110000;
 Best Local Similarity 76.4%; Pred. No. 1.1e-45;
 RESULT 830
 ID ACN44586 standard; DNA; 118931 BP.
 DE Human genomic sequence hCG30014.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 223.8; DB 11; Length 118931;
 Best Local Similarity 82.1%; Pred. No. 1.1e-45;
 RESULT 831
 ID AAC66548 standard; DNA; 121162 BP.
 DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
 PN WO200063375-A1.
 PD 26-OCT-2000.
 PA (GEST) GENSET.
 Query Match 9.8%; Score 223.8; DB 3; Length 121162;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 832
 ID ADL13941 standard; DNA; 125515 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #473.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.8%; Score 223.8; DB 10; Length 125515;
 Best Local Similarity 85.6%; Pred. No. 1.2e-45;
 RESULT 833

ID ABD32872 standard; DNA; 130244 BP.
DE Human cancer-associated genomic DNA HD17-083.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223.8; DB 13; Length 130244;
Best Local Similarity 85.6%; Pred. No. 1.2e-45;
RESULT 834
ID ACN44890 standard; DNA; 131576 BP.
DE Human genomic sequence hCG28994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 223.8; DB 11; Length 131576;
Best Local Similarity 85.6%; Pred. No. 1.2e-45;
RESULT 835
ID ABD32888 standard; DNA; 144068 BP.
DE Human cancer-associated genomic DNA HD18-013.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223.8; DB 13; Length 144068;
Best Local Similarity 83.2%; Pred. No. 1.2e-45;
RESULT 836
ID ACN44170 standard; DNA; 196686 BP.
DE Human genomic sequence hCG39530.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 223.8; DB 11; Length 196686;
Best Local Similarity 83.2%; Pred. No. 1.4e-45;
RESULT 837
ID ABD17970 standard; DNA; 209284 BP.
DE Human factor-related antisense polynucleotide.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 9.8%; Score 223.8; DB 11; Length 209284;
Best Local Similarity 82.4%; Pred. No. 1.5e-45;
RESULT 838
ID AD58279 standard; DNA; 226475 BP.
DE Human tumour suppressor gene, lmt reverse complement DNA.
PN WO2003066869-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 9.8%; Score 223.8; DB 9; Length 226475;
Best Local Similarity 83.2%; Pred. No. 1.5e-45;
RESULT 839
ID ADC86558 standard; DNA; 952 BP.
DE Human GPCR gene SEQ ID NO:1011.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 9.8%; Score 223.6; DB 10; Length 952;
Best Local Similarity 83.0%; Pred. No. 1.5e-46;
RESULT 840
ID ABZ74164 standard; DNA; 6404 BP.
DE Secreted protein gene 200 genomic fragment HMQA138, SEQ ID NO:1311.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.6; DB 8; Length 6404;
Best Local Similarity 76.1%; Pred. No. 3.4e-46;
RESULT 841
ID ADC20801 standard; DNA; 6404 BP.
DE Human secreted protein-related DNA sequence #219.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.6; DB 10; Length 6404;
Best Local Similarity 76.1%; Pred. No. 3.4e-46;
RESULT 842

ID AAK89070 standard; DNA; 11837 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2646.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.6; DB 4; Length 11837;
Best Local Similarity 82.7%; Pred. No. 4.5e-46;
RESULT 843
ID AAS33429 standard; DNA; 11837 BP.
DE DNA encoding human secreted protein, Seq ID No 712.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.6; DB 4; Length 11837;
Best Local Similarity 82.7%; Pred. No. 4.5e-46;
RESULT 844
ID AAK76413 standard; DNA; 21747 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31225.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.6; DB 4; Length 21747;
Best Local Similarity 82.7%; Pred. No. 5.9e-46;
RESULT 845
ID ABD33071 standard; DNA; 24529 BP.
DE Human cancer-associated (CA) gene HD07-001.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223.6; DB 13; Length 24529;
Best Local Similarity 86.3%; Pred. No. 6.3e-46;
RESULT 846
ID AEJ12996 standard; DNA; 24529 BP.
DE Cancer-associated gene sequence - SEQ ID 4.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR-) MORRIS D W.
PA (MALA-) MALANDRO M S.
Query Match 9.8%; Score 223.6; DB 15; Length 24529;
Best Local Similarity 86.3%; Pred. No. 6.3e-46;
RESULT 847
ID ADL13819 standard; DNA; 41150 BP.
DE Osteoarthritis-associated polymorphic nucleotide #351.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.8%; Score 223.6; DB 10; Length 41150;
Best Local Similarity 82.0%; Pred. No. 7.9e-46;
RESULT 848
ID AED18343 standard; DNA; 41150 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 594.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.8%; Score 223.6; DB 14; Length 41150;
Best Local Similarity 82.0%; Pred. No. 7.9e-46;
RESULT 849
ID ADN48556 standard; DNA; 44348 BP.
DE Human Notch3 genomic DNA #2.
PN US2004102390-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.8%; Score 223.6; DB 12; Length 44348;
Best Local Similarity 82.0%; Pred. No. 8.2e-46;
RESULT 850
ID ACN44146 standard; DNA; 50602 BP.
DE Human genomic sequence hCG28572.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 223.6; DB 11; Length 50602;
Best Local Similarity 83.9%; Pred. No. 8.7e-46;
RESULT 851

ID ACN45158 standard; DNA; 72705 BP.
DE Human genomic sequence hCG25130.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 223.6; DB 11; Length 72705;
Best Local Similarity 82.7%; Pred. No. 1e-45;
RESULT 852
ID ACN44438 standard; DNA; 73967 BP.
DE Human genomic sequence hCG27607.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.8%; Score 223.6; DB 11; Length 73967;
Best Local Similarity 85.3%; Pred. No. 1e-45;
RESULT 853
Query Match 9.8%; Score 223.6; DB 6; Length 91080;
Best Local Similarity 83.9%; Pred. No. 1.1e-45;
RESULT 854
Query Match 9.8%; Score 223.6; DB 12; Length 91134;
Best Local Similarity 83.9%; Pred. No. 1.1e-45;
RESULT 855
Query Match 9.8%; Score 223.6; DB 12; Length 91138;
Best Local Similarity 83.9%; Pred. No. 1.1e-45;
RESULT 856
Query Match 9.8%; Score 223.6; DB 12; Length 91139;
Best Local Similarity 83.9%; Pred. No. 1.1e-45;
RESULT 857
Query Match 9.8%; Score 223.6; DB 14; Length 91140;
Best Local Similarity 83.9%; Pred. No. 1.1e-45;
RESULT 858
ID AED99413 standard; DNA; 191343 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 53.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.8%; Score 223.6; DB 14; Length 191343;
Best Local Similarity 85.1%; Pred. No. 1.6e-45;
RESULT 859
ID AEL48676 standard; cDNA; 216498 BP.
DE Peptidyl arginine deiminase, type II, cDNA.
PN WO2006108135-A2.
PD 12-OCT-2006.
PA (YUJ/) YU J.
PA (JIAN/) JIANG Y.
PA (YANG/) YANG F.
PA (WANG/) WANG Y.
PA (LEHN/) LEHNHARDT S.
Query Match 9.8%; Score 223.6; DB 16; Length 216498;
Best Local Similarity 82.7%; Pred. No. 1.7e-45;
RESULT 860
ID AAK81896 standard; DNA; 7794 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36708.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 4; Length 7794;
Best Local Similarity 83.7%; Pred. No. 4.2e-46;
RESULT 861
ID AAS28608 standard; DNA; 7794 BP.
DE Genomic sequence #448 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 4; Length 7794;
Best Local Similarity 83.7%; Pred. No. 4.2e-46;
RESULT 862
ID ADG41804 standard; DNA; 7794 BP.
DE Human respiratory system associated genomic DNA seq id 1042.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 10; Length 7794;
Best Local Similarity 82.3%; Pred. No. 1.2e-45;
RESULT 863
ID ADI97578 standard; DNA; 7794 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID1042.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 11; Length 7794;
Best Local Similarity 83.7%; Pred. No. 4.2e-46;
RESULT 864
ID AEA61190 standard; DNA; 13989 BP.
DE Human PDK4 gene genomic sequence SEQ ID NO:100.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 9.8%; Score 223.4; DB 14; Length 13989;
Best Local Similarity 78.3%; Pred. No. 5.5e-46;
RESULT 865
ID AAK81246 standard; DNA; 26464 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36058.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 4; Length 26464;
Best Local Similarity 74.9%; Pred. No. 7.3e-46;
RESULT 866
ID AAS28363 standard; DNA; 32146 BP.
DE Genomic sequence #203 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 4; Length 32146;
Best Local Similarity 83.3%; Pred. No. 8e-46;
RESULT 867
ID ADG41559 standard; DNA; 32146 BP.
DE Human respiratory system associated genomic DNA seq id 797.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 10; Length 32146;
Best Local Similarity 83.3%; Pred. No. 8e-46;
RESULT 868
ID ADI97333 standard; DNA; 32146 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID797.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223.4; DB 11; Length 32146;
Best Local Similarity 83.3%; Pred. No. 8e-46;
RESULT 869
ID ADQ97910 standard; DNA; 44920 BP.
DE Human cancer associated sequence HD11-022, SEQ ID 887.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223.4; DB 12; Length 44920;
Best Local Similarity 82.1%; Pred. No. 9.2e-46;
RESULT 870
ID ABK85261 standard; DNA; 75899 BP.
DE Human genomic DNA for protein phosphatase 1B, PTP1B.
PN US2002055479-A1.
PD 09-MAY-2002.
PA (COWS/) COWSERT L M.
PA (WYAT/) WYATT J.
PA (FREI/) FREIER S M.
PA (MONI/) MONIA B P.
PA (BUTL/) BUTLER M M.
PA (MCKA/) MCKAY R.
Query Match 9.8%; Score 223.4; DB 6; Length 75899;
Best Local Similarity 82.3%; Pred. No. 1.2e-45;
RESULT 871
ID ADI13990 standard; DNA; 75899 BP.
DE Human protein phosphatase 1B (PTP1B) genomic DNA SeqID 243.

PN US2003220282-A1.
 PD 27-NOV-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.8%; Score 223.4; DB 12; Length 75899;
 Best Local Similarity 82.3%; Pred. No. 1.2e-45;
 RESULT 872
 ID ADZ56505 standard; DNA; 75899 BP.
 DE Human protein tyrosine phosphatase 1B genomic DNA SEQ ID NO:243.
 PN US2005095710-A1.
 PD 05-MAY-2005.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.8%; Score 223.4; DB 14; Length 75899;
 Best Local Similarity 82.3%; Pred. No. 1.2e-45;
 RESULT 873
 ID AEF59865 standard; DNA; 75899 BP.
 DE Human protein tyrosine phosphatase-1B DNA SEQ ID NO:243.
 PN US2006025372-A1.
 PD 02-FEB-2006.
 PA (BHAN/) BHANOT S.
 PA (COWS/) COWSERT L M.
 PA (WYAT/) WYATT J R.
 PA (MONI/) MONIA B P.
 PA (BUTL/) BUTLER M M.
 PA (MCKA/) MCKAY R. R.
 PA (FREI/) FREIER S M.
 PA (DOB1/) DOBIE K W.
 Query Match 9.8%; Score 223.4; DB 15; Length 75899;
 Best Local Similarity 82.3%; Pred. No. 1.2e-45;
 RESULT 874
 ID ACN44322 standard; DNA; 84073 BP.
 DE Human genomic sequence hCG28354.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 223.4; DB 11; Length 84073;
 Best Local Similarity 77.4%; Pred. No. 1.2e-45;
 RESULT 875
 ID ADQ97695 standard; DNA; 88892 BP.
 DE Human cancer associated sequence HD10-029, SEQ ID 672.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.8%; Score 223.4; DB 12; Length 88892;
 Best Local Similarity 87.1%; Pred. No. 1.3e-45;
 RESULT 876
 ID ABQ88176 standard; cDNA; 100301 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 83.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 9.8%; Score 223.4; DB 6; Length 100301;
 Best Local Similarity 78.3%; Pred. No. 1.3e-45;
 RESULT 877
 ID ADQ20754 standard; DNA; 100301 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3574.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.8%; Score 223.4; DB 12; Length 100301;
 Best Local Similarity 78.3%; Pred. No. 1.3e-45;
 RESULT 878
 ID ACN44150 standard; DNA; 438992 BP.
 DE Human genomic sequence hCG27278.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 223.4; DB 11; Length 110000;
 Best Local Similarity 85.8%; Pred. No. 1.4e-45;
 RESULT 879
 ID AAK73166 standard; DNA; 19965 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.
 PN WO200157182-A2.
 PD 09-AUG-2001.

ID AEH93956 standard; DNA; 118899 BP.
 DE DNMT31 variant full length coding sequence.
 PN US2006115829-A1.
 PD 01-JUN-2006.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match 9.8%; Score 223.4; DB 15; Length 118899;
 Best Local Similarity 85.8%; Pred. No. 1.4e-45;
 RESULT 881
 ID AEF74705 standard; DNA; 152037 BP.
 DE Human polynucleotide #219.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 9.8%; Score 223.4; DB 15; Length 152037;
 Best Local Similarity 82.1%; Pred. No. 1.6e-45;
 RESULT 882
 ID ADQ97433 standard; DNA; 295772 BP.
 DE Human cancer associated sequence HD08-047, SEQ ID 410.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.8%; Score 223.4; DB 12; Length 295772;
 Best Local Similarity 80.2%; Pred. No. 2.2e-45;
 RESULT 883
 ID AAD00684 standard; cDNA; 1413 BP.
 DE Human Hydrolase protein-9 (HYDRL-9) encoding cDNA.
 PN WO200028045-A2.
 PD 18-MAY-2000.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 9.8%; Score 223.2; DB 3; Length 1413;
 Best Local Similarity 81.0%; Pred. No. 2.2e-46;
 RESULT 884
 ID AAI59065 standard; cDNA; 2070 BP.
 DE Human polynucleotide SEQ ID NO 1268.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 2070;
 Best Local Similarity 71.8%; Pred. No. 2.6e-46;
 RESULT 885
 ID ADQ99288 standard; cDNA; 2070 BP.
 DE DNA encoding human GPCR-like protein seqid 958.
 PN US6569662-B1.
 PD 27-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.8%; Score 223.2; DB 5; Length 2070;
 Best Local Similarity 71.8%; Pred. No. 2.6e-46;
 RESULT 886
 ID ADB49048 standard; cDNA; 2070 BP.
 DE Novel human cDNA SEQ ID NO 958.
 PN US2003104529-A1.
 PD 05-JUN-2003.
 PA (ZHOU/) ZHOU P.
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (DRMA/) DRMANAC R T.
 Query Match 9.8%; Score 223.2; DB 9; Length 2070;
 Best Local Similarity 71.8%; Pred. No. 2.6e-46;
 RESULT 887
 ID AAK89199 standard; DNA; 10316 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 2975.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 10316;
 Best Local Similarity 85.5%; Pred. No. 5.4e-46;
 RESULT 888
 ID AAK73166 standard; DNA; 19965 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.
 PN WO200157182-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 19965;
 Best Local Similarity 86.6%; Pred. No. 7.2e-46;
 RESULT 889
 ID ABK69932 standard; DNA; 19965 BP.
 DE Human secreted protein gene 68 genomic DNA fragment #20.
 PN WO200226931-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 6; Length 19965;
 Best Local Similarity 86.6%; Pred. No. 7.2e-46;
 RESULT 890
 ID AAK73165 standard; DNA; 20420 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 20420;
 Best Local Similarity 86.6%; Pred. No. 7.3e-46;
 RESULT 891
 ID ABK69933 standard; DNA; 20420 BP.
 DE Human secreted protein gene 68 genomic DNA fragment #21.
 PN WO200226931-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 6; Length 20420;
 Best Local Similarity 86.6%; Pred. No. 7.3e-46;
 RESULT 892
 ID AAL35943 standard; DNA; 32132 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2308.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 32132;
 Best Local Similarity 70.6%; Pred. No. 8.9e-46;
 RESULT 893
 ID AAL07060 standard; DNA; 32132 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9748.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 4; Length 32132;
 Best Local Similarity 70.6%; Pred. No. 8.9e-46;
 RESULT 894
 ID ABX58931 standard; cDNA; 32132 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1275.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.8%; Score 223.2; DB 8; Length 32132;
 Best Local Similarity 70.6%; Pred. No. 8.9e-46;
 RESULT 895
 ID ADJ29681 standard; DNA; 32132 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2308.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 12; Length 32132;
 Best Local Similarity 70.6%; Pred. No. 8.9e-46;
 RESULT 896
 ID AEE04771 standard; DNA; 44633 BP.
 DE Cancer-associated gene SEQ ID NO:89.
 PN WO2005107396-A2.
 PD 17-NOV-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.8%; Score 223.2; DB 14; Length 44633;
 Best Local Similarity 86.5%; Pred. No. 1e-45;
 RESULT 898

ID ABZ74619 standard; DNA; 58181 BP.
 DE Secreted protein gene 372 genomic fragment HWBCN36, SEQ ID NO:1766.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 8; Length 58181;
 Best Local Similarity 70.6%; Pred. No. 1.2e-45;
 RESULT 899
 ID ADC21010 standard; DNA; 58181 BP.
 DE Human secreted protein-related DNA sequence #428.
 PN WO200292787-A2.
 PD 21-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 10; Length 58181;
 Best Local Similarity 70.6%; Pred. No. 1.2e-45;
 RESULT 900
 ID ABZ68140 standard; DNA; 58181 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1663.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223.2; DB 10; Length 58181;
 Best Local Similarity 70.6%; Pred. No. 1.2e-45;
 RESULT 901
 ID AAD58282 standard; DNA; 62782 BP.
 DE Human tumour suppressor gene, Lmt intron 3 DNA.
 PN WO2003066869-A1.
 PD 14-AUG-2003.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 Query Match 9.8%; Score 223.2; DB 9; Length 62782;
 Best Local Similarity 78.8%; Pred. No. 1.2e-45;
 RESULT 902
 ID AAD58281 standard; DNA; 62782 BP.
 DE Human tumour suppressor gene, Lmt intron 2 DNA.
 PN WO2003066869-A1.
 PD 14-AUG-2003.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 Query Match 9.8%; Score 223.2; DB 9; Length 62782;
 Best Local Similarity 78.8%; Pred. No. 1.2e-45;
 RESULT 903
 ID ADJ53477 standard; DNA; 70000 BP.
 DE Human PPP3CB genomic DNA #3.
 PN US2004023382-A1.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.8%; Score 223.2; DB 12; Length 70000;
 Best Local Similarity 85.3%; Pred. No. 1.3e-45;
 RESULT 904
 ID AAF30035 standard; DNA; 81001 BP.
 DE Human apolipoprotein A-IV-related protein (AA4RP) gene.
 PN WO200100803-A2.
 PD 04-JAN-2001.
 PA (GEST) GENSET.
 Query Match 9.8%; Score 223.2; DB 4; Length 81001;
 Best Local Similarity 85.5%; Pred. No. 1.4e-45;
 RESULT 905
 ID AEB77360 standard; DNA; 89014 BP.
 DE Human TGF beta receptor II complete antisense sequence SEQ ID NO 1.
 PN WO2005074981-A2.
 PD 18-AUG-2005.
 PA (BOGD/) BOGDH N U.
 Query Match 9.8%; Score 223.2; DB 14; Length 89014;
 Best Local Similarity 86.6%; Pred. No. 1.4e-45;
 RESULT 906
 ID AEG92754 standard; cDNA; 113681 BP.
 DE Human tumor cell cDNA SEQ ID NO:250.
 PN WO2006036025-A1.
 PD 06-APR-2006.
 PA (EISA) EISAI CO LTD.
 Query Match 9.8%; Score 223.2; DB 15; Length 113681;

Best Local Similarity 86.6%; Pred. No. 1.6e-45;
 RESULT 908
 ID AEH15864 standard; DNA; 114001 BP.
 DE Human estrogen reactivity gene, GREB1, SEQ ID 19.
 PN JP2006101790-A.
 PD 20-APR-2006.
 PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.
 Query Match 9.8%; Score 223.2; DB 15; Length 114001;
 Best Local Similarity 82.9%; Pred. No. 1.6e-45;
 RESULT 909
 ID AEB32396 standard; DNA; 119226 BP.
 DE Human genomic DNA #37.
 PN US2005147987-A1.
 PD 07-JUL-2005.
 PA (APPL-) APPLERA CORP NY.
 Query Match 9.8%; Score 223.2; DB 14; Length 119226;
 Best Local Similarity 81.8%; Pred. No. 1.6e-45;
 RESULT 910
 ID AEB32401 standard; DNA; 119313 BP.
 DE Human genomic DNA #42.
 PN US2005147987-A1.
 PD 07-JUL-2005.
 PA (APPL-) APPLERA CORP NY.
 Query Match 9.8%; Score 223.2; DB 14; Length 119313;
 Best Local Similarity 81.8%; Pred. No. 1.6e-45;
 RESULT 911
 ID ABD33616 standard; DNA; 122656 BP.
 DE Human cancer-associated (CA) gene HD07-125.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.8%; Score 223.2; DB 13; Length 122656;
 Best Local Similarity 85.3%; Pred. No. 1.6e-45;
 RESULT 912
 ID AEJ13838 standard; DNA; 122656 BP.
 DE Cancer-associated gene sequence - SEQ ID 846.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match 9.8%; Score 223.2; DB 15; Length 122656;
 Best Local Similarity 85.3%; Pred. No. 1.6e-45;
 RESULT 913
 ID ADH77370 standard; DNA; 137000 BP.
 DE Human PTPN12 polynucleotide #1.
 PN US2003232434-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 9.8%; Score 223.2; DB 12; Length 137000;
 Best Local Similarity 85.3%; Pred. No. 1.7e-45;
 RESULT 914
 ID ABE96219 standard; DNA; 137000 BP.
 DE Human PTPN12 genomic DNA.
 PN US2005282760-A1.
 PD 22-DEC-2005.
 PA (COWS/) COWSERT L M.
 PA (DOBI/) DOBIE K W.
 Query Match 9.8%; Score 223.2; DB 15; Length 137000;
 Best Local Similarity 85.3%; Pred. No. 1.7e-45;
 RESULT 915
 ID AAL38336 standard; DNA; 143899 BP.
 DE Genomic sequence encoding a human Ngr2 protein.
 PN WO200229059-A2.
 PD 11-APR-2002.
 PA (UYYA) UNIV YALE.
 PA (BIOJ) BIOGEN INC.
 Query Match 9.8%; Score 223.2; DB 6; Length 143899;
 Best Local Similarity 84.1%; Pred. No. 1.8e-45;
 RESULT 916
 ID AAD02697 standard; DNA; 160552 BP.
 DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
 PN WO200106015-A1.
 PD 25-JAN-2001.

PA (REGC) UNIV CALIFORNIA.
 Query Match 9.8%; Score 223.2; DB 4; Length 160552;
 Best Local Similarity 83.2%; Pred. No. 1.8e-45;
 RESULT 917
 ID AEB49487 standard; DNA; 180000 BP.
 DE Marfans' syndrome diagnosis associated DNA SEQ ID NO 1.
 PN WO2005116253-A1.
 PD 08-DEC-2005.
 PA (UYNA-) UNIV NAGASAKI.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Query Match 9.8%; Score 223.2; DB 15; Length 180000;
 Best Local Similarity 86.6%; Pred. No. 1.9e-45;
 RESULT 918
 ID AAD2832 standard; DNA; 180216 BP.
 DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.
 PN US2003170683-A1.
 PD 11-SEP-2003.
 PA (LEDE/) LEDER P.
 PA (LEAD/) LEADER B.
 Query Match 9.8%; Score 223.2; DB 10; Length 180216;
 Best Local Similarity 81.8%; Pred. No. 1.9e-45;
 RESULT 919
 ID ADL08108 standard; DNA; 188971 BP.
 DE Human gene associated with low HDL-C APOA1.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 9.8%; Score 223.2; DB 12; Length 188971;
 Best Local Similarity 85.5%; Pred. No. 2e-45;
 RESULT 920
 ID ADC87619 standard; DNA; 349981 BP.
 DE Human GPCR related polynucleotide SEQ ID NO:2072.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 9.8%; Score 223.2; DB 10; Length 349981;
 Best Local Similarity 84.1%; Pred. No. 2.6e-45;
 RESULT 921
 ID ADC86916 standard; DNA; 349989 BP.
 DE Human GPCR gene SEQ ID NO:1369.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 9.8%; Score 223.2; DB 10; Length 349989;
 Best Local Similarity 84.1%; Pred. No. 2.6e-45;
 RESULT 922
 ID ADQ63518 standard; cDNA; 3708 BP.
 DE Novel human cDNA sequence #679.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.8%; Score 223; DB 12; Length 3708;
 Best Local Similarity 81.4%; Pred. No. 3.8e-46;
 RESULT 923
 ID AAS16855 standard; DNA; 15714 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 2355.
 PN WO200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223; DB 4; Length 15714;
 Best Local Similarity 72.0%; Pred. No. 7.3e-46;
 RESULT 924
 ID ADE47549 standard; DNA; 15714 BP.
 DE Human cardiovascular system related genomic DNA #1115.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.8%; Score 223; DB 10; Length 15714;
 Best Local Similarity 72.0%; Pred. No. 7.3e-46;
 RESULT 925
 ID ADJ08967 standard; DNA; 15714 BP.

DE Human cardiovascular system associated polypeptide-related DNA SeqID2355.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 223; DB 13; Length 15714;
Best Local Similarity 72.0%; Pred. No. 7.3e-46;
RESULT 926
ID ADQ59185 standard; DNA; 38504 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:22.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match
Best Local Similarity 86.0%; Pred. No. 1.1e-45;
RESULT 927
ID AEG17800 standard; cDNA; 52280 BP.
DE Human plasminogen genomic cDNA.
PN US2006051780-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUKE.
PA (ROCH-) ROCHE PALO ALTO LLC.
Query Match 9.8%; Score 223; DB 15; Length 52280;
Best Local Similarity 75.9%; Pred. No. 1.3e-45;
RESULT 928
ID AAS20588 standard; DNA; 84495 BP.
DE Human methionine aminopeptidase protease genomic DNA.
PN US6329188-B1.
PD 11-DEC-2001.
PA (PEKE-) PE CORP NY.
Query Match 9.8%; Score 223; DB 6; Length 84495;
Best Local Similarity 81.4%; Pred. No. 1.6e-45;
RESULT 929
ID ADQ97846 standard; DNA; 94911 BP.
DE Human cancer associated sequence HD11-010, SEQ ID 823.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223; DB 12; Length 94911;
Best Local Similarity 83.6%; Pred. No. 1.6e-45;
RESULT 930
ID AAA10225 standard; DNA; 106746 BP.
DE Human PCTA-1 genomic DNA, SEQ ID NO:1.
PN WO9864590-A1.
PD 16-DEC-1999.
PA (GEST-) GENSET.
Query Match 9.8%; Score 223; DB 3; Length 106746;
Best Local Similarity 83.6%; Pred. No. 1.7e-45;
RESULT 931
ID ABD32653 standard; DNA; 117750 BP.
DE Human cancer-associated genomic DNA HD13-060.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 223; DB 13; Length 117750;
Best Local Similarity 79.4%; Pred. No. 1.8e-45;
RESULT 932
ID ABD18413 standard; DNA; 152811 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 664.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL-) UNIV FLORIDA RES FOUND INC.
Query Match 9.8%; Score 223; DB 14; Length 152811;
Best Local Similarity 82.5%; Pred. No. 2e-45;
RESULT 933
ID ACL56842 standard; cDNA; 573 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:2977.
PN WO2005000087-A2.
PD 06-JAN-2005.
PA (CHIR-) CHIRON CORP.
Query Match 9.8%; Score 222.8; DB 14; Length 573;

Best Local Similarity 82.0%; Pred. No. 1.9e-46;
RESULT 934
ID ADB82525 standard; cDNA; 714 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 837).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 9.8%; Score 222.8; DB 9; Length 714;
Best Local Similarity 82.0%; Pred. No. 2e-46;
RESULT 935
ID ABQ89583 standard; cDNA; 738 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 839.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 9.8%; Score 222.8; DB 6; Length 738;
Best Local Similarity 82.0%; Pred. No. 2.1e-46;
RESULT 936
ID ABK12093 standard; cDNA; 1380 BP.
DE cDNA encoding Phytochrome 9_9 protein.
PN WO200212309-A1.
PD 14-FEB-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 9.8%; Score 222.8; DB 6; Length 1380;
Best Local Similarity 82.0%; Pred. No. 2.8e-46;
RESULT 937
ID AAF97866 standard; DNA; 5301 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:80.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM-) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 9.8%; Score 222.8; DB 5; Length 5301;
Best Local Similarity 79.0%; Pred. No. 5e-46;
RESULT 938
ID ABK50893 standard; DNA; 7920 BP.
DE Human chromosome 19 bases 117001-124920, clone CTD-3093.
PN WO200220718-A2.
PD 14-MAR-2002.
PA (YTRQ-) UNIV ROCKEFELLER.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 9.8%; Score 222.8; DB 6; Length 7920;
Best Local Similarity 79.7%; Pred. No. 6e-46;
RESULT 939
ID ADS89069 standard; DNA; 15355 BP.
DE Human FGF1 gene SEQ ID NO:85.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 9.8%; Score 222.8; DB 13; Length 15355;
Best Local Similarity 81.0%; Pred. No. 8.1e-46;
RESULT 940
ID ADZ59511 standard; DNA; 37034 BP.
DE Secondary hyperparathyroidism detection human polymorphic gene, FGF1.
PN JP2005102601-A.
PD 21-APR-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (JIKI-) UNIV JIKEI.
Query Match 9.8%; Score 222.8; DB 14; Length 37034;
Best Local Similarity 81.0%; Pred. No. 1.2e-45;
RESULT 941
ID ADL13662 standard; DNA; 76416 BP.
DE Osteoarthritis-associated polymorphic nucleotide #194.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.8%; Score 222.8; DB 10; Length 76416;
Best Local Similarity 81.0%; Pred. No. 1.7e-45;
RESULT 942
ID ADS36495 standard; DNA; 77522 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1709.

PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.8%; Score 222.8; DB 13; Length 77522;
Best Local Similarity 81.0%; Pred. No. 1.7e-45;
RESULT 943
ID AAL57571 standard; cDNA; 83120 BP.
DE Human CGI-51 protein CDNA.
PN WO2003059148-A2.
PD 24-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (IGBI-) LG BIOMEDICAL INST.
Query Match 9.8%; Score 222.8; DB 9; Length 83120;
Best Local Similarity 85.5%; Pred. No. 1.7e-45;
RESULT 944
Query Match 9.8%; Score 222.8; DB 14; Length 110000;
Best Local Similarity 83.1%; Pred. No. 2e-45;
RESULT 945
ID ABN95044 standard; DNA; 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.8%; Score 222.8; DB 6; Length 110096;
Best Local Similarity 83.0%; Pred. No. 2e-45;
RESULT 946
ID AED18046 standard; DNA; 110096 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 297.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.8%; Score 222.8; DB 14; Length 110096;
Best Local Similarity 83.0%; Pred. No. 2e-45;
RESULT 947
ID AEF74649 standard; DNA; 110096 BP.
DE Human polynucleotide #163.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 9.8%; Score 222.8; DB 15; Length 110096;
Best Local Similarity 83.0%; Pred. No. 2e-45;
RESULT 948
ID AEF74540 standard; DNA; 110096 BP.
DE Human polynucleotide #54.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 9.8%; Score 222.8; DB 15; Length 110096;
Best Local Similarity 83.0%; Pred. No. 2e-45;
RESULT 949
ID AEF74955 standard; DNA; 110096 BP.
DE Human polynucleotide #469.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 9.8%; Score 222.8; DB 15; Length 110096;
Best Local Similarity 83.0%; Pred. No. 2e-45;
RESULT 950
ID AEF193838 standard; DNA; 134000 BP.
DE Human proline rich 4, PROL4, genomic sequence.
PN WO2006074061-A2.
PD 13-JUL-2006.
PA (SEQU-) SEQUENOM INC.
Query Match 9.8%; Score 222.8; DB 15; Length 134000;
Best Local Similarity 71.3%; Pred. No. 2.2e-45;
RESULT 951
ID AAD55694 standard; DNA; 175561 BP.
DE Human THBS4 reference gene (GI 14916146).
PN WO2003020120-A2.
PD 13-MAR-2003.

PA (VITI-) VITIVITY INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 9.8%; Score 222.8; DB 8; Length 175561;
Best Local Similarity 85.5%; Pred. No. 2.4e-45;
RESULT 952
ID ADL08129 standard; DNA; 175561 BP.
DE Human gene associated with low HDL-C THBS4.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 9.8%; Score 222.8; DB 12; Length 175561;
Best Local Similarity 85.5%; Pred. No. 2.4e-45;
RESULT 953
ID AAH16931 standard; cDNA; 556 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:16208.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.6; DB 4; Length 556;
Best Local Similarity 86.3%; Pred. No. 2.1e-46;
RESULT 954
ID ADB62815 standard; cDNA; 2477 BP.
DE Human cDNA encoding clone NTONG20005310.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.6; DB 10; Length 2477;
Best Local Similarity 82.7%; Pred. No. 4e-46;
RESULT 955
ID AAH17838 standard; cDNA; 2504 BP.
DE Human cDNA sequence SEQ ID NO:17524.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.6; DB 4; Length 2504;
Best Local Similarity 86.3%; Pred. No. 4.1e-46;
RESULT 956
ID AAK68368 standard; DNA; 5969 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23180.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 5969;
Best Local Similarity 85.0%; Pred. No. 6e-46;
RESULT 957
ID AAK73167 standard; DNA; 11746 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27979.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 11746;
Best Local Similarity 86.3%; Pred. No. 8.1e-46;
RESULT 958
ID ABK69935 standard; DNA; 11746 BP.
DE Human secreted protein gene 68 genomic DNA fragment #23.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 6; Length 11746;
Best Local Similarity 86.3%; Pred. No. 8.1e-46;
RESULT 959
ID ABK42245 standard; DNA; 12932 BP.
DE Genomic sequence #144 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 12932;
Best Local Similarity 83.8%; Pred. No. 8.5e-46;
RESULT 960
ID ADB60401 standard; DNA; 12932 BP.
DE Connective tissue related genomic DNA #144.
PN US2003054375-A1.

PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 9; Length 12932;
Best Local Similarity 83.8%; Pred. No. 8.5e-46;
RESULT 961
ID AAL05850 standard; DNA; 32184 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8538.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 32184;
Best Local Similarity 79.0%; Pred. No. 1.3e-45;
RESULT 962
ID ABL98414 standard; DNA; 32184 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3066.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 32184;
Best Local Similarity 79.0%; Pred. No. 1.3e-45;
RESULT 963
ID AAL36806 standard; DNA; 32185 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3171.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 32185;
Best Local Similarity 86.5%; Pred. No. 1.3e-45;
RESULT 964
ID ABX59794 standard; cDNA; 32185 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2138.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 222.6; DB 8; Length 32185;
Best Local Similarity 86.5%; Pred. No. 1.3e-45;
RESULT 965
ID ADJ30544 standard; DNA; 32185 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3171.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 12; Length 32185;
Best Local Similarity 86.5%; Pred. No. 1.3e-45;
RESULT 966
ID AAL05849 standard; DNA; 32204 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8537.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 32204;
Best Local Similarity 79.0%; Pred. No. 1.3e-45;
RESULT 967
ID ABL98413 standard; DNA; 32204 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3065.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 32204;
Best Local Similarity 79.0%; Pred. No. 1.3e-45;
RESULT 968
ID AEK79131 standard; DNA; 35320 BP.
DE Human DGK zeta gene, SEQ ID NO: 4.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 15; Length 35320;
Best Local Similarity 81.6%; Pred. No. 1.3e-45;
RESULT 969
ID AAK84729 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 222.6; DB 4; Length 48037;
Best Local Similarity 74.4%; Pred. No. 1.5e-45;
RESULT 970
ID AAK85983 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 48037;
Best Local Similarity 74.4%; Pred. No. 1.5e-45;
RESULT 971
ID AAK84730 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 48045;
Best Local Similarity 74.4%; Pred. No. 1.5e-45;
RESULT 972
ID AAK85984 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 48045;
Best Local Similarity 74.4%; Pred. No. 1.5e-45;
RESULT 973
ID AAK67426 standard; DNA; 55235 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22238.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.6; DB 4; Length 55235;
Best Local Similarity 85.0%; Pred. No. 1.6e-45;
RESULT 974
ID ADV09374 standard; DNA; 62520 BP.
DE Human helicase-like transcription factor (HLTF) genomic DNA.
PN US2004242510-A1.
PD 02-DEC-2004.
PA (MARK/) MARKOWITZ S D.
Query Match 9.7%; Score 222.6; DB 14; Length 62520;
Best Local Similarity 80.9%; Pred. No. 1.7e-45;
RESULT 975
ID AAV83940 standard; DNA; 80240 BP.
DE NC-contig derived from mardel(10) on chromosome 10q25.2.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 9.7%; Score 222.6; DB 2; Length 80240;
Best Local Similarity 85.0%; Pred. No. 1.9e-45;
RESULT 976
ID AAV83939 standard; DNA; 80595 BP.
DE HC-contig derived from normal human chromosome 10q25.2 region.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 9.7%; Score 222.6; DB 2; Length 80595;
Best Local Similarity 85.0%; Pred. No. 1.9e-45;
RESULT 977
ID ADP08388 standard; DNA; 95400 BP.
DE Human laminin alpha 4 (LAMA4) genomic DNA.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 9.7%; Score 222.6; DB 12; Length 95400;
Best Local Similarity 83.8%; Pred. No. 2.1e-45;
RESULT 978
ID AEK50257 standard; DNA; 95400 BP.
DE Human laminin, alpha 4 - LAMA4 genomic DNA.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 9.7%; Score 222.6; DB 15; Length 95400;
Best Local Similarity 83.8%; Pred. No. 2.1e-45;
RESULT 979
ID ADY70791 standard; DNA; 104424 BP.
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.
PN CN1548557-A.
PD 24-NOV-2004.

PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 9.7%; Score 222.6; DB 14; Length 104424;
Best Local Similarity 86.3%; Pred. No. 2.2e-45;
RESULT 980
ID ADZ46659 standard; DNA; 104424 BP.
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.
PN CN1548553-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 9.7%; Score 222.6; DB 14; Length 104424;
Best Local Similarity 86.3%; Pred. No. 2.2e-45;
RESULT 981
ID ABK83569 standard; cDNA; 122888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.7%; Score 222.6; DB 6; Length 122888;
Best Local Similarity 81.6%; Pred. No. 2.3e-45;
RESULT 982
ID ABK49450 standard; DNA; 147309 BP.
DE Human transporter genomic DNA sequence.
Query Match 9.7%; Score 222.6; DB 6; Length 147309;
Best Local Similarity 86.3%; Pred. No. 2.5e-45;
RESULT 983
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222.6; DB 12; Length 178024;
Best Local Similarity 80.5%; Pred. No. 2.8e-45;
RESULT 984
ID ABE04958 standard; DNA; 212235 BP.
DE Cancer-associated gene SEQ ID NO:276.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR-) CHIRON CORP.
Query Match 9.7%; Score 222.6; DB 14; Length 212235;
Best Local Similarity 86.3%; Pred. No. 3e-45;
RESULT 985
ID ACN44514 standard; DNA; 256493 BP.
DE Human genomic sequence hCG17361.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 222.6; DB 11; Length 256493;
Best Local Similarity 86.3%; Pred. No. 3.2e-45;
RESULT 986
ID ADP69744 standard; DNA; 312477 BP.
DE Human ROCK 1 DNA #2.
PN US2004115641-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.7%; Score 222.6; DB 12; Length 312477;
Best Local Similarity 77.7%; Pred. No. 3.5e-45;
RESULT 987
ID ABZ74324 standard; DNA; 518 BP.
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1471.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 8; Length 518;
Best Local Similarity 81.1%; Pred. No. 2.2e-46;
RESULT 988
ID ABZ67892 standard; DNA; 518 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1415.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 10; Length 518;
Best Local Similarity 81.1%; Pred. No. 2.2e-46;
RESULT 989

ID ABL37980 standard; cDNA; 577 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:1569.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.7%; Score 222.4; DB 6; Length 577;
Best Local Similarity 87.1%; Pred. No. 2.4e-46;
RESULT 990
ID ABV57704 standard; cDNA; 608 BP.
DE Human prostate expression marker cDNA 57695.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 9.7%; Score 222.4; DB 5; Length 608;
Best Local Similarity 80.1%; Pred. No. 2.4e-46;
RESULT 991
ID AAH16959 standard; cDNA; 1503 BP.
DE Human cDNA sequence SEQ ID NO:16245.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.4; DB 4; Length 1503;
Best Local Similarity 75.2%; Pred. No. 3.6e-46;
RESULT 992
ID ACAS4696 standard; cDNA; 2842 BP.
DE Human NF-kappaB associated polynucleotide sequence #136.
PN WO200286076-A2.
PD 31-OCT-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 9.7%; Score 222.4; DB 10; Length 2842;
Best Local Similarity 78.2%; Pred. No. 4.8e-46;
RESULT 993
ID ADU83314 standard; cDNA; 2842 BP.
DE Human NFkappaB-associated gene 40, cDNA #2.
PN WO2004100886-A2.
PD 25-NOV-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 9.7%; Score 222.4; DB 14; Length 2842;
Best Local Similarity 78.2%; Pred. No. 4.8e-46;
RESULT 994
ID ADQ87646 standard; cDNA; 2924 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4524.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 9.7%; Score 222.4; DB 12; Length 2924;
Best Local Similarity 87.1%; Pred. No. 4.9e-46;
RESULT 995
ID ACN37302 standard; cDNA; 2924 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323769, SEQ ID NO:95.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 9.7%; Score 222.4; DB 13; Length 2924;
Best Local Similarity 87.1%; Pred. No. 4.9e-46;
RESULT 996
ID ADP54897 standard; cDNA; 2924 BP.
DE Human PRO cDNA sequence SEQ ID NO:873.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 9.7%; Score 222.4; DB 13; Length 2924;
Best Local Similarity 87.1%; Pred. No. 4.9e-46;
RESULT 997
ID AAS92457 standard; cDNA; 7487 BP.
DE DNA encoding novel human diagnostic protein #28261.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSE INC.
Query Match 9.7%; Score 222.4; DB 5; Length 7487;
Best Local Similarity 81.1%; Pred. No. 7.5e-46;

RESULT 998
ID AB20857 standard; DNA; 11234 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13188.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 5; Length 11234;
Best Local Similarity 77.3%; Pred. No. 8.9e-46;
RESULT 999
ID AAK73037 standard; DNA; 12834 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27849.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 4; Length 12834;
Best Local Similarity 84.6%; Pred. No. 9.5e-46;
RESULT 1000
ID AAD16553 standard; DNA; 13021 BP.
DE Human novel protein-encoding gene 6 genomic DNA, SEQ ID NO:55.
PN WO200155311-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 4; Length 13021;
Best Local Similarity 83.3%; Pred. No. 9.6e-46;
RESULT 1001
ID AAG35084 standard; DNA; 13021 BP.
DE DNA #34 encoding human neoplastic disease associated polypeptide.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 4; Length 13021;
Best Local Similarity 83.3%; Pred. No. 9.6e-46;
RESULT 1002
ID ABS64143 standard; DNA; 13021 BP.
DE Human apoptosis related protein genomic DNA clone HOBY04 #1.
PN US2002086811-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 222.4; DB 6; Length 13021;
Best Local Similarity 83.3%; Pred. No. 9.6e-46;
RESULT 1003
ID ADC46526 standard; DNA; 13021 BP.
DE Human neoplastic disease-associated gene 61 DNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 10; Length 13021;
Best Local Similarity 83.3%; Pred. No. 9.6e-46;
RESULT 1004
ID AAD60452 standard; DNA; 13021 BP.
DE Human secreted protein-encoding genomic DNA, SEQ ID NO:55.
PN US2003092615-A1.
PD 15-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 10; Length 13021;
Best Local Similarity 83.3%; Pred. No. 9.6e-46;
RESULT 1005
ID AAF97862 standard; DNA; 22081 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:76.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 9.7%; Score 222.4; DB 5; Length 22081;
Best Local Similarity 84.5%; Pred. No. 1.2e-45;
RESULT 1006
ID ABE04761 standard; DNA; 22659 BP.
DE Cancer-associated gene SEQ ID NO:79.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.

Query Match 9.7%; Score 222.4; DB 14; Length 22659;
Best Local Similarity 82.2%; Pred. No. 1.2e-45;
RESULT 1007
ID AAL56668 standard; DNA; 23324 BP.
DE Human G-CSF stimulated clone 1 (hGC-1) genomic DNA.
PN WO2003050293-A2.
PD 19-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 9.7%; Score 222.4; DB 9; Length 23324;
Best Local Similarity 78.2%; Pred. No. 1.2e-45;
RESULT 1008
ID AAK75632 standard; DNA; 23802 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30444.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.4; DB 4; Length 23802;
Best Local Similarity 68.5%; Pred. No. 1.3e-45;
RESULT 1009
ID ACN43922 standard; DNA; 45864 BP.
DE Human genomic sequence hCG27363.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 222.4; DB 11; Length 45864;
Best Local Similarity 82.4%; Pred. No. 1.7e-45;
RESULT 1010
ID ABN89533 standard; DNA; 48436 BP.
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
PN US2002061562-A1.
PD 23-MAY-2002.
PA (FUKU/) FUKUDA M N.
PA (AKAM/) AKAMA T O.
Query Match 9.7%; Score 222.4; DB 6; Length 48436;
Best Local Similarity 78.6%; Pred. No. 1.7e-45;
RESULT 1011
ID ABS98185 standard; DNA; 53099 BP.
DE Human multidrug resistance gene exons 4-28 sequence.
PN WO200257410-A2.
PD 25-JUL-2002.
PA (DNAS-) DNA SCI LAB INC.
Query Match 9.7%; Score 222.4; DB 6; Length 53099;
Best Local Similarity 74.6%; Pred. No. 1.8e-45;
RESULT 1012
ID ADH56439 standard; DNA; 95001 BP.
DE Human hypothetical tumour endothelial marker DNA.
PN US2003232770-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.7%; Score 222.4; DB 12; Length 95001;
Best Local Similarity 83.3%; Pred. No. 2.3e-45;
RESULT 1013
ID ABD32669 standard; DNA; 106544 BP.
DE Human cancer-associated genomic DNA HD13-073.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222.4; DB 13; Length 106544;
Best Local Similarity 85.8%; Pred. No. 2.5e-45;
RESULT 1014
ID ADH99063 standard; DNA; 118518 BP.
DE Human NF-kappa-B p50 subunit full length DNA.
PN US2004005569-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 9.7%; Score 222.4; DB 12; Length 118518;
Best Local Similarity 68.5%; Pred. No. 2.6e-45;
RESULT 1016
ID ACF62749 standard; DNA; 128993 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:681.

PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 9.7%; Score 222.4; DB 8; Length 128993;
Best Local Similarity 74.6%; Pred. No. 2.7e-45;
RESULT 1017
ID ADB20868 standard; DNA; 128993 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:681.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 9.7%; Score 222.4; DB 8; Length 128993;
Best Local Similarity 74.6%; Pred. No. 2.7e-45;
RESULT 1018
ID ADB87957 standard; DNA; 128993 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:681.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 9.7%; Score 222.4; DB 10; Length 128993;
Best Local Similarity 74.6%; Pred. No. 2.7e-45;
RESULT 1019
ID ADB96940 standard; DNA; 128993 BP.
DE Human WDR1 related DNA sequence SEQ ID NO:681.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 9.7%; Score 222.4; DB 10; Length 128993;
Best Local Similarity 74.6%; Pred. No. 2.7e-45;
RESULT 1020
ID ADB92131 standard; DNA; 128993 BP.
DE Human WDR1 related DNA sequence SEQ ID NO:681.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 9.7%; Score 222.4; DB 10; Length 128993;
Best Local Similarity 74.6%; Pred. No. 2.7e-45;
RESULT 1021
ID ABD33163 standard; DNA; 138837 BP.
DE Human cancer-associated (CA) gene HD07-022.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222.4; DB 13; Length 138837;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
RESULT 1022
ID AEJ13138 standard; DNA; 138837 BP.
DE Cancer-associated gene sequence - SEQ ID 146.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.7%; Score 222.4; DB 15; Length 138837;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
RESULT 1023
ID AED89419 standard; DNA; 168656 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 59.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.7%; Score 222.4; DB 14; Length 168656;
Best Local Similarity 83.3%; Pred. No. 3e-45;
RESULT 1024
ID AED89418 standard; DNA; 170285 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 58.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.7%; Score 222.4; DB 14; Length 170285;
Best Local Similarity 83.3%; Pred. No. 3e-45;
RESULT 1025
ID ABK83571 standard; cDNA; 175737 BP.
DE Human cDNA differentially expressed in granulocytic cells #142.

PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.7%; Score 222.4; DB 6; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1026
ID ADL13596 standard; DNA; 175737 BP.
DE Osteoarthritis-associated polymorphic nucleotide #128.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.7%; Score 222.4; DB 10; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1027
ID ADQ18934 standard; DNA; 175737 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.7%; Score 222.4; DB 12; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1028
ID AEC32799 standard; DNA; 175737 BP.
DE Breast cancer detection expression profile gene, SEQ ID 34.
PN US2005186577-A1.
PD 25-AUG-2005.
PA (WANG/) WANG Y.
Query Match 9.7%; Score 222.4; DB 14; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1029
ID AEC8466 standard; cDNA; 175737 BP.
DE Breast cancer associated cDNA SEQ ID NO 34.
PN WO2005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 9.7%; Score 222.4; DB 14; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1030
ID AED18210 standard; DNA; 175737 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 461.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.7%; Score 222.4; DB 14; Length 175737;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1031
ID AEK17570 standard; DNA; 242981 BP.
DE Cell/tissue epigenetic characterization human gene, SEQ ID NO:22.
PN WO2006094836-A2.
PD 14-SEP-2006.
PA (EPIO-) EPIONTIS GMBH.
Query Match 9.7%; Score 222.4; DB 15; Length 242981;
Best Local Similarity 84.5%; Pred. No. 3.6e-45;
RESULT 1032
ID ABD33276 standard; DNA; 256190 BP.
DE Human cancer-associated (CA) gene HD07-048.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222.4; DB 13; Length 256190;
Best Local Similarity 84.6%; Pred. No. 3.6e-45;
RESULT 1033
ID AEJ13312 standard; DNA; 256190 BP.
DE Cancer-associated gene sequence - SEQ ID 320.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.7%; Score 222.4; DB 15; Length 256190;
Best Local Similarity 84.6%; Pred. No. 3.6e-45;
RESULT 1034
ID AAH71089 standard; cDNA; 366 BP.
DE Human cervical cancer marker nucleic acid 2363.

PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 9.7%; Score 222.2; DB 4; Length 366;
Best Local Similarity 85.2%; Pred. No. 2.2e-46;
RESULT 1035
ID ABR65466 standard; cDNA; 509 BP.
DE Human cancer related polynucleotide SEQ ID NO 5433.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 222.2; DB 6; Length 509;
Best Local Similarity 71.8%; Pred. No. 2.5e-46;
RESULT 1036
ID AAH98536 standard; cDNA; 859 BP.
DE Human EST-derived coding sequence SEQ ID NO: 393.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 222.2; DB 4; Length 859;
Best Local Similarity 83.9%; Pred. No. 3.2e-46;
RESULT 1037
ID AAD34114 standard; cDNA; 921 BP.
DE Human secreted protein-encoding gene 9 cDNA clone HE8N042, SEQ ID NO:19.
PN WO200222654-A1.
PD 21-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 6; Length 921;
Best Local Similarity 85.2%; Pred. No. 3.3e-46;
RESULT 1038
ID AAH17382 standard; cDNA; 2835 BP.
DE Human cDNA sequence SEQ ID NO:16817.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.2; DB 4; Length 2835;
Best Local Similarity 81.8%; Pred. No. 5.4e-46;
RESULT 1039
ID ADO63525 standard; cDNA; 3871 BP.
DE Novel human cDNA sequence #686.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 222.2; DB 12; Length 3871;
Best Local Similarity 84.0%; Pred. No. 6.2e-46;
RESULT 1040
ID AAH18205 standard; cDNA; 3877 BP.
DE Human cDNA sequence SEQ ID NO:18124.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 222.2; DB 4; Length 3877;
Best Local Similarity 85.2%; Pred. No. 6.2e-46;
RESULT 1041
ID AAK80271 standard; DNA; 6418 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35083.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 4; Length 6418;
Best Local Similarity 84.1%; Pred. No. 7.8e-46;
RESULT 1042
ID ADH10009 standard; DNA; 8949 BP.
DE Human FUS II exon A and A1 DNA.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 9.7%; Score 222.2; DB 10; Length 8949;
Best Local Similarity 85.2%; Pred. No. 9.1e-46;
RESULT 1043
ID ADL13829 standard; DNA; 12414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #361.

PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.7%; Score 222.2; DB 10; Length 12414;
Best Local Similarity 81.8%; Pred. No. 1.1e-45;
RESULT 1044
ID AAK67239 standard; DNA; 30393 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22051.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 4; Length 30393;
Best Local Similarity 81.9%; Pred. No. 1.6e-45;
RESULT 1045
ID AAI99255 standard; DNA; 32127 BP.
DE Human excretory related polynucleotide SEQ ID NO 1019.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 4; Length 32127;
Best Local Similarity 84.0%; Pred. No. 1.6e-45;
RESULT 1046
ID AAI63605 standard; DNA; 32127 BP.
DE Human kidney related polynucleotide SEQ ID NO 920.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 5; Length 32127;
Best Local Similarity 84.0%; Pred. No. 1.6e-45;
RESULT 1047
ID AAK82338 standard; DNA; 48908 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 4; Length 48908;
Best Local Similarity 84.0%; Pred. No. 1.9e-45;
RESULT 1048
ID ADC86870 standard; DNA; 69770 BP.
DE Human GPCR gene SEQ ID NO:1323.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 9.7%; Score 222.2; DB 10; Length 69770;
Best Local Similarity 78.8%; Pred. No. 2.3e-45;
RESULT 1049
ID AAK86832 standard; DNA; 72215 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41644.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222.2; DB 4; Length 72215;
Best Local Similarity 84.0%; Pred. No. 2.3e-45;
RESULT 1050
ID ADP08387 standard; DNA; 94400 BP.
DE Human glycoprotein VI (platelet) (GP6/GPIV/GPVI) genomic DNA.
Query Match 9.7%; Score 222.2; DB 12; Length 94400;
Best Local Similarity 84.0%; Pred. No. 2.6e-45;
RESULT 1051
ID AEK50256 standard; DNA; 94400 BP.
DE Human glycoprotein VI (platelet) - GP6 genomic DNA.
PN US2006204967-A1.
PD 14-SEP-2006.
PA (ROTH/) ROTH R. B.
PA (BRAU/) BRAUN A.
PA (KAMM/) KAMMERER S M.
PA (NELS/) NELSON M R.
PA (RENE/) RENELAND R H.
Query Match 9.7%; Score 222.2; DB 15; Length 94400;
Best Local Similarity 84.0%; Pred. No. 2.6e-45;
RESULT 1052
ID ADX98574 standard; DNA; 95050 BP.

DE Human LOC145197 genomic DNA.
Query Match 9.7%; Score 222.2; DB 14; Length 95050;
Best Local Similarity 81.8%; Pred. No. 2.6e-45;
RESULT 1053
ID AEG24777 standard; DNA; 98800 BP.
DE Human TRPS1 DNA.
PN WO2006022636-A1.
PD 02-MAR-2006.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222.2; DB 15; Length 98800;
Best Local Similarity 70.5%; Pred. No. 2.7e-45;
RESULT 1054
ID AEI93841 standard; DNA; 100000 BP.
DE Human glutathione peroxidase 3, GPX3, genomic sequence.
PN WO2006074061-A2.
PD 13-JUL-2006.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222.2; DB 15; Length 100000;
Best Local Similarity 75.8%; Pred. No. 2.7e-45;
RESULT 1055
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 10; Length 128034;
Best Local Similarity 85.2%; Pred. No. 3e-45;
RESULT 1056
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 10; Length 128034;
Best Local Similarity 85.2%; Pred. No. 3e-45;
RESULT 1057
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 12; Length 128034;
Best Local Similarity 85.2%; Pred. No. 3e-45;
RESULT 1058
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 12; Length 128034;
Best Local Similarity 85.2%; Pred. No. 3e-45;
RESULT 1059
ID ABZ35015 standard; cDNA; 136328 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 127.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 9.7%; Score 222.2; DB 6; Length 136328;
Best Local Similarity 87.9%; Pred. No. 3.1e-45;
RESULT 1060
ID ABT10718 standard; cDNA; 185371 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 852.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.7%; Score 222.2; DB 6; Length 185371;
Best Local Similarity 81.8%; Pred. No. 3.5e-45;
RESULT 1061
ID ADM69029 standard; DNA; 191150 BP.
DE Human platelet derived growth factor receptor alpha wild-type gDNA.
PN WO2003105773-A2.

PD 24-DEC-2003.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBEN CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
Query Match 9.7%; Score 222.2; DB 12; Length 191150;
Best Local Similarity 82.1%; Pred. No. 3.6e-45;
RESULT 1062
ID ADL13719 standard; DNA; 199878 BP.
DE Osteoarthritis-associated polymorphic nucleotide #251.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.7%; Score 222.2; DB 10; Length 199878;
Best Local Similarity 73.1%; Pred. No. 3.7e-45;
RESULT 1063
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 10; Length 202100;
Best Local Similarity 85.2%; Pred. No. 3.7e-45;
RESULT 1064
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 9.7%; Score 222.2; DB 12; Length 202100;
Best Local Similarity 85.2%; Pred. No. 3.7e-45;
RESULT 1065
ID ACN44070 standard; DNA; 344548 BP.
DE Human genomic sequence hCG36954.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 222.2; DB 11; Length 344548;
Best Local Similarity 87.9%; Pred. No. 4.7e-45;
RESULT 1066
ID AAK78857 standard; DNA; 358 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33669.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 358;
Best Local Similarity 78.4%; Pred. No. 2.4e-46;
RESULT 1067
ID AAK78858 standard; DNA; 358 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33670.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 358;
Best Local Similarity 78.4%; Pred. No. 2.4e-46;
RESULT 1068
ID ACN40083 standard; cDNA; 2417 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326241, SEQ ID NO:4645.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 222; DB 13; Length 2417;
Best Local Similarity 84.8%; Pred. No. 5.7e-46;
RESULT 1069
ID ADM20191 standard; cDNA; 6491 BP.
DE Alternative nucleotide for novel channel/transporter cDNA #212.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 5; Length 6491;
Best Local Similarity 82.4%; Pred. No. 8.9e-46;
RESULT 1070

ID ADC20800 standard; DNA; 10115 BP.
DE Human secreted protein-related DNA sequence #218.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 10; Length 10115;
Best Local Similarity 83.5%; Pred. No. 1.1e-45;
RESULT 1071
ID ABZ74163 standard; DNA; 10116 BP.
DE Secreted protein gene 200 genomic fragment HMQAI38, SEQ ID NO:1310.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 8; Length 10116;
Best Local Similarity 83.5%; Pred. No. 1.1e-45;
RESULT 1072
ID ABZ74318 standard; DNA; 11168 BP.
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1465.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 8; Length 11168;
Best Local Similarity 82.4%; Pred. No. 1.1e-45;
RESULT 1073
ID ABZ67886 standard; DNA; 11168 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1409.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 10; Length 11168;
Best Local Similarity 82.4%; Pred. No. 1.1e-45;
RESULT 1074
ID AAI99007 standard; DNA; 11992 BP.
DE Human excretory related polynucleotide SEQ ID NO 771.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 11992;
Best Local Similarity 80.3%; Pred. No. 1.2e-45;
RESULT 1075
ID AAK80050 standard; DNA; 11992 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34862.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 11992;
Best Local Similarity 80.3%; Pred. No. 1.2e-45;
RESULT 1076
ID AAI63357 standard; DNA; 11992 BP.
DE Human kidney related polynucleotide SEQ ID NO 672.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 5; Length 11992;
Best Local Similarity 80.3%; Pred. No. 1.2e-45;
RESULT 1077
ID ABZ74319 standard; DNA; 12212 BP.
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1466.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 8; Length 12212;
Best Local Similarity 82.4%; Pred. No. 1.2e-45;
RESULT 1078
ID ABZ67887 standard; DNA; 12212 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1410.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 10; Length 12212;
Best Local Similarity 82.4%; Pred. No. 1.2e-45;
RESULT 1079
ID AAS42069 standard; DNA; 17687 BP.

DE Genomic sequence #385 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 17687;
Best Local Similarity 68.6%; Pred. No. 1.4e-45;
RESULT 1080
ID AAS42064 standard; DNA; 19815 BP.
DE Genomic sequence #380 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 19815;
Best Local Similarity 68.6%; Pred. No. 1.5e-45;
RESULT 1081
ID ABD33582 standard; DNA; 21823 BP.
DE Human cancer-associated (CA) gene HD07-117.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222; DB 13; Length 21823;
Best Local Similarity 84.7%; Pred. No. 1.5e-45;
RESULT 1082
ID ABJ13786 standard; DNA; 21823 BP.
DE Cancer-associated gene sequence - SEQ ID 794.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORA/) MORRIS D W.
Query Match 9.7%; Score 222; DB 15; Length 21823;
Best Local Similarity 84.7%; Pred. No. 1.5e-45;
RESULT 1083
ID AAL05336 standard; DNA; 32249 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8024.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 32249;
Best Local Similarity 72.6%; Pred. No. 1.8e-45;
RESULT 1084
ID ABL98205 standard; DNA; 32249 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2857.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 222; DB 4; Length 32249;
Best Local Similarity 72.6%; Pred. No. 1.8e-45;
RESULT 1085
ID ACN44094 standard; DNA; 35236 BP.
DE Human genomic sequence hCG23314.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 222; DB 11; Length 35236;
Best Local Similarity 82.4%; Pred. No. 1.9e-45;
RESULT 1086
ID ADQ97207 standard; DNA; 56181 BP.
DE Human cancer associated sequence HD08-013, SEQ ID 183.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222; DB 12; Length 56181;
Best Local Similarity 82.4%; Pred. No. 2.3e-45;
RESULT 1087
ID AAC89559 standard; DNA; 80331 BP.
DE Human histone deacetylase HDAC-C coding sequence.
PN WO200071703-A2.
PD 30-NOV-2000.
PA (METH-) METHYLGENE INC.
Query Match 9.7%; Score 222; DB 4; Length 80331;
Best Local Similarity 70.9%; Pred. No. 2.7e-45;
RESULT 1088
ID ADQ97846 standard; DNA; 94911 BP.

DE Human cancer associated sequence HD11-010, SEQ ID 823.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222; DB 12; Length 94911;
Best Local Similarity 83.5%; Pred. No. 3e-45;
RESULT 1099
ID ABQ88125 standard; cDNA; 109201 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 32.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 9.7%; Score 222; DB 6; Length 109201;
Best Local Similarity 83.5%; Pred. No. 3.1e-45;
RESULT 1090
ID ACN44674 standard; DNA; 129042 BP.
DE Human genomic sequence HCG27276.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 222; DB 11; Length 129042;
Best Local Similarity 86.0%; Pred. No. 3.4e-45;
RESULT 1091
ID AED18548 standard; DNA; 150147 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 799.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYEL) UNIV FLORIDA RES FOUND INC.
Query Match 9.7%; Score 222; DB 14; Length 150147;
Best Local Similarity 85.0%; Pred. No. 3.6e-45;
RESULT 1092
ID AAD28763 standard; DNA; 154465 BP.
DE Human AKAP allelic variant (AKAP10-1) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 6; Length 154465;
Best Local Similarity 81.3%; Pred. No. 3.7e-45;
RESULT 1093
ID AAD28762 standard; DNA; 158245 BP.
DE Human AKAP allelic variant (AKAP10) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 6; Length 158245;
Best Local Similarity 81.3%; Pred. No. 3.7e-45;
RESULT 1094
ID AED89421 standard; DNA; 159497 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.7%; Score 222; DB 14; Length 159497;
Best Local Similarity 82.4%; Pred. No. 3.7e-45;
RESULT 1095
ID AAH02340 standard; DNA; 161425 BP.
DE Human AKAP10 gene SEQ ID NO: 36.
PN WO200127857-A2.
PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 4; Length 161425;
Best Local Similarity 81.3%; Pred. No. 3.7e-45;
RESULT 1096
ID AAH02339 standard; DNA; 162025 BP.
DE Human AKAP10 gene SEQ ID NO: 35.
PN WO200127857-A2.
PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 4; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1097
ID AAD28758 standard; DNA; 162025 BP.

DE Human AKAP allelic variant (AKAP10-6) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 6; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1098
ID AAD28759 standard; DNA; 162025 BP.
DE Human AKAP allelic variant (AKAP10-7) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 6; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1099
ID ADS75958 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-6 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 13; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1100
ID ADS75959 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-7 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 13; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1101
ID ADS75963 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-1 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 13; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1102
ID ADS75962 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 wild type genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 9.7%; Score 222; DB 13; Length 162025;
Best Local Similarity 81.3%; Pred. No. 3.8e-45;
RESULT 1103
ID ABE05008 standard; DNA; 246386 BP.
DE Cancer-associated gene SEQ ID NO:326.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.7%; Score 222; DB 14; Length 246386;
Best Local Similarity 84.7%; Pred. No. 4.5e-45;
RESULT 1104
ID ADQ97557 standard; DNA; 254396 BP.
DE Human cancer associated sequence HD09-013, SEQ ID 534.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 222; DB 12; Length 254396;
Best Local Similarity 75.0%; Pred. No. 4.6e-45;
RESULT 1105
ID ADP65796 standard; DNA; 270150 BP.
DE Human 16p133 sequence section 7 of 8 DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 9.7%; Score 222; DB 11; Length 270150;
Best Local Similarity 68.8%; Pred. No. 4.7e-45;
RESULT 1106
ID ABQ92014 standard; cDNA; 4236 BP.
DE Human polynucleotide SEQ ID NO 11.

PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 9.7%; Score 221.8; DB 6; Length 4236;
Best Local Similarity 83.0%; Pred. No. 8.2e-46;
RESULT 1107
ID AAV61487 standard; cDNA; 4237 BP.
DE Human secreted protein fe366_1 cDNA.
PN WO9841539-A2.
PD 24-SEP-1998.
PA (GEMV) GENETICS INST INC.
Query Match 9.7%; Score 221.8; DB 2; Length 4237;
Best Local Similarity 83.0%; Pred. No. 8.2e-46;
RESULT 1108
ID AAK66570 standard; DNA; 10708 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21382.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 4; Length 10708;
Best Local Similarity 83.1%; Pred. No. 1.2e-45;
RESULT 1109
ID ABA16244 standard; DNA; 11715 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8575.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 5; Length 11715;
Best Local Similarity 84.2%; Pred. No. 1.3e-45;
RESULT 1110
ID ADG20558 standard; DNA; 15620 BP.
DE Human RNASEL nucleotide sequence SEQ ID NO:2.
PN WO2003106617-A2.
PD 24-DEC-2003.
PA (TELA-) TEL AVIV MEDICAL CENT RES DEV FUND.
Query Match 9.7%; Score 221.8; DB 12; Length 15620;
Best Local Similarity 83.1%; Pred. No. 1.5e-45;
RESULT 1111
ID AAS36927 standard; DNA; 20869 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2427.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 4; Length 20869;
Best Local Similarity 84.2%; Pred. No. 1.7e-45;
RESULT 1112
ID AAK85001 standard; DNA; 20869 BP..
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39813.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 4; Length 20869;
Best Local Similarity 84.2%; Pred. No. 1.7e-45;
RESULT 1113
ID ABA16245 standard; DNA; 20869 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8576.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 5; Length 20869;
Best Local Similarity 84.2%; Pred. No. 1.7e-45;
RESULT 1114
ID ADE47621 standard; DNA; 20869 BP.
DE Human cardiovascular system related genomic DNA #1187.
PN US2003059908-A1.
PD 27-MAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 10; Length 20869;
Best Local Similarity 84.2%; Pred. No. 1.7e-45;
RESULT 1115
ID ADJ09039 standard; DNA; 20869 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2427.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 13; Length 20869;
Best Local Similarity 84.2%; Pred. No. 1.7e-45;
RESULT 1116
ID AAL03917 standard; DNA; 22299 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6605.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 4; Length 22299;
Best Local Similarity 75.5%; Pred. No. 1.7e-45;
RESULT 1117
ID AAS40317 standard; DNA; 22299 BP.
DE DNA encoding human prostate cancer antigen, Seq ID No 469.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 5; Length 22299;
Best Local Similarity 75.5%; Pred. No. 1.7e-45;
RESULT 1118
ID ADJ09523 standard; DNA; 22299 BP.
DE Human prostate cancer associated gene-related DNA SeqID469.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 11; Length 22299;
Best Local Similarity 75.5%; Pred. No. 1.7e-45;
RESULT 1119
ID ACN44866 standard; DNA; 27204 BP.
DE Human genomic sequence hCG23376.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 221.8; DB 11; Length 27204;
Best Local Similarity 82.1%; Pred. No. 1.9e-45;
RESULT 1120
ID ABK86948 standard; DNA; 28444 BP.
DE Human glutathione synthetase (GSS) gene sequence.
PN WO200238585-A2.
PD 16-MAY-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 9.7%; Score 221.8; DB 6; Length 28444;
Best Local Similarity 82.0%; Pred. No. 1.9e-45;
RESULT 1121
ID AEB31548 standard; DNA; 29764 BP.
DE Glutathione synthetase (GSS) DNA.
PN WO2005068649-A1.
PD 28-JUL-2005.
PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG.
Query Match 9.7%; Score 221.8; DB 14; Length 29764;
Best Local Similarity 82.0%; Pred. No. 2e-45;
RESULT 1122
ID AAK69758 standard; DNA; 32986 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24570.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.8; DB 4; Length 32986;
Best Local Similarity 84.3%; Pred. No. 2.1e-45;
RESULT 1123
ID AAK84629 standard; DNA; 32986 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39441.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 221.8; DB 4; Length 32986;
 Best Local Similarity 84.3%; Pred. No. 2.1e-45;
 RESULT 1124
 ID AAK87512 standard; DNA; 41488 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42324.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 221.8; DB 4; Length 41488;
 Best Local Similarity 76.6%; Pred. No. 2.3e-45;
 RESULT 1125
 ID ADC86998 standard; DNA; 43419 BP.
 DE Human GPCR gene SEQ ID NO:1451.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 9.7%; Score 221.8; DB 10; Length 43419;
 Best Local Similarity 82.0%; Pred. No. 2.3e-45;
 RESULT 1126
 ID AED18692 standard; DNA; 59102 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 943.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 9.7%; Score 221.8; DB 14; Length 59102;
 Best Local Similarity 82.0%; Pred. No. 2.7e-45;
 RESULT 1127
 ID AED18692 standard; DNA; 59102 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 943.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 9.7%; Score 221.8; DB 14; Length 59102;
 Best Local Similarity 82.0%; Pred. No. 2.7e-45;
 RESULT 1128
 ID ABK90695 standard; DNA; 73467 BP.
 DE DNA encoding human transporter protein.
 Query Match 9.7%; Score 221.8; DB 6; Length 73467;
 Best Local Similarity 83.1%; Pred. No. 3e-45;
 RESULT 1129
 ID ABK95843 standard; DNA; 73467 BP.
 DE Genomic DNA encoding novel human transporter protein.
 Query Match 9.7%; Score 221.8; DB 8; Length 73467;
 Best Local Similarity 83.1%; Pred. No. 3e-45;
 RESULT 1130
 ID AEC00670 standard; DNA; 73467 BP.
 DE Human sodium/glucose cotransporter related genomic DNA, SEQ ID NO: 3.
 Query Match 9.7%; Score 221.8; DB 14; Length 73467;
 Best Local Similarity 83.1%; Pred. No. 3e-45;
 RESULT 1131
 ID ABD33179 standard; DNA; 100445 BP.
 DE Human cancer-associated (CA) gene HD07-026.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRIS DISCOVERY INC.
 Query Match 9.7%; Score 221.8; DB 13; Length 100445;
 Best Local Similarity 84.5%; Pred. No. 3.4e-45;
 RESULT 1132
 ID AEJ13162 standard; DNA; 100445 BP.
 DE Cancer-associated gene sequence - SEQ ID 170.
 PN US2006154250-A1.
 PD 13-JUL-2006.
 PA (MORR/) MORRIS D W.
 PA (MALA/) MALANDRO M S.
 Query Match 9.7%; Score 221.8; DB 15; Length 100445;
 Best Local Similarity 84.5%; Pred. No. 3.4e-45;
 RESULT 1133
 ID ABD32988 standard; DNA; 115611 BP.
 DE Human cancer-associated genomic DNA HD21-012.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRIS DISCOVERY INC.

Query Match 9.7%; Score 221.8; DB 13; Length 115611;
 Best Local Similarity 85.5%; Pred. No. 3.6e-45;
 RESULT 1134
 ID ADZ12550 standard; DNA; 117730 BP.
 DE Human cancer-associated genomic DNA #8.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.7%; Score 221.8; DB 14; Length 117730;
 Best Local Similarity 83.1%; Pred. No. 3.7e-45;
 RESULT 1135
 ID ADS36461 standard; DNA; 158417 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 9.7%; Score 221.8; DB 13; Length 158417;
 Best Local Similarity 77.6%; Pred. No. 4.2e-45;
 RESULT 1136
 ID ABK83497 standard; cDNA; 227968 BP.
 DE Human cDNA differentially expressed in granulocytic cells #68.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.7%; Score 221.8; DB 6; Length 227968;
 Best Local Similarity 83.1%; Pred. No. 4.9e-45;
 RESULT 1137
 ID ADQ18538 standard; DNA; 227968 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 9.7%; Score 221.8; DB 12; Length 227968;
 Best Local Similarity 83.1%; Pred. No. 4.9e-45;
 RESULT 1138
 ID AED17856 standard; DNA; 227968 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 107.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 9.7%; Score 221.8; DB 14; Length 227968;
 Best Local Similarity 83.1%; Pred. No. 4.9e-45;
 RESULT 1139
 ID AEF51726 standard; DNA; 304486 BP.
 DE Human p21-activated kinase 5 (PAK5) encoding DNA.
 PN EP1619504-A1.
 PD 25-JAN-2006.
 PA (FRAU-) FRAUNHOFER INST TOXIKOLOGIE & EXPERIMENT.
 Query Match 9.7%; Score 221.8; DB 15; Length 304486;
 Best Local Similarity 85.5%; Pred. No. 5.6e-45;
 RESULT 1140
 ID ADM81937 standard; DNA; 408 BP.
 DE NBP3K9 marker amplicon #182.
 PN WO2005007144-A2.
 PD 27-JAN-2005.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 9.7%; Score 221.6; DB 14; Length 408;
 Best Local Similarity 78.2%; Pred. No. 3.2e-46;
 RESULT 1141
 ID AEK86105 standard; DNA; 408 BP.
 DE Human chromosome-14 microsatellite, SEQ ID NO:1278.
 PN WO2006081555-A2.
 PD 03-AUG-2006.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 9.7%; Score 221.6; DB 15; Length 408;
 Best Local Similarity 78.2%; Pred. No. 3.2e-46;
 RESULT 1142
 ID ABN65219 standard; cDNA; 602 BP.
 DE Human cancer related polynucleotide SEQ ID NO 5186.
 PN WO200214500-A2.
 PD 21-FEB-2002.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 221.6; DB 6; Length 602;
Best Local Similarity 81.5%; Pred. No. 3.9e-46;
RESULT 1143
ID ACL58593 standard; cDNA; 602 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:4728.
PN WO200500087-A2.
PA (CHIR) CHIRON CORP.
Query Match 9.7%; Score 221.6; DB 14; Length 602;
Best Local Similarity 81.5%; Pred. No. 3.9e-46;
RESULT 1144
ID AAI59074 standard; cDNA; 1426 BP.
DE Human polynucleotide SEQ ID NO 1277.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 221.6; DB 4; Length 1426;
Best Local Similarity 80.7%; Pred. No. 5.7e-46;
RESULT 1145
ID ADQ99297 standard; cDNA; 1426 BP.
DE DNA encoding human GPCR-like protein seqid 967.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 221.6; DB 5; Length 1426;
Best Local Similarity 80.7%; Pred. No. 5.7e-46;
RESULT 1146
ID ADB49057 standard; cDNA; 1426 BP.
DE Novel human cDNA SEQ ID NO 967.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 9.7%; Score 221.6; DB 9; Length 1426;
Best Local Similarity 80.7%; Pred. No. 5.7e-46;
RESULT 1147
ID ADM01487 standard; cDNA; 2345 BP.
DE Human cDNA of the invention SEQ ID NO:172.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 221.6; DB 11; Length 2345;
Best Local Similarity 85.0%; Pred. No. 7.1e-46;
RESULT 1148
ID AEC94417 standard; cDNA; 2345 BP.
DE Human cDNA clone BRACE20228480, SEQ ID 172.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 221.6; DB 14; Length 2345;
Best Local Similarity 85.0%; Pred. No. 7.1e-46;
RESULT 1149
ID ADB63298 standard; cDNA; 2405 BP.
DE Human cDNA encoding clone TEST120057200.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 221.6; DB 10; Length 2405;
Best Local Similarity 82.6%; Pred. No. 7.2e-46;
RESULT 1150
ID ARAH4554 standard; cDNA; 2918 BP.
DE Human cDNA sequence SEQ ID NO:12123.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 221.6; DB 4; Length 2918;
Best Local Similarity 86.2%; Pred. No. 7.8e-46;
RESULT 1151
ID AFG92703 standard; cDNA; 2921 BP.

DE Human tumor cell cDNA SEQ ID NO:199.
PN WO2006036025-A1.
PD 06-APR-2006.
PA (EISA) EISAI CO LTD.
Query Match 9.7%; Score 221.6; DB 15; Length 2921;
Best Local Similarity 86.2%; Pred. No. 7.8e-46;
RESULT 1152
ID AEG5422 standard; DNA; 3102 BP..
DE Human Kir6.2 genomic DNA.
PN WO2006027128-A1.
PD 16-MAR-2006.
PA (SNFI) SANOFI-AVENTIS DEUT GMBH.
Query Match 9.7%; Score 221.6; DB 15; Length 3102;
Best Local Similarity 82.6%; Pred. No. 8e-46;
RESULT 1153
ID AEE83655 standard; cDNA; 3807 BP.
DE Human cDNA differentially expressed in asthma, SEQ ID NO:63.
PN WO2005118403-A2.
PD 15-DEC-2005.
PA (LINK-) LINKAGENE LTD.
Query Match 9.7%; Score 221.6; DB 15; Length 3807;
Best Local Similarity 76.8%; Pred. No. 8.8e-46;
RESULT 1154
ID ABZ20987 standard; DNA; 5278 BP.
DE Human thyroid tumour associated CAT-A genomic sequence SEQ ID NO: 12.
PN WO200283727-A2.
PD 24-OCT-2002.
PA (BULL/) BULLERDIEK J.
Query Match 9.7%; Score 221.6; DB 10; Length 5278;
Best Local Similarity 81.5%; Pred. No. 1e-45;
RESULT 1155
ID ADX08890 standard; DNA; 7639 BP.
DE Human matrix metalloproteinase 9 gene.
PN WO2005017113-A2.
PD 24-FEB-2005.
PA (LOVE-) LOVEACE RESPIRATORY RES INST.
Query Match 9.7%; Score 221.6; DB 14; Length 7639;
Best Local Similarity 85.0%; Pred. No. 1.2e-45;
RESULT 1156
ID AAK81565 standard; DNA; 14897 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36377.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.6; DB 4; Length 14897;
Best Local Similarity 76.8%; Pred. No. 1.6e-45;
RESULT 1157
ID AAK81510 standard; DNA; 15651 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36322.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.6; DB 4; Length 15651;
Best Local Similarity 86.2%; Pred. No. 1.7e-45;
RESULT 1158
ID AEN89476 standard; cDNA; 19806 BP.
DE Human dehydrogenase genomic DNA SEQ ID NO:3.
PN WO200250255-A2.
PD 27-JUN-2002.
PA (PEKE) PE CORP NY.
Query Match 9.7%; Score 221.6; DB 6; Length 19806;
Best Local Similarity 86.2%; Pred. No. 1.8e-45;
RESULT 1159
ID ABD33092 standard; DNA; 21602 BP.
DE Human cancer-associated (CA) gene HD07-006.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.6; DB 13; Length 21602;
Best Local Similarity 76.3%; Pred. No. 1.9e-45;
RESULT 1160
ID AEJ13028 standard; DNA; 21602 BP.
DE Cancer-associated gene sequence - SEQ ID 36.

RESULT 1179
ID ABL78937 standard; DNA; 6458 BP.
DE Type-II diabetes susceptibility gene KCN11.
PN CN171550-A.
PD 18-JAN-2006.
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MED.
Query Match 9.7%; Score 221.4; DB 15; Length 6458;
Best Local Similarity 83.3%; Pred. No. 1.3e-45;
RESULT 1180
ID ABA07082 standard; DNA; 9721 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 401.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 9721;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1181
ID AAK89292 standard; DNA; 9721 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2868.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 9721;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1182
ID AAK65483 standard; DNA; 11127 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 20295.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 9721;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1183
ID AAL05506 standard; DNA; 11127 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8194.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 11127;
Best Local Similarity 82.2%; Pred. No. 1.6e-45;
RESULT 1184
ID AAS0353 standard; DNA; 12482 BP.
DE Human Goodpasture antigen binding protein gene.
PN WO200050607-A2.
PD 31-AUG-2000.
PA (SAUS/) SAUS J.
Query Match 9.7%; Score 221.4; DB 3; Length 12482;
Best Local Similarity 77.6%; Pred. No. 1.7e-45;
RESULT 1185
ID ABS64477 standard; DNA; 12482 BP.
DE Human Goodpasture binding protein, GPBP, genomic DNA.
PN WO200261430-A2.
PD 08-AUG-2002.
PA (SAUS/) SAUS J.
Query Match 9.7%; Score 221.4; DB 6; Length 12482;
Best Local Similarity 77.6%; Pred. No. 1.7e-45;
RESULT 1186
ID ADF69350 standard; DNA; 12482 BP.
DE Human Goodpasture antigen binding protein (GPBP) genomic DNA.
PN US2003054488-A1.
PD 20-MAR-2003.
PA (SAUS/) SAUS J.
Query Match 9.7%; Score 221.4; DB 10; Length 12482;
Best Local Similarity 77.6%; Pred. No. 1.7e-45;
RESULT 1187
ID AAK69721 standard; DNA; 16086 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 24533.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 16086;
Best Local Similarity 84.5%; Pred. No. 1.9e-45;
RESULT 1188
ID AAL36020 standard; DNA; 16086 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2385.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 4; Length 16086;
Best Local Similarity 84.5%; Pred. No. 1.9e-45;
RESULT 1189
ID ABX59008 standard; cDNA; 16086 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1352.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 221.4; DB 8; Length 16086;
Best Local Similarity 84.5%; Pred. No. 1.9e-45;
RESULT 1190
ID ADJ23758 standard; DNA; 16086 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2385.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.4; DB 12; Length 16086;
Best Local Similarity 84.5%; Pred. No. 1.9e-45;
RESULT 1191
ID ABD33005 standard; DNA; 31840 BP.
DE Human cancer-associated genomic DNA HD21-026.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.4; DB 13; Length 31840;
Best Local Similarity 82.2%; Pred. No. 2.6e-45;
RESULT 1192
ID ABK84372 standard; cDNA; 37160 BP.
DE Human cDNA differentially expressed in granulocytic cells #943.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.7%; Score 221.4; DB 6; Length 37160;
Best Local Similarity 87.0%; Pred. No. 2.8e-45;
RESULT 1193
ID AAL57448 standard; DNA; 39726 BP.
DE Human NSD1 genomic DNA sequence.
PN EP1321533-A2.
PD 25-JUN-2003.
PA (UYNA-) UNIV NAGASAKI.
Query Match 9.7%; Score 221.4; DB 9; Length 39726;
Best Local Similarity 79.1%; Pred. No. 2.8e-45;
RESULT 1194
ID ADB16926 standard; DNA; 50000 BP.
DE Human DYX1C1 DNA, chromosomal gene region nucleotides 1-50000.
PN WO2003068814-A1.
PD 21-AUG-2003.
PA (LICN) LICENTIA LTD.
Query Match 9.7%; Score 221.4; DB 9; Length 50000;
Best Local Similarity 83.4%; Pred. No. 3.2e-45;
RESULT 1195
ID ADQ97986 standard; DNA; 86899 BP.
DE Human cancer associated sequence HD11-036, SEQ ID 963.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.4; DB 12; Length 86899;
Best Local Similarity 82.3%; Pred. No. 4e-45;
RESULT 1196
ID ADQ19501 standard; DNA; 135005 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.7%; Score 221.4; DB 12; Length 135005;
Best Local Similarity 84.5%; Pred. No. 4.9e-45;

RESULT 1197
ID AED89414 standard; DNA; 150450 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 54.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.7%; Score 221.4; DB 14; Length 150450;
Best Local Similarity 84.5%; Pred. No. 5.2e-45;
RESULT 1198
ID AEF19127 standard; DNA; 188056 BP.
DE Human NIPBL genomic sequence.
PN US2006003354-A1.
PD 05-JAN-2006.
PA (KRAN/) KRANTZ I D.
PA (JACK/) JACKSON L G.
Query Match 9.7%; Score 221.4; DB 15; Length 188056;
Best Local Similarity 88.0%; Pred. No. 5.7e-45;
RESULT 1199
ID AEA17302 standard; DNA; 197140 BP.
DE Human GNAI gene locus Seq 12.
PN WO2005047318-A1.
PD 26-MAY-2005.
PA (ASTR-) ASTRAZENECA AB.
PA (ASTR-) ASTRAZENECA UK LTD.
Query Match 9.7%; Score 221.4; DB 14; Length 197140;
Best Local Similarity 84.5%; Pred. No. 5.8e-45;
RESULT 1200
ID AED89381 standard; DNA; 207908 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 21.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 9.7%; Score 221.4; DB 14; Length 207908;
Best Local Similarity 85.7%; Pred. No. 6e-45;
RESULT 1201
ID AAH17100 standard; cDNA; 1803 BP.
DE Human cDNA sequence SEQ ID NO:16426.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.7%; Score 221.2; DB 4; Length 1803;
Best Local Similarity 85.4%; Pred. No. 8e-46;
RESULT 1202
ID AAS21879 standard; DNA; 1867 BP.
DE Human collagen gene COL9A1 5' UTR.
PN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
Query Match 9.7%; Score 221.2; DB 5; Length 1867;
Best Local Similarity 81.7%; Pred. No. 8.1e-46;
RESULT 1203
ID ABA14499 standard; DNA; 2229 BP.
DE Human nervous system related polynucleotide SEQ ID NO 6830.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 5; Length 2229;
Best Local Similarity 85.2%; Pred. No. 8.8e-46;
RESULT 1204
ID AAK69791 standard; DNA; 2784 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24603.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 2784;
Best Local Similarity 80.7%; Pred. No. 9.7e-46;
RESULT 1205
ID AAK69792 standard; DNA; 2787 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24604.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 2787;
Best Local Similarity 80.7%; Pred. No. 9.7e-46;
RESULT 1206
ID AAL05661 standard; DNA; 2787 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8349.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 2787;
Best Local Similarity 80.7%; Pred. No. 9.7e-46;
RESULT 1207
ID ABA07987 standard; DNA; 2787 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 782.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 2787;
Best Local Similarity 80.7%; Pred. No. 9.7e-46;
RESULT 1208
ID AAL36019 standard; DNA; 5930 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2384.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 5930;
Best Local Similarity 85.2%; Pred. No. 1.4e-45;
RESULT 1209
ID ABX59007 standard; cDNA; 5930 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1351.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 221.2; DB 8; Length 5930;
Best Local Similarity 85.2%; Pred. No. 1.4e-45;
RESULT 1210
ID ADJ29757 standard; DNA; 5930 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2384.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 12; Length 5930;
Best Local Similarity 85.2%; Pred. No. 1.4e-45;
RESULT 1211
ID ABZ09913 standard; DNA; 6289 BP.
DE Human 5' and/or regulatory region of RBL2 DNA SEQ ID NO:53.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 9.7%; Score 221.2; DB 8; Length 6289;
Best Local Similarity 86.5%; Pred. No. 1.4e-45;
RESULT 1212
ID ADE84033 standard; DNA; 9289 BP.
DE 5' regulatory region of human gene RBL2.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 9.7%; Score 221.2; DB 10; Length 9289;
Best Local Similarity 86.5%; Pred. No. 1.7e-45;
RESULT 1213
ID AAL05679 standard; DNA; 10680 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8367.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 10680;
Best Local Similarity 80.4%; Pred. No. 1.8e-45;
RESULT 1214
ID AAK68712 standard; DNA; 11482 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 11482;
Best Local Similarity 78.7%; Pred. No. 1.8e-45;
RESULT 1215
ID AAK71246 standard; DNA; 11482 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 11482;
Best Local Similarity 78.7%; Pred. No. 1.8e-45;
RESULT 1216
ID AEG35806 standard; DNA; 23880 BP.
DE Human calcium channel 1D subunit G16155 allele DNA sequence SEQ ID NO: 4.
PN JP2006067886-A.
PD 16-MAR-2006.
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.
Query Match 9.7%; Score 221.2; DB 15; Length 23880;
Best Local Similarity 85.2%; Pred. No. 2.5e-45;
RESULT 1217
ID AEG35818 standard; DNA; 23880 BP.
DE Human calcium channel 1D subunit A16155 allele DNA sequence.
PN JP2006067886-A.
PD 16-MAR-2006.
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.
Query Match 9.7%; Score 221.2; DB 15; Length 23880;
Best Local Similarity 85.2%; Pred. No. 2.5e-45;
RESULT 1218
ID AAS21771 standard; DNA; 24183 BP.
DE Human gene for collagen COL9A1.
PN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
Query Match 9.7%; Score 221.2; DB 5; Length 24183;
Best Local Similarity 81.7%; Pred. No. 2.6e-45;
RESULT 1219
ID ACN44954 standard; DNA; 31116 BP.
DE Human genomic sequence HCG38622.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 221.2; DB 11; Length 31116;
Best Local Similarity 80.9%; Pred. No. 2.9e-45;
RESULT 1220
ID AD213255 standard; DNA; 31279 BP.
DE Human cancer-associated genomic DNA #63.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 9.7%; Score 221.2; DB 14; Length 31279;
Best Local Similarity 80.9%; Pred. No. 2.9e-45;
RESULT 1221
ID AAK77458 standard; DNA; 44196 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32270.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221.2; DB 4; Length 44196;
Best Local Similarity 82.9%; Pred. No. 3.4e-45;
RESULT 1222
ID ABE05072 standard; DNA; 50244 BP.
DE Cancer-associated gene SEQ ID NO:390.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR-) CHIRON CORP.
Query Match 9.7%; Score 221.2; DB 14; Length 50244;
Best Local Similarity 84.3%; Pred. No. 3.6e-45;
RESULT 1223
ID ADC87618 standard; DNA; 58366 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2071.

PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 9.7%; Score 221.2; DB 10; Length 58366;
Best Local Similarity 86.5%; Pred. No. 3.8e-45;
RESULT 1224
ID ADA02540 standard; DNA; 58822 BP.
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 221.2; DB 9; Length 58822;
Best Local Similarity 80.9%; Pred. No. 3.8e-45;
RESULT 1225
ID ADB72278 standard; DNA; 58822 BP.
DE Human TCOF1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 221.2; DB 10; Length 58822;
Best Local Similarity 80.9%; Pred. No. 3.8e-45;
RESULT 1226
ID ADE95788 standard; DNA; 58822 BP.
DE Human TCOF1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 221.2; DB 10; Length 58822;
Best Local Similarity 80.9%; Pred. No. 3.8e-45;
RESULT 1227
ID AEK60059 standard; DNA; 58822 BP.
DE Human TCOF1 genomic sequence, SEQ ID NO:46.
PN US2006204982-A1.
PD 14-SEP-2006.
PA (MORR-) MORRIS D W.
PA (ENGEL-) ENGELHARD E K.
Query Match 9.7%; Score 221.2; DB 15; Length 58822;
Best Local Similarity 80.9%; Pred. No. 3.8e-45;
RESULT 1228
ID AEQ88096 standard; cDNA; 92638 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 3.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 9.7%; Score 221.2; DB 6; Length 92638;
Best Local Similarity 80.4%; Pred. No. 4.7e-45;
RESULT 1229
ID ADQ97313 standard; DNA; 121062 BP.
DE Human cancer associated sequence HD08-030, SEQ ID 290.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.2; DB 12; Length 121062;
Best Local Similarity 82.8%; Pred. No. 5.3e-45;
RESULT 1230
ID ADX06911 standard; DNA; 131078 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1476.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 9.7%; Score 221.2; DB 14; Length 131078;
Best Local Similarity 80.7%; Pred. No. 5.5e-45;
RESULT 1231
ID AEE04699 standard; DNA; 151790 BP.
DE Cancer-associated gene SEQ ID NO:17.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR-) CHIRON CORP.
Query Match 9.7%; Score 221.2; DB 14; Length 151790;
Best Local Similarity 84.3%; Pred. No. 5.8e-45;
RESULT 1232

ID ADQ59422 standard; DNA; 246940 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.2; DB 12; Length 246940;
Best Local Similarity 80.7%; Pred. No. 7.3e-45;
RESULT 1233
ID ADQ59416 standard; DNA; 337022 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:52.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 221.2; DB 12; Length 337022;
Best Local Similarity 85.2%; Pred. No. 8.4e-45;
RESULT 1234
ID ADZ13691 standard; DNA; 338780 BP.
DE Human cancer-associated genomic DNA #105.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.7%; Score 221.2; DB 14; Length 338780;
Best Local Similarity 85.2%; Pred. No. 8.4e-45;
RESULT 1235
ID ADC86642 standard; DNA; 349881 BP.
DE Human GPCR gene SEQ ID NO:1095.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 9.7%; Score 221.2; DB 10; Length 349881;
Best Local Similarity 86.5%; Pred. No. 8.5e-45;
RESULT 1236
ID ADQ64631 standard; cDNA; 1955 BP.
DE Novel human cDNA sequence #1792.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 221; DB 12; Length 1955;
Best Local Similarity 83.5%; Pred. No. 9.3e-46;
RESULT 1237
ID AAA40727 standard; DNA; 2561 BP.
DE Wild type human CD36 nucleic acid sequence SEQ ID NO:101.
PN WO200019883-A2.
PD 13-APR-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
Query Match 9.7%; Score 221; DB 3; Length 2561;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1238
ID AAA40745 standard; DNA; 2561 BP.
DE Wild type human CD36 nucleic acid sequence SEQ ID NO:119.
PN WO200019883-A2.
PD 13-APR-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
Query Match 9.7%; Score 221; DB 3; Length 2561;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1239
ID ADL13540 standard; DNA; 2561 BP.
DE Osteoarthritis-associated polymorphic nucleotide #72.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.7%; Score 221; DB 10; Length 2561;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1240

ID ADO15852 standard; DNA; 3442 BP.
DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 114.
PN WO2004039975-A1.
PD 13-MAY-2004.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 9.7%; Score 221; DB 12; Length 3442;
Best Local Similarity 82.4%; Pred. No. 1.2e-45;
RESULT 1241
ID ADQ63041 standard; cDNA; 4161 BP.
DE Novel human cDNA sequence #202.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 221; DB 12; Length 4161;
Best Local Similarity 83.5%; Pred. No. 1.3e-45;
RESULT 1242
ID ADG32780 standard; DNA; 5957 BP.
DE Human DNA differentially expressed in patients with SLE SeqID104.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 9.7%; Score 221; DB 10; Length 5957;
Best Local Similarity 80.2%; Pred. No. 1.5e-45;
RESULT 1243
ID ADR24391 standard; DNA; 5957 BP.
DE Breast cancer prognosis marker #252.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 9.7%; Score 221; DB 13; Length 5957;
Best Local Similarity 80.2%; Pred. No. 1.5e-45;
RESULT 1244
ID AAK78524 standard; DNA; 8912 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33336.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221; DB 4; Length 8912;
Best Local Similarity 71.4%; Pred. No. 1.8e-45;
RESULT 1245
ID AAK78525 standard; DNA; 9857 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33337.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221; DB 4; Length 9857;
Best Local Similarity 71.4%; Pred. No. 1.9e-45;
RESULT 1246
ID AAL05479 standard; DNA; 9857 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8167.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221; DB 4; Length 9857;
Best Local Similarity 71.4%; Pred. No. 1.9e-45;
RESULT 1247
ID ABL98332 standard; DNA; 9857 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2984.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 221; DB 4; Length 9857;
Best Local Similarity 71.4%; Pred. No. 1.9e-45;
RESULT 1248
ID ADB99091 standard; cDNA; 14581 BP.
DE Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #1.
PN US2003096750-A1.
PD 22-MAY-2003.
PA (TOMB/) TOMBRAN-TINK J.
PA (STEE/) STEELE F R.
PA (CHAD/) CHADER G J.

PA (BECE/) BECERRA S P.
 PA (JOHN/) JOHNSON L V.
 PA (RODR/) RODRIGUEZ I R.
 Query Match 9.7%; Score 221; DB 10; Length 14581;
 Best Local Similarity 84.7%; Pred. No. 2.3e-45;
 RESULT 1249
 ID ABS57267 standard; DNA; 14581 BP.
 DE Partial sequence #1 of genomic DNA encoding human PEDF.
 PN US6451763-B1.
 PD 17-SEP-2002.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 9.7%; Score 221; DB 10; Length 14581;
 Best Local Similarity 84.7%; Pred. No. 2.3e-45;
 RESULT 1250
 ID AAS34685 standard; DNA; 19205 BP.
 DE Human DNA for a novel foetal antigen, SEQ ID NO 2109.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 221; DB 5; Length 19205;
 Best Local Similarity 87.0%; Pred. No. 2.6e-45;
 RESULT 1251
 ID AAK90824 standard; DNA; 21393 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 4400.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 221; DB 4; Length 21393;
 Best Local Similarity 82.4%; Pred. No. 2.7e-45;
 RESULT 1252
 ID AAS11948 standard; DNA; 21393 BP.
 DE Human DNA for novel secreted protein.
 PN WO200155200-A1.
 PD 02-AUG-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 221; DB 5; Length 21393;
 Best Local Similarity 82.4%; Pred. No. 2.7e-45;
 RESULT 1253
 ID AAT11658 standard; DNA; 22481 BP.
 DE PEDF full length sequence and flanking sequences.
 PN WO9533480-A1.
 PD 14-DEC-1995.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 9.7%; Score 221; DB 2; Length 22481;
 Best Local Similarity 84.7%; Pred. No. 2.8e-45;
 RESULT 1254
 ID ABA98882 standard; DNA; 22484 BP.
 DE Nucleotide sequence related to the SLED sequence of the invention.
 PN US2002002131-A1.
 PD 03-JAN-2002.
 PA (BOUC/) BOUCK N P.
 PA (DAWS/) DAWSON D W.
 PA (GILL/) GILLIS P R.
 Query Match 9.7%; Score 221; DB 6; Length 22484;
 Best Local Similarity 84.7%; Pred. No. 2.8e-45;
 RESULT 1255
 ID ABA05882 standard; DNA; 22484 BP.
 DE Angiogenesis inhibition method related DNA.
 PN US2001049355-A1.
 PD 06-DEC-2001.
 PA (BOUC/) BOUCK N P.
 PA (DAWS/) DAWSON D W.
 PA (GILL/) GILLIS P R.
 Query Match 9.7%; Score 221; DB 6; Length 22484;
 Best Local Similarity 84.7%; Pred. No. 2.8e-45;
 RESULT 1256
 ID ABO88196 standard; cDNA; 22484 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 103.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 9.7%; Score 221; DB 6; Length 22484;
 Best Local Similarity 84.7%; Pred. No. 2.8e-45;

RESULT 1257
 ID ABN96844 standard; DNA; 22484 BP.
 DE Gene #3342 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.7%; Score 221; DB 6; Length 22484;
 Best Local Similarity 84.7%; Pred. No. 2.8e-45;
 RESULT 1258
 ID ABK14446 standard; DNA; 26201 BP.
 DE Human HMGCL gene, generic sequence.
 PN WO200198315-A2.
 PD 27-DEC-2001.
 PA (GENA-) GENAISANCE PHARM INC.
 Query Match 9.7%; Score 221; DB 6; Length 26201;
 Best Local Similarity 83.5%; Pred. No. 3e-45;
 RESULT 1259
 ID ABK14039 standard; DNA; 26201 BP.
 DE Human 3-hydroxy-3-methylglutaryl coenzyme A lyase (HMGCL) gene sequence.
 PN WO200198315-A2.
 PD 27-DEC-2001.
 PA (GENA-) GENAISANCE PHARM INC.
 Query Match 9.7%; Score 221; DB 6; Length 26201;
 Best Local Similarity 83.5%; Pred. No. 3e-45;
 RESULT 1260
 ID ABS54327 standard; DNA; 32654 BP.
 DE Gene encoding human kinase.
 DE Gene encoding human kinase.
 Query Match 9.7%; Score 221; DB 6; Length 32654;
 Best Local Similarity 85.0%; Pred. No. 3.3e-45;
 RESULT 1261
 ID ABZ09862 standard; DNA; 35962 BP.
 DE Human 5' and/or regulatory region of ABL1 DNA SEQ ID NO:2.
 PN WO200277272-A2.
 PD 03-OCT-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 9.7%; Score 221; DB 8; Length 35962;
 Best Local Similarity 83.5%; Pred. No. 3.4e-45;
 RESULT 1262
 ID ADL13478 standard; DNA; 35962 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #10.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 9.7%; Score 221; DB 10; Length 35962;
 Best Local Similarity 83.5%; Pred. No. 3.4e-45;
 RESULT 1263
 ID ADR52883 standard; DNA; 35962 BP.
 DE Drug therapy altered expressed gene #234.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC/) BURCZYNSKI M.
 PA (TWIN/) TWINE N.
 PA (DORN/) DORNER A J.
 PA (TREP/) TREPICCHIO W L.
 Query Match 9.7%; Score 221; DB 13; Length 35962;
 Best Local Similarity 83.5%; Pred. No. 3.4e-45;
 RESULT 1264
 Query Match 9.7%; Score 221; DB 10; Length 54391;
 Best Local Similarity 82.4%; Pred. No. 4.1e-45;
 RESULT 1265
 Query Match 9.7%; Score 221; DB 14; Length 54396;
 Best Local Similarity 82.4%; Pred. No. 4.1e-45;
 RESULT 1266
 ID ACN44198 standard; DNA; 63313 BP.
 DE Human genomic sequence hCG19397.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.7%; Score 221; DB 11; Length 63313;
 Best Local Similarity 86.0%; Pred. No. 4.4e-45;
 RESULT 1267
 ID ACN44362 standard; DNA; 68255 BP.

DE Human genomic sequence HCG39597.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.7%; Score 221; DB 11; Length 68255;
 Best Local Similarity 80.3%; Pred. No. 4.6e-45;
 RESULT 1268
 ID ADZ10962 standard; DNA; 74424 BP.
 DE Human STAT3 DNA sequence - SEQ ID 153.
 PN US2005074879-A1.
 PD 07-APR-2005.
 PA (KARR/) KARRAS J G.
 Query Match 9.7%; Score 221; DB 14; Length 74424;
 Best Local Similarity 82.4%; Pred. No. 4.8e-45;
 RESULT 1269
 ID AEK52879 standard; DNA; 74424 BP.
 DE Human chromosome 17 genomic contig DNA SEQ ID: 153.
 PN US2006217319-A1.
 PD 28-SEP-2006.
 PA (KARR/) KARRAS J G.
 Query Match 9.7%; Score 221; DB 15; Length 74424;
 Best Local Similarity 82.4%; Pred. No. 4.8e-45;
 RESULT 1270
 ID AEG05665 standard; DNA; 79950 BP.
 DE Human FLJ14297 genomic DNA SEQ ID NO 2.
 PN WO2006022629-A1.
 PD 02-MAR-2006.
 PA (SEU-) SEQUENOM INC.
 Query Match 9.7%; Score 221; DB 15; Length 79950;
 Best Local Similarity 63.2%; Pred. No. 4.9e-45;
 RESULT 1271
 ID ABD32673 standard; DNA; 91359 BP.
 DE Human cancer-associated genomic DNA HD13-075.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.7%; Score 221; DB 13; Length 91359;
 Best Local Similarity 81.3%; Pred. No. 5.2e-45;
 RESULT 1272
 Query Match 9.7%; Score 221; DB 4; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1273
 Query Match 9.7%; Score 221; DB 4; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1274
 Query Match 9.7%; Score 221; DB 6; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1275
 Query Match 9.7%; Score 221; DB 6; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1276
 Query Match 9.7%; Score 221; DB 11; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1277
 Query Match 9.7%; Score 221; DB 12; Length 110000;
 Best Local Similarity 81.6%; Pred. No. 5.7e-45;
 RESULT 1278
 ID AEE04879 standard; DNA; 681142 BP.
 DE Cancer-associated gene SEQ ID NO:197.
 PN WO2005107396-A2.
 PD 17-NOV-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.7%; Score 221; DB 14; Length 110000;
 Best Local Similarity 84.7%; Pred. No. 5.7e-45;
 RESULT 1279
 ID ABN95044 standard; DNA; 110096 BP.
 DE Gene #1542 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.7%; Score 221; DB 6; Length 110096;
 Best Local Similarity 83.5%; Pred. No. 5.7e-45;
 RESULT 1280

ID AED18046 standard; DNA; 110096 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 297.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 9.7%; Score 221; DB 14; Length 110096;
 Best Local Similarity 83.5%; Pred. No. 5.7e-45;
 RESULT 1281
 ID AEF74649 standard; DNA; 110096 BP.
 DE Human polynucleotide #163.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 9.7%; Score 221; DB 15; Length 110096;
 Best Local Similarity 83.5%; Pred. No. 5.7e-45;
 RESULT 1282
 ID AEF74540 standard; DNA; 110096 BP.
 DE Human polynucleotide #54.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 9.7%; Score 221; DB 15; Length 110096;
 Best Local Similarity 83.5%; Pred. No. 5.7e-45;
 RESULT 1283
 ID AEF74955 standard; DNA; 110096 BP.
 DE Human polynucleotide #469.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 9.7%; Score 221; DB 15; Length 110096;
 Best Local Similarity 83.5%; Pred. No. 5.7e-45;
 RESULT 1284
 ID ADP84158 standard; DNA; 129017 BP.
 DE Human AST-1 locus DNA representing part of the GPRA gene SeqID 1.
 PN WO2005012875-A2.
 PD 10-FEB-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 9.7%; Score 221; DB 14; Length 131078;
 Best Local Similarity 86.0%; Pred. No. 6.2e-45;
 RESULT 1286
 ID ACF62732 standard; DNA; 177531 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.
 PN WO2003013534-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.7%; Score 221; DB 8; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1287
 ID ADB20847 standard; DNA; 177531 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:660.
 PN WO2003013533-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.7%; Score 221; DB 8; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1288
 ID ADB87936 standard; DNA; 177531 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:660.
 PN WO2003013536-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.7%; Score 221; DB 10; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1289
 ID ADB96919 standard; DNA; 177531 BP.

DE Human MDR1 related DNA sequence SEQ ID NO:660.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.7%; Score 221; DB 10; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1290
 ID ADB921110 standard; DNA; 177531 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:660.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 9.7%; Score 221; DB 10; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1291
 ID ADH74617 standard; DNA; 177531 BP.
 DE Human BAC clone GSI-259H13 CYP3A5 genomic DNA.
 PN US2003143537-A1.
 PD 31-JUL-2003.
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 Query Match 9.7%; Score 221; DB 10; Length 177531;
 Best Local Similarity 82.4%; Pred. No. 7.1e-45;
 RESULT 1292
 ID ACN44170 standard; DNA; 196686 BP.
 DE Human genomic sequence HCG39530.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.7%; Score 221; DB 11; Length 196686;
 Best Local Similarity 80.2%; Pred. No. 7.4e-45;
 RESULT 1293
 ID AEF95801 standard; DNA; 207740 BP.
 DE Human chromosome 20 partial genomic sequence SEQ ID NO:1.
 PN JP2006042735-A.
 PD 16-FEB-2006.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
 Query Match 9.7%; Score 221; DB 15; Length 207740;
 Best Local Similarity 86.0%; Pred. No. 7.6e-45;
 RESULT 1294
 ID ACN44046 standard; DNA; 260027 BP.
 DE Human genomic sequence HCG1735292.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.7%; Score 221; DB 11; Length 260027;
 Best Local Similarity 86.0%; Pred. No. 8.4e-45;
 RESULT 1295
 ID ADE86352 standard; DNA; 300000 BP.
 DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.
 PN WO2003029422-A2.
 PD 10-APR-2003.
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 Query Match 9.7%; Score 221; DB 10; Length 300000;
 Best Local Similarity 83.5%; Pred. No. 8.9e-45;
 RESULT 1296
 ID ADO14076 standard; DNA; 300001 BP.
 DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.
 PN WO2004041216-A2.
 PD 21-MAY-2004.
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.
 Query Match 9.7%; Score 221; DB 12; Length 300001;
 Best Local Similarity 83.5%; Pred. No. 8.9e-45;
 RESULT 1297
 ID ABL86091 standard; cDNA; 392 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:9069.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 9.7%; Score 220.8; DB 6; Length 392;
 Best Local Similarity 84.0%; Pred. No. 5.1e-46;
 RESULT 1298

ID ACH74861 standard; DNA; 573 BP.
 DE Human genome derived single exon probe #8056.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 9.7%; Score 220.8; DB 12; Length 573;
 Best Local Similarity 77.0%; Pred. No. 6e-46;
 RESULT 1299
 ID AAL07263 standard; DNA; 1367 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9951.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 220.8; DB 4; Length 1367;
 Best Local Similarity 85.4%; Pred. No. 8.9e-46;
 RESULT 1300
 ID ABL98809 standard; DNA; 1367 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3461.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 220.8; DB 4; Length 1367;
 Best Local Similarity 85.4%; Pred. No. 8.9e-46;
 RESULT 1301
 ID ADD18515 standard; DNA; 2227 BP.
 DE Human prostate cancer diagnosis related DNA sequence SeqID87.
 PN WO2003012067-A2.
 PD 13-FEB-2003.
 PA (UNMI) UNIV MICHIGAN.
 Query Match 9.7%; Score 220.8; DB 10; Length 2227;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 1302
 ID ADR67013 standard; cDNA; 2502 BP.
 DE Human cancer associated gene cDNA sequence SEQ ID NO:59.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.7%; Score 220.8; DB 13; Length 2502;
 Best Local Similarity 84.3%; Pred. No. 1.2e-45;
 RESULT 1303
 ID ADZ12882 standard; cDNA; 2502 BP.
 DE Human cancer-associated cDNA #120.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.7%; Score 220.8; DB 14; Length 2502;
 Best Local Similarity 84.3%; Pred. No. 1.2e-45;
 RESULT 1304
 ID ADR08039 standard; cDNA; 3071 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1545.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 9.7%; Score 220.8; DB 13; Length 3071;
 Best Local Similarity 83.0%; Pred. No. 1.3e-45;
 RESULT 1305
 ID ACN44535 standard; cDNA; 4779 BP.
 DE Human mRNA sequence hCT29338.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.7%; Score 220.8; DB 11; Length 4779;
 Best Local Similarity 84.5%; Pred. No. 1.6e-45;
 RESULT 1306
 ID ABA15436 standard; DNA; 11726 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7767.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.7%; Score 220.8; DB 5; Length 11726;
 Best Local Similarity 83.3%; Pred. No. 2.3e-45;

RESULT 1307
ID ABZ73812 standard; DNA; 11726 BP.
DE Secreted protein gene s4 genomic fragment HCE1G78, SEQ ID NO:959.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 8; Length 11726;
Best Local Similarity 83.3%; Pred. No. 2.3e-45;
RESULT 1308
ID ADA98478 standard; DNA; 11726 BP.
DE Human secreted protein-related DNA sequence #71.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 8; Length 11726;
Best Local Similarity 83.3%; Pred. No. 2.3e-45;
RESULT 1309
ID AAS33411 standard; DNA; 18595 BP.
DE DNA encoding human secreted protein, Seq ID No 694.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 4; Length 18595;
Best Local Similarity 76.2%; Pred. No. 2.9e-45;
RESULT 1310
ID AAL37007 standard; DNA; 18966 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3372.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 4; Length 18966;
Best Local Similarity 85.4%; Pred. No. 2.9e-45;
RESULT 1311
ID ABA20628 standard; DNA; 18966 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12959.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 5; Length 18966;
Best Local Similarity 85.4%; Pred. No. 2.9e-45;
RESULT 1312
ID ABX59995 standard; cDNA; 18966 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2339.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 220.8; DB 8; Length 18966;
Best Local Similarity 85.4%; Pred. No. 2.9e-45;
RESULT 1313
ID ADJ30745 standard; DNA; 18966 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3372.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 12; Length 18966;
Best Local Similarity 85.4%; Pred. No. 2.9e-45;
RESULT 1314
ID ACN43982 standard; DNA; 24898 BP.
DE Human genomic sequence hCG23625.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 11; Length 24898;
Best Local Similarity 84.3%; Pred. No. 3.3e-45;
RESULT 1315
ID AAD47150 standard; DNA; 31814 BP.
DE Human Ras-like protein encoding gene.
PN WO200277190-A2.
PD 03-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 9.7%; Score 220.8; DB 10; Length 31814;

Best Local Similarity 84.2%; Pred. No. 3.7e-45;
RESULT 1316
ID AAS30619 standard; DNA; 31994 BP.
DE DNA encoding novel lung cancer antigen, Seq ID No 71.
PN WO200155300-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 4; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1317
ID AAS28165 standard; DNA; 31994 BP.
DE Genomic sequence #5 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 4; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1318
ID ACA03382 standard; DNA; 31994 BP.
DE DNA encoding human lung cancer antigen HCLCR09.
PN US2002173454-A1.
PD 21-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.7%; Score 220.8; DB 8; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1319
ID ADB96730 standard; DNA; 31994 BP.
DE Novel lung cancer antigen genomic DNA #1.
PN US2003049703-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 9; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1320
ID ADG41361 standard; DNA; 31994 BP.
DE Human respiratory system associated genomic DNA seq id 599.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 10; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1321
ID ADI97135 standard; DNA; 31994 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID599.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 11; Length 31994;
Best Local Similarity 76.7%; Pred. No. 3.7e-45;
RESULT 1322
ID AAS36516 standard; DNA; 32219 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2016.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 4; Length 32219;
Best Local Similarity 79.1%; Pred. No. 3.7e-45;
RESULT 1323
ID ADE47210 standard; DNA; 32219 BP.
DE Human cardiovascular system related genomic DNA #776.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.8; DB 10; Length 32219;
Best Local Similarity 79.1%; Pred. No. 3.7e-45;
RESULT 1324
ID ADJ08628 standard; DNA; 32219 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2016.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 220.8; DB 13; Length 32219;
Best Local Similarity 79.1%; Pred. No. 3.7e-45;
RESULT 1325
ID ADR67012 standard; DNA; 32229 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:58.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.7%; Score 220.8; DB 13; Length 32229;
Best Local Similarity 84.3%; Pred. No. 3.7e-45;
RESULT 1326
ID ADZ12877 standard; DNA; 32229 BP.
DE Human cancer-associated genomic DNA #34.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.7%; Score 220.8; DB 14; Length 32229;
Best Local Similarity 84.3%; Pred. No. 3.7e-45;
RESULT 1327
ID ACN44534 standard; DNA; 39768 BP.
DE Human genomic sequence hCG38101.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 11; Length 39768;
Best Local Similarity 84.5%; Pred. No. 4.1e-45;
RESULT 1328
ID ACN44798 standard; DNA; 40491 BP.
DE Human genomic sequence hCG41911.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 11; Length 40491;
Best Local Similarity 83.1%; Pred. No. 4.1e-45;
RESULT 1329
ID ADA02858 standard; DNA; 53795 BP.
DE Human LMO2 carcinoma associated gene, SEQ ID NO:1376.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 9; Length 53795;
Best Local Similarity 83.0%; Pred. No. 4.6e-45;
RESULT 1330
ID ADB72596 standard; DNA; 53795 BP.
DE Human LMO2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 53795;
Best Local Similarity 83.0%; Pred. No. 4.6e-45;
RESULT 1331
ID ADC85337 standard; DNA; 53795 BP.
DE Mouse Lmo2 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 53795;
Best Local Similarity 83.0%; Pred. No. 4.6e-45;
RESULT 1332
ID ADM74453 standard; DNA; 53795 BP.
DE Human carcinoma associated (CA) nucleic acid #61.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENG/) ENGELHARD E K.
Query Match 9.7%; Score 220.8; DB 12; Length 53795;
Best Local Similarity 83.0%; Pred. No. 4.6e-45;
RESULT 1333
ID ADC87426 standard; DNA; 59588 BP.
DE Human GPCR gene SEQ ID NO:1879.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 9.7%; Score 220.8; DB 10; Length 59588;
Best Local Similarity 82.1%; Pred. No. 4.9e-45;
RESULT 1334
ID ABX13172 standard; DNA; 65464 BP.
DE Human gene encoding a Noelin-1-like secreted protein.
PN US2002173459-A1.
PD 21-NOV-2002.
PA (PEKE) PE CORP NY.
Query Match 9.7%; Score 220.8; DB 8; Length 65464;
Best Local Similarity 85.7%; Pred. No. 5.1e-45;
RESULT 1335
ID ACN44450 standard; DNA; 75252 BP.
DE Human genomic sequence hCG27772.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 11; Length 75252;
Best Local Similarity 80.8%; Pred. No. 5.4e-45;
RESULT 1336
ID ADC85476 standard; DNA; 96594 BP.
DE Human Msf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 96594;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1337
ID ADE95974 standard; DNA; 96594 BP.
DE Human SYK gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 96594;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1338
ID ADA02726 standard; DNA; 96595 BP.
DE Human SYK carcinoma associated gene, SEQ ID NO:1244.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 9; Length 96595;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1339
ID ADA02996 standard; DNA; 96595 BP.
DE Human Msf carcinoma associated gene, SEQ ID NO:1514.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 9; Length 96595;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1340
ID ADB72464 standard; DNA; 96595 BP.
DE Human SYK gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 96595;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1341
ID ADB72734 standard; DNA; 96595 BP.
DE Human Msf gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.8; DB 10; Length 96595;
Best Local Similarity 85.4%; Pred. No. 6e-45;
RESULT 1342
ID ADM74591 standard; DNA; 96595 BP.
DE Human carcinoma associated (CA) nucleic acid #130.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.

PA (ENGELHARD E K.
 Query Match 9.7%; Score 220.8; DB 12; Length 96595;
 Best Local Similarity 85.4%; Pred. No. 6e-45;
 RESULT 1343
 ID AEKG0245 standard; DNA; 96595 BP.
 DE Human SYK genomic sequence, SEQ ID NO: 232.
 PN US2006204982-A1.
 PD 14-SEP-2006.
 PA (MORRIS D W.
 PA (ENGELHARD E K.
 Query Match 9.7%; Score 220.8; DB 15; Length 96595;
 Best Local Similarity 85.4%; Pred. No. 6e-45;
 RESULT 1344
 ID ABN96931 standard; DNA; 99014 BP.
 DE Gene #3429 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.7%; Score 220.8; DB 6; Length 99014;
 Best Local Similarity 81.9%; Pred. No. 6.1e-45;
 RESULT 1345
 Query Match 9.7%; Score 220.8; DB 4; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1346
 Query Match 9.7%; Score 220.8; DB 4; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1347
 Query Match 9.7%; Score 220.8; DB 6; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1348
 Query Match 9.7%; Score 220.8; DB 6; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1349
 ID ABOQ3210 standard; DNA; 397658 BP.
 DE Human transporter protein genomic DNA SEQ ID NO:3.
 Query Match 9.7%; Score 220.8; DB 8; Length 110000;
 Best Local Similarity 83.3%; Pred. No. 6.4e-45;
 RESULT 1350
 Query Match 9.7%; Score 220.8; DB 11; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1351
 Query Match 9.7%; Score 220.8; DB 12; Length 110000;
 Best Local Similarity 83.7%; Pred. No. 6.4e-45;
 RESULT 1352
 ID ABK83567 standard; cDNA; 112460 BP.
 DE Human cDNA differentially expressed in granulocytic cells #138.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 9.7%; Score 220.8; DB 6; Length 112460;
 Best Local Similarity 80.8%; Pred. No. 6.5e-45;
 RESULT 1353
 ID AEF92731 standard; DNA; 112460 BP.
 DE Human chromosome 22 sequence, contains MGAT3 gene.
 PN WO2006020269-A2.
 PD 23-FEB-2006.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 9.7%; Score 220.8; DB 15; Length 112460;
 Best Local Similarity 80.8%; Pred. No. 6.5e-45;
 RESULT 1354
 ID ABD32872 standard; DNA; 130244 BP.
 DE Human cancer-associated genomic DNA HD17-083.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGRES) SAGRES DISCOVERY INC.
 Query Match 9.7%; Score 220.8; DB 13; Length 130244;
 Best Local Similarity 86.7%; Pred. No. 6.9e-45;
 RESULT 1355
 ID RAD54538 standard; DNA; 133893 BP.
 DE Human phosphatidylinositol biphosphate (PIB) DNA #1.
 PN WO200299125-A1.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.

Query Match 9.7%; Score 220.8; DB 9; Length 133893;
 Best Local Similarity 83.3%; Pred. No. 7e-45;
 RESULT 1356
 ID AAZ93815 standard; DNA; 144460 BP.
 DE Olfactory receptor operon.
 PN WO200021985-A2.
 PD 20-APR-2000.
 PA (GEST) GENSET.
 Query Match 9.7%; Score 220.8; DB 3; Length 144460;
 Best Local Similarity 72.5%; Pred. No. 7.2e-45;
 RESULT 1357
 ID ADP65423 standard; DNA; 154068 BP.
 DE Human sequence from clone RP11-363122 on chromosome 1, complete DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 9.7%; Score 220.8; DB 11; Length 154068;
 Best Local Similarity 83.0%; Pred. No. 7.4e-45;
 RESULT 1358
 ID AED89402 standard; DNA; 155515 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 42.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 9.7%; Score 220.8; DB 14; Length 155515;
 Best Local Similarity 84.3%; Pred. No. 7.5e-45;
 RESULT 1359
 ID AED89421 standard; DNA; 159497 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 9.7%; Score 220.8; DB 14; Length 159497;
 Best Local Similarity 81.9%; Pred. No. 7.6e-45;
 RESULT 1360
 ID AED89403 standard; DNA; 159660 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 43.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 9.7%; Score 220.8; DB 14; Length 159660;
 Best Local Similarity 84.3%; Pred. No. 7.6e-45;
 RESULT 1361
 ID ADZ13837 standard; DNA; 188267 BP.
 DE Human cancer-associated genomic DNA #115.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.7%; Score 220.8; DB 14; Length 188267;
 Best Local Similarity 86.7%; Pred. No. 8.2e-45;
 RESULT 1362
 ID AED89391 standard; DNA; 207600 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 31.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 9.7%; Score 220.8; DB 14; Length 207600;
 Best Local Similarity 85.4%; Pred. No. 8.5e-45;
 RESULT 1363
 ID ADP75187 standard; DNA; 302603 BP.
 DE Human Endophilin 1 gene.
 PN WO2003031594-A2.
 PD 17-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 9.7%; Score 220.8; DB 11; Length 302603;
 Best Local Similarity 74.6%; Pred. No. 1e-44;
 RESULT 1364
 ID ACF91253 standard; DNA; 459 BP.
 DE Human SIRS/sepsis diagnostic marker DNA fragment 10113.
 PN WO2004087949-A2.
 PD 14-OCT-2004.
 PA (SIRS-) SIRS LAB GMBH.
 Query Match 9.7%; Score 220.6; DB 13; Length 459;

Best Local Similarity 87.5%; Pred. No. 6.1e-46;
RESULT 1365
ID AAK70773 standard; DNA; 831 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25585.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 831;
Best Local Similarity 83.7%; Pred. No. 8e-46;
RESULT 1366
ID ADNA1750 standard; DNA; 2034 BP.
DE Novel human secreted protein polynucleotide seqid 872.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KIYAW/) Kiyaw H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFLE/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 9.7%; Score 220.6; DB 12; Length 2034;
Best Local Similarity 83.7%; Pred. No. 1.2e-45;
RESULT 1367
ID AAH19188 standard; cDNA; 2912 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HBW155, SEQ ID NO:29.
PN WO200132910-A2.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 2912;
Best Local Similarity 84.9%; Pred. No. 1.4e-45;
RESULT 1368
ID AAS41970 standard; DNA; 3702 BP.
DE Genomic sequence #286 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 3702;
Best Local Similarity 84.7%; Pred. No. 1.6e-45;
RESULT 1369
ID AAS41971 standard; DNA; 3842 BP.
DE Genomic sequence #287 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 3842;
Best Local Similarity 84.7%; Pred. No. 1.6e-45;
RESULT 1370
ID ABK92513 standard; DNA; 6096 BP.
DE Human prostate specific nucleic acid #132.
PN WO200239810-A2.
PD 16-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 9.7%; Score 220.6; DB 6; Length 6096;
Best Local Similarity 87.5%; Pred. No. 2e-45;
RESULT 1371
ID ABA20383 standard; DNA; 7074 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12714.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 5; Length 7074;
Best Local Similarity 86.2%; Pred. No. 2.1e-45;
RESULT 1372
ID AAK83072 standard; DNA; 10102 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37884.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 10102;
Best Local Similarity 70.3%; Pred. No. 2.5e-45;
RESULT 1373
ID ABA20382 standard; DNA; 10642 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12713.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 5; Length 10642;
Best Local Similarity 86.2%; Pred. No. 2.5e-45;
RESULT 1374
ID AAI99283 standard; DNA; 15037 BP.
DE Human excretory related polynucleotide SEQ ID NO 1047.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 15037;
Best Local Similarity 81.5%; Pred. No. 2.9e-45;
RESULT 1375
ID AAI63633 standard; DNA; 15037 BP.
DE Human kidney related polynucleotide SEQ ID NO 948.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 5; Length 15037;
Best Local Similarity 81.5%; Pred. No. 2.9e-45;
RESULT 1376
ID ABK42539 standard; DNA; 16181 BP.
DE Genomic sequence #438 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 16181;
Best Local Similarity 82.8%; Pred. No. 3e-45;
RESULT 1377
ID AAL04268 standard; DNA; 16181 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6956.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 16181;
Best Local Similarity 82.8%; Pred. No. 3e-45;
RESULT 1378
ID ADB60695 standard; DNA; 16181 BP.
DE Connective tissue related genomic DNA #438.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 9; Length 16181;
Best Local Similarity 82.8%; Pred. No. 3e-45;
RESULT 1379
ID ABZ73855 standard; DNA; 28482 BP.
DE Secreted protein gene 64 genomic fragment HCEGX05, SEQ ID NO:1002.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 28482;
Best Local Similarity 81.5%; Pred. No. 3.9e-45;
RESULT 1380
ID ADA44262 standard; DNA; 28482 BP.
DE Human secreted protein DNA SEQ ID 455.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 28482;
Best Local Similarity 81.5%; Pred. No. 3.9e-45;
RESULT 1381
ID AAS28674 standard; DNA; 32170 BP.
DE Genomic sequence #514 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 32170;
Best Local Similarity 83.7%; Pred. No. 4.1e-45;
RESULT 1382
ID ADG41870 standard; DNA; 32170 BP.
DE Human respiratory system associated genomic DNA seq id 1108.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 10; Length 32170;
Best Local Similarity 83.7%; Pred. No. 4.1e-45;
RESULT 1383
ID ADI97644 standard; DNA; 32170 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID1108.
PN US200307704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 11; Length 32170;
Best Local Similarity 83.7%; Pred. No. 4.1e-45;
RESULT 1384
ID ABZ74517 standard; DNA; 32681 BP.
DE Secreted protein gene 329 genomic fragment HTLBT80, SEQ ID NO:1664.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1385
ID ABZ73854 standard; DNA; 32681 BP.
DE Secreted protein gene 64 genomic fragment HCEGX05, SEQ ID NO:1001.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1386
ID ADA98915 standard; DNA; 32681 BP.
DE Human secreted protein-related DNA sequence #508.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1387
ID ADA44261 standard; DNA; 32681 BP.
DE Human secreted protein DNA SEQ ID 454.
PN WO2003000855-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1388
ID ADA44519 standard; DNA; 32681 BP.
DE Human secreted protein DNA SEQ ID 712.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 8; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1389
ID ADC20949 standard; DNA; 32681 BP.
DE Human secreted protein-related DNA sequence #367.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 10; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1390
ID ABZ68053 standard; DNA; 32681 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1576.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 220.6; DB 10; Length 32681;
Best Local Similarity 81.5%; Pred. No. 4.2e-45;
RESULT 1391
ID AEH64934 standard; DNA; 35579 BP.
DE Human 2,4-dienoyl-CoA reductase (DCR-AKL) gene, SEQ ID 27.
PN JP2005253434-A.
PD 22-SEP-2005.
PA (HOKK-) HOKKAIDO TLO KK.
Query Match 9.7%; Score 220.6; DB 15; Length 35579;
Best Local Similarity 78.0%; Pred. No. 4.3e-45;
RESULT 1392
ID AAK64829 standard; DNA; 36501 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19641.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 220.6; DB 4; Length 36501;
Best Local Similarity 83.7%; Pred. No. 4.4e-45;
RESULT 1393
ID AEA61173 standard; DNA; 37577 BP.
DE Human IL1R2 gene genomic sequence SEQ ID NO:83.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 9.7%; Score 220.6; DB 14; Length 37577;
Best Local Similarity 81.5%; Pred. No. 4.4e-45;
RESULT 1394
ID ADZ70415 standard; cDNA; 43284 BP.
DE Human cDNA from lung cancer marker, SEQ ID 100.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 9.7%; Score 220.6; DB 14; Length 43284;
Best Local Similarity 84.9%; Pred. No. 4.7e-45;
RESULT 1395
ID ADX98572 standard; DNA; 86950 BP.
DE Human HT014/LOC148902/LYPLA2/GALE genomic DNA.
Query Match 9.7%; Score 220.6; DB 14; Length 86950;
Best Local Similarity 83.2%; Pred. No. 6.5e-45;
RESULT 1396
ID ACN44742 standard; DNA; 87731 BP.
DE Human genomic sequence hCG1738334.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.6; DB 11; Length 87731;
Best Local Similarity 83.7%; Pred. No. 6.5e-45;
RESULT 1397
Query Match 9.7%; Score 220.6; DB 11; Length 110000;
Best Local Similarity 83.7%; Pred. No. 7.2e-45;
RESULT 1398
Query Match 9.7%; Score 220.6; DB 11; Length 110000;
Best Local Similarity 84.9%; Pred. No. 7.2e-45;
RESULT 1399
Query Match 9.7%; Score 220.6; DB 14; Length 110000;
Best Local Similarity 84.9%; Pred. No. 7.2e-45;
RESULT 1400
ID AED18450 standard; DNA; 138839 BP.
DE Fibrinolytic disorder associated polynucleotide SEQ ID NO 701.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.7%; Score 220.6; DB 14; Length 138839;
Best Local Similarity 79.8%; Pred. No. 8e-45;
RESULT 1401
ID ACN45146 standard; DNA; 226215 BP.
DE Human genomic sequence hCG1639824.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.7%; Score 220.6; DB 11; Length 226215;
Best Local Similarity 82.6%; Pred. No. 1e-44;
RESULT 1402

ID AAL02996 standard; DNA; 1160 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5684.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 1160;
Best Local Similarity 86.9%; Pred. No. 1e-45;
RESULT 1403
ID ABL97343 standard; DNA; 1160 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 1995.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 1160;
Best Local Similarity 86.9%; Pred. No. 1e-45;
RESULT 1404
ID AAK70288 standard; DNA; 1746 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 25100.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 1746;
Best Local Similarity 84.4%; Pred. No. 1.3e-45;
RESULT 1405
ID AAK70289 standard; DNA; 1746 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 25101.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 1746;
Best Local Similarity 84.4%; Pred. No. 1.3e-45;
RESULT 1406
ID AAH14059 standard; cDNA; 2544 BP.
DE Human cDNA sequence SEQ ID NO: 11193.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.6%; Score 220.4; DB 4; Length 2544;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1407
ID AEL63133 standard; DNA; 2576 BP.
DE Human protooncogene TRG4.
PN WO2006109942-A1.
PD 19-OCT-2006.
PA (KIMH/) KIM H.
Query Match 9.6%; Score 220.4; DB 15; Length 2576;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1408
ID AAK65774 standard; DNA; 2635 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 20586.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 2635;
Best Local Similarity 82.1%; Pred. No. 1.5e-45;
RESULT 1409
ID ADF69151 standard; cDNA; 5223 BP.
DE Human MP53 nucleotide sequence SEQ ID NO: 9.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 9.6%; Score 220.4; DB 10; Length 5223;
Best Local Similarity 87.0%; Pred. No. 2.1e-45;
RESULT 1410
ID AAQ44278 standard; DNA; 17327 BP.
DE Serglycin - proteoglycan peptide core.
PN WO9313119-A1.
PD 08-JUL-1993.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 9.6%; Score 220.4; DB 2; Length 17327;
Best Local Similarity 85.7%; Pred. No. 3.5e-45;
RESULT 1411
ID ADR67006 standard; DNA; 22608 BP.

DE Human cancer associated gene genomic sequence SEQ ID NO: 52.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.6%; Score 220.4; DB 13; Length 22608;
Best Local Similarity 81.0%; Pred. No. 4e-45;
RESULT 1412
ID ADZ12855 standard; DNA; 22608 BP.
DE Human cancer-associated genomic DNA #32.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.6%; Score 220.4; DB 14; Length 22608;
Best Local Similarity 81.0%; Pred. No. 4e-45;
RESULT 1413
ID AAK77173 standard; DNA; 23394 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 31985.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 4; Length 23394;
Best Local Similarity 82.1%; Pred. No. 4e-45;
RESULT 1414
ID ADM57790 standard; DNA; 29485 BP.
DE Human pres gene.
PN US2003216564-A1.
PD 20-NOV-2003.
PA (DALL/) DALLOS P.
PA (ZHEN/) ZHENG J.
PA (WADI/) MADISON L D.
Query Match 9.6%; Score 220.4; DB 11; Length 29485;
Best Local Similarity 83.2%; Pred. No. 4.5e-45;
RESULT 1415
ID ADE86101 standard; DNA; 29485 BP.
DE BAC clone containing DNA encoding human prestin protein.
PN US6602992-B1.
PD 05-AUG-2003.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 9.6%; Score 220.4; DB 12; Length 29485;
Best Local Similarity 83.2%; Pred. No. 4.5e-45;
RESULT 1416
ID ABK87970 standard; DNA; 29912 BP.
DE Human prolactin receptor (PRLR) genomic DNA.
PN WO200250098-A2.
PD 27-JUN-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 9.6%; Score 220.4; DB 6; Length 29912;
Best Local Similarity 74.7%; Pred. No. 4.5e-45;
RESULT 1417
ID ABA15643 standard; DNA; 30610 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7974.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.4; DB 5; Length 30610;
Best Local Similarity 82.1%; Pred. No. 4.6e-45;
RESULT 1418
ID ABD33628 standard; DNA; 36714 BP.
DE Human cancer-associated (CA) gene HD07-128.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.6%; Score 220.4; DB 13; Length 36714;
Best Local Similarity 85.7%; Pred. No. 5e-45;
RESULT 1419
ID AEJ13856 standard; DNA; 36714 BP.
DE Cancer-associated gene sequence - SEQ ID 864.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Query Match 9.6%; Score 220.4; DB 15; Length 36714;
Best Local Similarity 85.7%; Pred. No. 5e-45;

RESULT 1420
 ID ADZ13602 standard; DNA; 36724 BP.
 DE Human cancer-associated genomic DNA #96.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 9.6%; Score 220.4; DB 14; Length 36724;
 Best Local Similarity 85.7%; Pred. No. 5e-45;
 RESULT 1421
 ID AAL51353 standard; DNA; 39776 BP.
 DE Human secreted protein genomic DNA sequence.
 PN WO200299072-A2.
 PD 12-DEC-2002.
 PA (PEKE) PE CORP NY.
 Query Match 9.6%; Score 220.4; DB 10; Length 39776;
 Best Local Similarity 75.5%; Pred. No. 5.1e-45;
 RESULT 1422
 ID AEA61140 standard; DNA; 40085 BP.
 DE Human FMO5 gene genomic sequence SEQ ID NO:50.
 PN US2005130172-A1.
 PD 16-JUN-2005.
 PA (FARB) BAYER CORP.
 Query Match 9.6%; Score 220.4; DB 14; Length 40085;
 Best Local Similarity 83.2%; Pred. No. 5.2e-45;
 RESULT 1423
 ID ACN44386 standard; DNA; 40136 BP.
 DE Human genomic sequence hCG18551.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 9.8%; Score 220.4; DB 11; Length 40136;
 Best Local Similarity 85.9%; Pred. No. 5.2e-45;
 RESULT 1424
 ID ABD32754 standard; DNA; 62124 BP.
 DE Human cancer-associated genomic DNA HD16-028.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 9.6%; Score 220.4; DB 13; Length 62124;
 Best Local Similarity 85.7%; Pred. No. 6.3e-45;
 RESULT 1425
 ID ABS52847 standard; DNA; 90541 BP.
 DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.
 PN US2002094560-A1.
 PD 18-JUL-2002.
 PA (ABUT/) ABU-THREIDEN J.
 PA (GONG/) GONG F. K.
 PA (KETC/) KETCHUM K. A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E. M.
 Query Match 9.6%; Score 220.4; DB 6; Length 90541;
 Best Local Similarity 83.2%; Pred. No. 7.4e-45;
 RESULT 1426
 ID ADJ37690 standard; DNA; 90541 BP.
 DE Human kinase genomic DNA.
 PN US2003175927-A1.
 PD 18-SEP-2003.
 PA (APPL-) APPLERA CORP.
 Query Match 9.8%; Score 220.4; DB 10; Length 90541;
 Best Local Similarity 83.2%; Pred. No. 7.4e-45;
 RESULT 1427
 ID ADR31219 standard; DNA; 90541 BP.
 DE Human SRPK2 kinase protein alternative splice form genomic DNA.
 PN US2004157297-A1.
 PD 12-AUG-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 9.6%; Score 220.4; DB 13; Length 90541;
 Best Local Similarity 83.2%; Pred. No. 7.4e-45;
 RESULT 1428
 ID AAL54213 standard; DNA; 113033 BP.
 DE SR protein-specific kinase-1 DNA, SEQ ID No 5.
 PN WO200299427-A1.
 PD 12-DEC-2002.

PA (EXEL-) EXELIXIS INC.
 Query Match 9.6%; Score 220.4; DB 8; Length 113033;
 Best Local Similarity 83.2%; Pred. No. 8.2e-45;
 RESULT 1429
 ID ADZ70593 standard; cDNA; 114596 BP.
 DE Human cDNA from lung cancer marker gene B4GALT5.
 PN WO2005032495-A2.
 PD 14-APR-2005.
 PA (FARB) BAYER PHARM CORP.
 Query Match 9.6%; Score 220.4; DB 14; Length 114596;
 Best Local Similarity 82.1%; Pred. No. 8.3e-45;
 RESULT 1430
 ID AEJ41365 standard; DNA; 119600 BP.
 DE Human c10orf24 gene.
 PN WO2006069592-A2.
 PD 06-JUL-2006.
 PA (VECH-) VER CHRISTELIJK WETENSCHAPPELIJK ONDERW.
 Query Match 9.6%; Score 220.4; DB 15; Length 119600;
 Best Local Similarity 83.2%; Pred. No. 8.4e-45;
 RESULT 1431
 ID AEB45166 standard; DNA; 170001 BP.
 DE Human FAT gene SEQ ID NO 1.
 PN WO2005071104-A1.
 PD 04-AUG-2005.
 PA (GARV-) GARVAN INST MEDICAL RES.
 Query Match 9.6%; Score 220.4; DB 14; Length 170001;
 Best Local Similarity 83.2%; Pred. No. 9.9e-45;
 RESULT 1432
 ID ADV16961 standard; DNA; 290040 BP.
 DE Human protein associated with myc (PAM) genomic DNA.
 PN EP1481685-A1.
 PD 01-DEC-2004.
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 Query Match 9.6%; Score 220.4; DB 14; Length 290040;
 Best Local Similarity 85.7%; Pred. No. 1.3e-44;
 RESULT 1433
 ID ADU92049 standard; DNA; 290040 BP.
 DE Human PAM (protein associated with myc) genomic DNA.
 PN EP1481680-A1.
 PD 01-DEC-2004.
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 Query Match 9.6%; Score 220.4; DB 14; Length 290040;
 Best Local Similarity 85.7%; Pred. No. 1.3e-44;
 RESULT 1434
 ID AEB33438 standard; DNA; 601 BP.
 DE Human DNA polymorphic region #1018.
 PN US2005147987-A1.
 PD 07-JUL-2005.
 PA (APPL-) APPLERA CORP NY.
 Query Match 9.6%; Score 220.2; DB 14; Length 601;
 Best Local Similarity 84.6%; Pred. No. 8.8e-46;
 RESULT 1435
 ID ADY78516 standard; cDNA; 675 BP.
 DE Human cDNA predominantly expressed in blood cells, PREB-084.
 PN WO2005026314-A2.
 PD 24-MAR-2005.
 PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
 PA (GENE-) GENEDESIGN INC.
 Query Match 9.6%; Score 220.2; DB 14; Length 675;
 Best Local Similarity 84.0%; Pred. No. 9.3e-46;
 RESULT 1436
 ID ABA15638 standard; DNA; 10489 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7969.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220.2; DB 5; Length 10489;
 Best Local Similarity 79.6%; Pred. No. 3.2e-45;
 RESULT 1437
 ID AAK66569 standard; DNA; 10689 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21381.
 PN WO200157182-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 10689;
Best Local Similarity 82.8%; Pred. No. 3.2e-45;
RESULT 1438
ID AAK80647 standard; DNA; 11632 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35459.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 11632;
Best Local Similarity 77.6%; Pred. No. 3.3e-45;
RESULT 1439
ID ABE88112 standard; cDNA; 18687 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 19.
PN W0200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 9.6%; Score 220.2; DB 6; Length 18687;
Best Local Similarity 80.6%; Pred. No. 4.1e-45;
RESULT 1440
ID ADL15086 standard; DNA; 18687 BP.
DE Human C1 inhibitor DNA for cancer treatment.
PN W02003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 9.6%; Score 220.2; DB 10; Length 18687;
Best Local Similarity 80.6%; Pred. No. 4.1e-45;
RESULT 1441
ID ADR52914 standard; DNA; 18687 BP.
DE Drug therapy altered expressed gene #265.
PN W02004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC) BURCZYNSKI M.
PA (TWIN) TWINE N.
PA (DORN) DORNER A J.
PA (TREP) TREPICCHIO W L.
Query Match 9.6%; Score 220.2; DB 13; Length 18687;
Best Local Similarity 80.6%; Pred. No. 4.1e-45;
RESULT 1442
ID ADL62089 standard; DNA; 18968 BP.
DE Human ovarian cancer DNA marker #20301.
PN W0200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 9.6%; Score 220.2; DB 5; Length 18968;
Best Local Similarity 84.2%; Pred. No. 4.1e-45;
RESULT 1443
ID AAL04782 standard; DNA; 22927 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7470.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 22927;
Best Local Similarity 82.8%; Pred. No. 4.5e-45;
RESULT 1444
ID ABL97677 standard; DNA; 22927 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.
PN W0200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 22927;
Best Local Similarity 82.8%; Pred. No. 4.5e-45;
RESULT 1445
ID ASB31547 standard; DNA; 23353 BP.
DE Glutamate-cysteine ligase modulating subunit (GCLM) DNA.
PN W02005068649-A1.
PD 28-JUL-2005.
PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG.
Query Match 9.6%; Score 220.2; DB 14; Length 23353;
Best Local Similarity 76.8%; Pred. No. 4.5e-45;
RESULT 1446

ID ACN44242 standard; DNA; 26318 BP.
DE Human genomic sequence hCG20537.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.6%; Score 220.2; DB 11; Length 26318;
Best Local Similarity 83.9%; Pred. No. 4.8e-45;
RESULT 1447
ID ADZ12935 standard; DNA; 28320 BP.
DE Human cancer-associated genomic DNA #39.
PN W02005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 9.6%; Score 220.2; DB 14; Length 28320;
Best Local Similarity 83.9%; Pred. No. 5e-45;
RESULT 1448
ID AAL05628 standard; DNA; 32176 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8316.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 32176;
Best Local Similarity 87.8%; Pred. No. 5.3e-45;
RESULT 1449
ID ADA02960 standard; DNA; 44325 BP.
DE Human DAD1 carcinoma associated gene, SEQ ID NO:1478.
PN W02003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.6%; Score 220.2; DB 9; Length 44325;
Best Local Similarity 86.4%; Pred. No. 6.1e-45;
RESULT 1450
ID ADB72698 standard; DNA; 44325 BP.
DE Human DAD1 gene.
PN W02003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.6%; Score 220.2; DB 10; Length 44325;
Best Local Similarity 86.4%; Pred. No. 6.1e-45;
RESULT 1451
ID ADC85440 standard; DNA; 44325 BP.
DE Human Dad1 genomic sequence.
PN W02003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.6%; Score 220.2; DB 10; Length 44325;
Best Local Similarity 86.4%; Pred. No. 6.1e-45;
RESULT 1452
ID ADM74555 standard; DNA; 44325 BP.
DE Human carcinoma associated (CA) nucleic acid #112.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR) MORRIS D W.
PA (ENGEL) ENGELHARD E K.
Query Match 9.6%; Score 220.2; DB 12; Length 44325;
Best Local Similarity 86.4%; Pred. No. 6.1e-45;
RESULT 1453
ID ABS57422 standard; DNA; 46718 BP.
DE Human protease genomic DNA.
PN US2002137180-A1.
PD 26-SEP-2002.
PA (GANW) GAN W.
PA (YEJ) YE J.
PA (DFRA) DI FRANCESCO V.
PA (BEAS) BEASLEY E M.
Query Match 9.6%; Score 220.2; DB 8; Length 46718;
Best Local Similarity 84.2%; Pred. No. 6.2e-45;
RESULT 1454
ID ADG62974 standard; DNA; 46718 BP.
DE Human protease genomic DNA.
PN US2003054489-A1.
PD 20-MAR-2003.
PA (APPL-) APPLERA CORP.

Query Match 9.6%; Score 220.2; DB 10; Length 46718;
Best Local Similarity 84.2%; Pred. No. 6.2e-45;
RESULT 1455
ID AAK86671 standard; DNA; 53075 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41483.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220.2; DB 4; Length 53075;
Best Local Similarity 82.0%; Pred. No. 6.6e-45;
RESULT 1456
ID ACN43874 standard; DNA; 58845 BP.
DE Human genomic sequence hCG25637.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 9.6%; Score 220.2; DB 11; Length 58845;
Best Local Similarity 83.9%; Pred. No. 6.9e-45;
RESULT 1457
ID ADH10008 standard; DNA; 85873 BP.
DE Human chromosome 3p25 DNA fragment.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 9.6%; Score 220.2; DB 10; Length 85873;
Best Local Similarity 83.9%; Pred. No. 8.2e-45;
RESULT 1458
ID AEC82644 standard; cDNA; 90901 BP.
DE Breast cancer associated cDNA SEQ ID NO 212.
PN WO2005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 9.6%; Score 220.2; DB 14; Length 90901;
Best Local Similarity 82.8%; Pred. No. 8.4e-45;
RESULT 1459
Query Match 9.6%; Score 220.2; DB 6; Length 110000;
Best Local Similarity 82.8%; Pred. No. 9.1e-45;
RESULT 1460
Query Match 9.6%; Score 220.2; DB 12; Length 110000;
Best Local Similarity 82.8%; Pred. No. 9.1e-45;
RESULT 1461
Query Match 9.6%; Score 220.2; DB 12; Length 110000;
Best Local Similarity 82.8%; Pred. No. 9.1e-45;
RESULT 1462
Query Match 9.6%; Score 220.2; DB 12; Length 110000;
Best Local Similarity 82.8%; Pred. No. 9.1e-45;
RESULT 1463
Query Match 9.6%; Score 220.2; DB 14; Length 110000;
Best Local Similarity 82.8%; Pred. No. 9.1e-45;
RESULT 1464
Query Match 9.6%; Score 220.2; DB 15; Length 110000;
Best Local Similarity 85.1%; Pred. No. 9.1e-45;
RESULT 1465
ID ABK83569 standard; cDNA; 128888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.6%; Score 220.2; DB 6; Length 122888;
Best Local Similarity 80.8%; Pred. No. 9.6e-45;
RESULT 1466
ID AEF51725 standard; DNA; 126932 BP.
DE Human ribosomal S6 kinase 4 (RSK4) encoding DNA.
PN EP1619504-A1.
PD 25-JAN-2006.
PA (FRAU-) FRAUNHOFER INST TOXIKOLOGIE & EXPERIMENT.
Query Match 9.6%; Score 220.2; DB 15; Length 126932;
Best Local Similarity 85.1%; Pred. No. 9.7e-45;
RESULT 1467
ID ADP5634 standard; DNA; 137908 BP.
DE Human sequence from clone 914P14 on chromosome Xq23 Contains DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 9.6%; Score 220.2; DB 11; Length 137908;
Best Local Similarity 82.8%; Pred. No. 1e-44;
RESULT 1468
ID ABK49586 standard; DNA; 143306 BP.
DE Human transporter protein gene.
Query Match 9.6%; Score 220.2; DB 6; Length 143306;
Best Local Similarity 84.0%; Pred. No. 1e-44;
RESULT 1469
ID ADL13739 standard; DNA; 147620 BP.
DE Osteoarthritis-associated polymorphic nucleotide #271.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.6%; Score 220.2; DB 10; Length 147620;
Best Local Similarity 77.3%; Pred. No. 1e-44;
RESULT 1470
ID ADQ19948 standard; DNA; 147620 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2768.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.6%; Score 220.2; DB 12; Length 147620;
Best Local Similarity 77.3%; Pred. No. 1e-44;
RESULT 1471
ID ADL08124 standard; DNA; 176080 BP.
DE Human gene associated with low HDL-C LRPAP1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 9.6%; Score 220.2; DB 12; Length 176080;
Best Local Similarity 84.0%; Pred. No. 1.1e-44;
RESULT 1472
ID AED18538 standard; DNA; 184666 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 9.6%; Score 220.2; DB 14; Length 184666;
Best Local Similarity 84.2%; Pred. No. 1.2e-44;
RESULT 1473
ID ABX16034 standard; DNA; 203654 BP.
DE Human gene encoding calcium channel transporter family member.
PN US2002142938-A1.
PD 03-OCT-2002.
PA (YANC/) YAN C.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 9.6%; Score 220.2; DB 10; Length 203654;
Best Local Similarity 75.2%; Pred. No. 1.2e-44;
RESULT 1474
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.6%; Score 220.2; DB 11; Length 304905;
Best Local Similarity 82.8%; Pred. No. 1.4e-44;
RESULT 1475
ID AAD58431 standard; DNA; 322101 BP.
DE Human PAOD1 genomic DNA.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 9.6%; Score 220.2; DB 10; Length 322101;
Best Local Similarity 81.7%; Pred. No. 1.5e-44;
RESULT 1476
ID ADI35046 standard; DNA; 322101 BP.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) genomic DNA sequence.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.

Query Match 9.6%; Score 220.2; DB 12; Length 322101;
 Best Local Similarity 81.7%; Pred. No. 1.5e-44;
 RESULT 1477
 ID AAL02649 standard; cDNA; 499 BP.
 DE Human reproductive system related antigen cDNA SEQ ID NO: 2650.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 499;
 Best Local Similarity 84.6%; Pred. No. 9.1e-46;
 RESULT 1478
 ID ABA07691 standard; cDNA; 499 BP.
 DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 248.
 PN WO200155325-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 499;
 Best Local Similarity 84.6%; Pred. No. 9.1e-46;
 RESULT 1479
 ID ABA07691 standard; cDNA; 499 BP.
 DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 248.
 PN WO200155325-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 499;
 Best Local Similarity 84.6%; Pred. No. 9.1e-46;
 RESULT 1480
 ID ABA16111 standard; DNA; 1314 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8442.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 5; Length 1314;
 Best Local Similarity 74.9%; Pred. No. 1.4e-45;
 RESULT 1481
 ID ADT61904 standard; cDNA; 3154 BP.
 DE Human PRO92240 cDNA.
 PN US2004198969-A1.
 PD 07-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 9.6%; Score 220; DB 13; Length 3154;
 Best Local Similarity 78.2%; Pred. No. 2.1e-45;
 RESULT 1482
 ID ADU46702 standard; cDNA; 3154 BP.
 DE DNA340535 encoding human PRO92240.
 PN WO2004096124-A2.
 PD 11-NOV-2004.
 PA (GETH) GENENTECH INC.
 Query Match 9.6%; Score 220; DB 13; Length 3154;
 Best Local Similarity 78.2%; Pred. No. 2.1e-45;
 RESULT 1483
 ID AAK65080 standard; DNA; 8925 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19892.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 8925;
 Best Local Similarity 82.6%; Pred. No. 3.3e-45;
 RESULT 1484
 ID ADC86204 standard; DNA; 14325 BP.
 DE Human GPCR gene SEQ ID NO:657.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 9.6%; Score 220; DB 10; Length 14325;
 Best Local Similarity 84.6%; Pred. No. 4.1e-45;
 RESULT 1485
 ID AAS41688 standard; DNA; 14332 BP.
 DE Genomic sequence #4 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.6%; Score 220; DB 4; Length 14332;
 Best Local Similarity 82.3%; Pred. No. 4.1e-45;
 RESULT 1486
 ID AAK81810 standard; DNA; 14332 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36622.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 14332;
 Best Local Similarity 82.3%; Pred. No. 4.1e-45;
 RESULT 1487
 ID AAK84386 standard; DNA; 14332 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39198.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 14332;
 Best Local Similarity 82.3%; Pred. No. 4.1e-45;
 RESULT 1488
 ID AAK84803 standard; DNA; 17154 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19615.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 17154;
 Best Local Similarity 85.9%; Pred. No. 4.5e-45;
 RESULT 1489
 ID ABZ20990 standard; DNA; 24801 BP.
 DE Human thyroid tumour associated PKCG genomic sequence SEQ ID NO: 18.
 PN WO200283727-A2.
 PD 24-OCT-2002.
 PA (BULL/) BULLERDIEK J.
 Query Match 9.6%; Score 220; DB 10; Length 24801;
 Best Local Similarity 83.7%; Pred. No. 5.3e-45;
 RESULT 1490
 ID ADO01541 standard; DNA; 25301 BP.
 DE Human protein kinase C gamma (PRKCG) genomic DNA.
 PN US2004106138-A1.
 PD 03-JUN-2004.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 9.6%; Score 220; DB 12; Length 25301;
 Best Local Similarity 83.7%; Pred. No. 5.3e-45;
 RESULT 1491
 ID AAL36313 standard; DNA; 26591 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2678.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 4; Length 26591;
 Best Local Similarity 82.3%; Pred. No. 5.4e-45;
 RESULT 1492
 ID ABX59301 standard; cDNA; 26591 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1645.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 9.6%; Score 220; DB 8; Length 26591;
 Best Local Similarity 82.3%; Pred. No. 5.4e-45;
 RESULT 1493
 ID ADJ30051 standard; DNA; 26591 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2678.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 220; DB 12; Length 26591;
 Best Local Similarity 82.3%; Pred. No. 5.4e-45;
 RESULT 1494
 ID AEC82969 standard; cDNA; 28247 BP.
 DE Breast cancer associated cDNA SEQ ID NO 537.
 PN WO2005083429-A2.
 PD 09-SEP-2005.

PA (VERI-) VERIDEX LLC.
Query Match 9.6%; Score 220; DB 14; Length 28247;
Best Local Similarity 85.9%; Pred. No. 5.6e-45;
RESULT 1495
ID ABL68824 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7161.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.6%; Score 220; DB 6; Length 38374;
Best Local Similarity 81.2%; Pred. No. 6.4e-45;
RESULT 1496
ID ABL68363 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6700.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.6%; Score 220; DB 6; Length 38374;
Best Local Similarity 81.2%; Pred. No. 6.4e-45;
RESULT 1497
ID ABL68364 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6701.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 9.6%; Score 220; DB 6; Length 38374;
Best Local Similarity 81.2%; Pred. No. 6.4e-45;
RESULT 1498
ID ABN96966 standard; DNA; 38374 BP.
DE Gene #3464 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 9.6%; Score 220; DB 6; Length 38374;
Best Local Similarity 81.2%; Pred. No. 6.4e-45;
RESULT 1499
ID AAK78847 standard; DNA; 57296 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33659.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220; DB 4; Length 57296;
Best Local Similarity 82.3%; Pred. No. 7.7e-45;
RESULT 1500
ID AAK78170 standard; DNA; 57296 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32982.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 220; DB 4; Length 57296;
Best Local Similarity 82.3%; Pred. No. 7.7e-45;

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2007, 20:07:09 ; Search time 872 Seconds
(without alignments)
9811.899 Million cell updates/sec

Title: US-09-944-929-82

Perfect score: 2284

Sequence: 1 gcggagcatccgcgcggtc.....ataaatctttgtactcaa 2284

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents_NA.*
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2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq.*
3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq.*
4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq.*
5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq.*
6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq.*
7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq.*
8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq.*
9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq.*
10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq.*
11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2284	100.0	2284	3	US-09-944-457-82
3	2284	100.0	2284	3	US-09-945-584-82
4	2284	100.0	2284	3	US-09-991-181-514
5	2284	100.0	2284	3	US-09-944-944-82
6	2284	100.0	2284	3	US-09-990-444-514
7	2284	100.0	2284	3	US-09-945-587-82
8	2284	100.0	2284	3	US-09-997-333-514
9	2284	100.0	2284	3	US-09-992-598-514
10	2284	100.0	2284	4	US-09-989-735-514
11	2284	100.0	2284	5	US-09-989-726-514
12	2284	100.0	2284	5	US-09-944-884-82
13	2284	100.0	2284	5	US-09-997-514-514
14	2284	100.0	2284	5	US-09-989-728-514
15	2284	100.0	2284	5	US-09-997-349-514
16	2284	100.0	2284	5	US-09-997-653-514
17	2284	100.0	2284	5	US-09-989-293A-514
18	2284	100.0	2284	5	US-09-989-732-514
19	2284	100.0	2284	5	US-09-990-441-514
20	2284	100.0	2284	5	US-09-989-328-514
21	2284	100.0	2284	5	US-09-989-724-514
22	2284	100.0	2284	5	US-09-989-733-514

23	2284	100.0	2284	5	US-09-993-583-514	Sequence 514, App
24	2284	100.0	2284	5	US-09-989-279-514	Sequence 514, App
25	2284	100.0	2284	5	US-09-991-157-514	Sequence 514, App
26	2284	100.0	2284	5	US-09-990-439-514	Sequence 514, App
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28	2284	100.0	2284	5	US-09-987-384-514	Sequence 514, App
29	2284	100.0	2284	5	US-09-989-730-514	Sequence 514, App
30	2284	100.0	2284	5	US-09-997-585-514	Sequence 514, App
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33	2284	100.0	2284	5	US-09-997-666-514	Sequence 514, App
34	342.6	15.0	343	7	US-09-925-065A-474441	Sequence 474441, A
35	270.2	11.8	295	3	US-09-513-999C-9897	Sequence 9897, Ap
36	270.2	11.8	295	3	US-10-793-479-9897	Sequence 9897, Ap
37	244	10.4	29930	3	US-09-949-016-15326	Sequence 15326, A
38	241.4	10.6	547	7	US-09-925-065A-517320	Sequence 517320, A
39	240.8	10.5	59828	3	US-09-949-016-16238	Sequence 16238, A
40	240.8	10.5	85963	3	US-09-949-016-13804	Sequence 13804, A
41	240.4	10.5	601	3	US-09-949-016-69955	Sequence 69955, A
42	238.6	10.4	566	7	US-09-925-065A-604542	Sequence 604542, A
43	237.6	10.4	62873	3	US-09-949-016-15676	Sequence 15676, A
44	237.4	10.4	1937	7	US-09-925-065A-681005	Sequence 681005, A
45	237.4	10.4	1937	7	US-09-925-065A-681006	Sequence 681006, A
46	237.4	10.4	15007	3	US-09-949-016-15279	Sequence 15279, A
47	237.4	10.4	74545	3	US-09-949-002-606	Sequence 606, App
48	237.4	10.4	131860	3	US-09-949-002-730	Sequence 730, App
49	237	10.4	566	7	US-09-925-065A-604543	Sequence 604543, A
50	237	10.4	566	7	US-09-925-065A-604544	Sequence 604544, A
51	237	10.4	601	3	US-09-949-002-1635	Sequence 1635, Ap
52	237	10.4	601	3	US-09-949-002-5643	Sequence 5643, Ap
53	237	10.4	38009	3	US-09-949-016-13617	Sequence 13617, A
54	237	10.4	150780	3	US-09-949-016-14711	Sequence 14711, A
55	236.8	10.4	10427	3	US-09-949-016-15785	Sequence 15785, A
56	236.8	10.4	20901	3	US-09-949-016-11866	Sequence 11866, A
57	236.6	10.4	100463	3	US-09-949-016-12511	Sequence 12511, A
58	236.6	10.4	100468	3	US-09-949-016-13725	Sequence 13725, A
59	236.4	10.4	627	7	US-09-925-065A-497272	Sequence 497272, A
60	236.2	10.3	175265	3	US-09-949-016-16089	Sequence 16089, A
61	236	10.3	168174	3	US-10-071-411A-63	Sequence 63, Appl
62	236	10.3	168273	3	US-10-071-411A-2	Sequence 2, Appl
63	235.8	10.3	18888	3	US-09-949-016-16386	Sequence 16386, A
64	235.8	10.3	105168	3	US-09-949-016-13286	Sequence 13286, A
65	235.6	10.3	611	7	US-09-925-065A-809034	Sequence 809034, A
66	235.6	10.3	611	7	US-09-925-065A-809035	Sequence 809035, A
67	235.6	10.3	614	7	US-09-925-065A-893913	Sequence 893913, A
68	235.6	10.3	622	7	US-09-925-065A-895353	Sequence 895353, A
69	235.6	10.3	71574	3	US-09-949-016-15580	Sequence 15580, A
70	235.4	10.3	578	7	US-09-925-065A-792832	Sequence 792832, A
71	235.4	10.3	58397	3	US-09-949-016-14469	Sequence 14469, A
72	235.4	10.3	59076	3	US-09-949-016-15097	Sequence 15097, A
73	235.2	10.3	62386	3	US-09-949-016-12823	Sequence 12823, A
74	235	10.3	601	3	US-09-949-016-94321	Sequence 94321, A
75	235	10.3	601	3	US-09-949-016-94322	Sequence 94322, A
76	235	10.3	625	7	US-09-925-065A-808258	Sequence 808258, A
77	234.6	10.3	597	7	US-09-925-065A-823703	Sequence 823703, A
78	234.6	10.3	639	7	US-09-925-065A-863172	Sequence 863172, A
79	234.2	10.3	5819	3	US-09-949-016-14050	Sequence 14050, A
80	234.2	10.3	5822	3	US-09-949-016-15657	Sequence 15657, A
81	234.2	10.3	50836	3	US-09-949-016-16722	Sequence 16722, A
82	234	10.2	24299	3	US-09-949-016-15452	Sequence 15452, A
83	233.8	10.2	601	3	US-09-949-016-18060	Sequence 18060, A
84	233.6	10.2	601	3	US-09-949-016-197087	Sequence 197087, A
85	233.6	10.2	160552	3	US-09-593-828-11	Sequence 11, Appl
86	233.6	10.2	160552	5	US-10-697-828-11	Sequence 11, Appl
87	233.4	10.2	27702	3	US-09-949-016-11795	Sequence 11795, A
88	233.4	10.2	32278	3	US-09-949-016-14575	Sequence 14575, A
89	233.2	10.2	1701	3	US-09-078-294-9	Sequence 9, Appl
90	233.2	10.2	1701	5	US-09-728-552A-9	Sequence 9, Appl
91	233	10.2	597	7	US-09-925-065A-751914	Sequence 751914, A
92	233	10.2	597	7	US-09-925-065A-751915	Sequence 751915, A
93	232.8	10.2	601	3	US-09-949-016-45773	Sequence 45773, A
94	232.8	10.2	601	3	US-09-949-016-45774	Sequence 45774, A
95	232.6	10.2	601	3	US-09-949-016-87766	Sequence 87766, A

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97	232.6	10.2	17370	3	US-09-949-016-17331	Sequence 17331, A	170	229.4	10.0	571	7	US-09-925-065A-327161	Sequence 327161,
98	232.6	10.2	74881	3	US-09-949-016-15545	Sequence 15545, A	c 171	229.4	10.0	619	7	US-09-925-065A-536043	Sequence 536043, A
99	232.6	10.2	74914	3	US-09-949-016-12286	Sequence 12286, A	c 172	229.4	10.0	713	7	US-09-925-065A-93712	Sequence 93712, A
100	232.6	10.2	246230	3	US-09-949-016-17019	Sequence 17019, A	c 173	229.4	10.0	1412	7	US-09-925-065A-63600	Sequence 63600, A
101	232.6	10.2	246230	3	US-09-949-016-17020	Sequence 17020, A	c 174	229.4	10.0	1412	7	US-09-925-065A-63601	Sequence 63601, A
102	232.6	10.2	246230	3	US-09-949-016-17021	Sequence 17021, A	c 175	229.4	10.0	1412	7	US-09-925-065A-63602	Sequence 63602, A
103	232.6	10.2	246230	3	US-09-949-016-17022	Sequence 17022, A	c 176	229.4	10.0	1412	7	US-09-925-065A-63603	Sequence 63603, A
104	232.4	10.2	31385	3	US-09-949-016-13358	Sequence 13358, A	c 177	229.4	10.0	37976	3	US-09-949-016-13441	Sequence 13441, A
105	232.4	10.2	73788	3	US-09-949-016-12358	Sequence 12358, A	c 178	229.4	10.0	43560	5	US-09-949-016-13441	Sequence 13441, A
c 106	232.2	10.2	605	7	US-09-925-065A-878037	Sequence 878037, A	c 179	229.4	10.0	72602	3	US-09-949-016-14385	Sequence 14385, A
c 107	232.2	10.2	607	7	US-09-925-065A-873360	Sequence 873360, A	c 180	229.4	10.0	98302	3	US-09-949-016-16847	Sequence 16847, A
108	232.2	10.2	614	7	US-09-925-065A-878367	Sequence 878367, A	c 181	229.4	10.0	112507	3	US-09-949-016-12420	Sequence 12420, A
109	232.2	10.2	18008	3	US-09-949-016-13291	Sequence 13291, A	c 182	229.4	10.0	112507	3	US-09-949-016-12794	Sequence 12794, A
c 110	232	10.2	488	7	US-09-925-065A-850388	Sequence 850388, A	c 183	229.4	10.0	112508	3	US-09-949-016-15589	Sequence 15589, A
c 111	232	10.2	489	7	US-09-925-065A-842830	Sequence 842830, A	c 184	229.4	10.0	112508	3	US-09-949-016-16590	Sequence 16590, A
c 112	231.8	10.1	601	3	US-09-949-002-6961	Sequence 6961, Ap	c 185	229.4	10.0	113042	3	US-09-949-016-12343	Sequence 12343, A
c 113	231.8	10.1	970	7	US-09-925-065A-727962	Sequence 727962, A	c 186	229.4	10.0	113042	3	US-09-949-016-15246	Sequence 15246, A
c 114	231.8	10.1	18396	3	US-09-949-002-763	Sequence 763, App	c 187	229.4	10.0	162025	3	US-09-834-700-13	Sequence 13, Appl
c 115	231.8	10.1	18700	3	US-09-949-016-13140	Sequence 13140, A	c 188	229.4	10.0	162025	3	US-09-834-700-14	Sequence 14, Appl
c 116	231.6	10.1	40951	3	US-09-949-016-15846	Sequence 15846, A	c 189	229.4	10.0	162025	3	US-09-834-700-17	Sequence 17, Appl
c 117	231.6	10.1	45299	3	US-09-949-016-12465	Sequence 12465, A	c 190	229.4	10.0	162025	3	US-09-834-700-18	Sequence 18, Appl
c 118	231.6	10.1	45300	3	US-09-949-016-13045	Sequence 13045, A	c 191	229.4	10.0	177979	3	US-09-949-016-14125	Sequence 14125, A
c 119	231.6	10.1	54711	3	US-09-949-016-17489	Sequence 17489, A	c 192	229.4	10.0	227979	3	US-09-949-016-11842	Sequence 11842, A
c 120	231.6	10.1	105045	3	US-09-949-002-663	Sequence 663, App	c 193	229.2	10.0	601	3	US-09-949-016-141088	Sequence 141088, A
c 121	231.6	10.1	107045	3	US-09-949-002-772	Sequence 772, App	c 194	229.2	10.0	601	3	US-09-949-016-154401	Sequence 154401, A
c 122	231.6	10.1	118923	3	US-09-949-016-13227	Sequence 13227, A	c 195	229.2	10.0	601	3	US-09-949-016-154402	Sequence 154402, A
c 123	231.6	10.1	304533	3	US-09-949-016-15371	Sequence 15371, A	c 196	229.2	10.0	656	7	US-09-925-065A-675446	Sequence 675446, A
c 124	231.6	10.1	304533	3	US-09-949-016-15372	Sequence 15372, A	c 197	229.2	10.0	19377	3	US-09-949-016-15198	Sequence 15198, A
c 125	231.4	10.1	601	3	US-09-949-002-6962	Sequence 6962, Ap	c 198	229.2	10.0	129554	3	US-09-949-002-765	Sequence 765, App
c 126	231.4	10.1	970	7	US-09-925-065A-727961	Sequence 727961, A	c 199	229.2	10.0	193169	3	US-09-949-016-15091	Sequence 15091, A
c 127	231.4	10.1	1463	7	US-09-925-065A-678834	Sequence 678834, A	c 200	229	10.0	601	3	US-09-949-016-51144	Sequence 51144, A
c 128	231.4	10.1	18700	3	US-09-949-016-13140	Sequence 13140, A	c 201	229	10.0	601	3	US-09-949-016-109427	Sequence 109427, A
c 129	231.4	10.1	44244	3	US-09-949-016-11743	Sequence 11743, A	c 202	229	10.0	601	7	US-09-925-065A-811520	Sequence 811520, A
c 130	231.4	10.1	44245	3	US-09-949-016-13579	Sequence 13579, A	c 203	229	10.0	601	7	US-09-925-065A-812401	Sequence 812401, A
c 131	231.4	10.1	58014	3	US-09-949-016-17448	Sequence 17448, A	c 204	229	10.0	609	7	US-09-925-065A-809539	Sequence 809539, A
c 132	231.4	10.1	87648	3	US-09-949-016-13655	Sequence 13655, A	c 205	229	10.0	653	7	US-09-925-065A-698440	Sequence 698440, A
c 133	231.4	10.1	670689	3	US-09-949-016-12507	Sequence 12507, A	c 206	229	10.0	713	7	US-09-925-065A-93711	Sequence 93711, A
c 134	231.4	10.1	670690	3	US-09-949-016-14207	Sequence 14207, A	c 207	229	10.0	722	7	US-09-925-065A-31275	Sequence 31275, A
c 135	231.2	10.1	14084	3	US-09-949-016-13889	Sequence 13889, A	c 208	229	10.0	2495	3	US-09-771-357-104	Sequence 104, App
c 136	231.2	10.1	44019	3	US-09-949-016-14902	Sequence 14902, A	c 209	229	10.0	2495	3	US-10-059-579A-104	Sequence 104, App
c 137	231	10.1	601	3	US-09-949-016-87765	Sequence 87765, A	c 210	229	10.0	9900	3	US-09-949-016-13392	Sequence 13392, A
c 138	231	10.1	1833	3	US-09-925-065A-68653	Sequence 68653, A	c 211	229	10.0	65744	3	US-09-949-016-12591	Sequence 12591, A
c 139	231	10.1	3165	7	US-09-925-065A-688877	Sequence 688877, A	c 212	229	10.0	65745	3	US-09-949-016-15871	Sequence 15871, A
c 140	231	10.1	3165	7	US-09-925-065A-688878	Sequence 688878, A	c 213	228.8	10.0	560	3	US-09-925-065A-589226	Sequence 589226, A
c 141	231	10.1	40168	3	US-09-949-016-13225	Sequence 13225, A	c 214	228.8	10.0	601	3	US-09-949-016-120456	Sequence 120456, A
c 142	230.8	10.1	679	7	US-09-925-065A-532787	Sequence 532787, A	c 215	228.8	10.0	36618	3	US-09-949-016-15723	Sequence 15723, A
c 143	230.8	10.1	17628	3	US-09-949-016-16718	Sequence 16718, A	c 216	228.8	10.0	65990	3	US-09-949-016-11830	Sequence 11830, A
c 144	230.8	10.1	71879	3	US-09-949-016-17465	Sequence 17465, A	c 217	228.6	10.0	601	3	US-09-949-016-19500	Sequence 19500, A
c 145	230.6	10.1	601	3	US-09-949-016-68606	Sequence 68606, A	c 218	228.6	10.0	601	3	US-09-949-016-205300	Sequence 205300, A
c 146	230.6	10.1	616	7	US-09-925-065A-931112	Sequence 931112, A	c 219	228.6	10.0	601	3	US-09-949-002-2639	Sequence 2639, Ap
c 147	230.6	10.1	24005	3	US-09-949-016-13758	Sequence 13758, A	c 220	228.6	10.0	601	3	US-09-949-002-2640	Sequence 2640, Ap
c 148	230.6	10.1	25859	3	US-09-949-016-15052	Sequence 15052, A	c 221	228.6	10.0	601	3	US-09-949-002-9909	Sequence 9909, Ap
c 149	230.4	10.1	601	3	US-09-949-016-120457	Sequence 120457, A	c 222	228.6	10.0	601	3	US-09-949-002-9910	Sequence 9910, Ap
c 150	230.4	10.1	601	3	US-09-949-016-120458	Sequence 120458, A	c 223	228.6	10.0	13203	3	US-09-949-016-17544	Sequence 17544, A
c 151	230.4	10.1	631	7	US-09-925-065A-499794	Sequence 499794, A	c 224	228.6	10.0	16273	3	US-09-949-016-11826	Sequence 11826, A
c 152	230.2	10.1	1427	7	US-09-925-065A-726021	Sequence 726021, A	c 225	228.6	10.0	39480	3	US-09-949-016-13634	Sequence 13634, A
c 153	230.2	10.1	10281	3	US-09-949-016-15812	Sequence 15812, A	c 226	228.6	10.0	46725	3	US-09-949-016-15680	Sequence 15680, A
c 154	230.2	10.1	10465	3	US-09-949-016-13136	Sequence 13136, A	c 227	228.6	10.0	98828	3	US-09-949-016-16630	Sequence 16630, A
c 155	230.2	10.1	68452	3	US-09-949-016-13305	Sequence 13305, A	c 228	228.6	10.0	235452	3	US-09-949-016-13675	Sequence 13675, A
c 156	230.2	10.1	325791	3	US-09-768-185A-1	Sequence 1, Appl	c 229	228.6	10.0	294836	3	US-09-949-016-15974	Sequence 15974, A
c 157	230	10.1	955	3	US-09-620-312D-228	Sequence 228, App	c 230	228.6	10.0	312470	3	US-09-949-016-14043	Sequence 14043, A
c 158	230	10.1	40512	3	US-09-949-016-16612	Sequence 16612, A	c 231	228.6	10.0	336024	3	US-09-949-016-12373	Sequence 12373, A
c 159	229.8	10.1	489	7	US-09-925-065A-469133	Sequence 469133, A	c 232	228.4	10.0	599	7	US-09-925-065A-557593	Sequence 557593, A
c 160	229.8	10.1	591	7	US-09-925-065A-526304	Sequence 526304, A	c 233	228.4	10.0	626	7	US-09-925-065A-709437	Sequence 709437, A
c 161	229.8	10.1	619	7	US-09-925-065A-536042	Sequence 536042, A	c 234	228.4	10.0	15849	3	US-09-054-272-50	Sequence 50, Appl
c 162	229.8	10.1	38206	3	US-09-949-016-15527	Sequence 15527, A	c 235	228.4	10.0	23801	4	US-09-880-107-2362	Sequence 2362, Ap
c 163	229.6	10.1	20840	3	US-09-949-016-14115	Sequence 14115, A	c 236	228.4	10.0	15849	3	US-09-949-016-16773	Sequence 16773, A
c 164	229.6	10.1	36731	3	US-09-949-016-13770	Sequence 13770, A	c 237	228.4	10.0	146428	3	US-09-949-016-12620	Sequence 12620, A
c 165	229.6	10.1	64291	3	US-09-949-016-16278	Sequence 16278, A	c 238	228.4	10.0	146438	3	US-09-949-016-12081	Sequence 12081, A
c 166	229.6	10.1	84587	3	US-09-949-016-15733	Sequence 15733, A	c 239	228.4	10.0	150833	3	US-09-949-016-14859	Sequence 14859, A
c 167	229.6	10.1	117410	3	US-09-949-016-12262	Sequence 12262, A	c 240	228.4	10.0	159963	3	US-09-949-016-14858	Sequence 14858, A
c 168	229.6	10.1	144362	3	US-09-949-016-16066	Sequence 16066, A	c 241	228.4	10.0	171130	3	US-09-949-016-14861	Sequence 14861, A

C 242	228.4	10.0	201529	3	US-09-949-016-12740	Sequence 12740, A	C 315	227	9.9	26721	3	US-09-949-002-820	Sequence 820, App
C 243	228.2	10.0	546	7	US-09-925-065A-799095	Sequence 799095, A	C 316	227	9.9	27692	3	US-09-949-002-680	Sequence 680, App
C 244	228.2	10.0	601	3	US-09-949-016-64930	Sequence 64930, A	C 317	227	9.9	28228	5	US-10-021-698A-4530	Sequence 4530, Ap
C 245	228.2	10.0	601	3	US-09-949-016-172794	Sequence 172794, A	C 318	227	9.9	47030	3	US-09-949-016-13037	Sequence 13037, A
C 246	228.2	10.0	601	3	US-09-949-002-3497	Sequence 3497, Ap	C 319	227	9.9	47030	3	US-09-949-016-13038	Sequence 13038, A
C 247	228.2	10.0	601	3	US-09-949-002-9469	Sequence 9469, Ap	C 320	227	9.9	47030	3	US-09-949-016-15039	Sequence 15039, A
C 248	228.2	10.0	604	7	US-09-925-065A-799096	Sequence 799096, A	C 321	227	9.9	47030	3	US-09-949-016-15040	Sequence 15040, A
C 249	228.2	10.0	635	7	US-09-925-065A-856307	Sequence 856307, A	C 322	227	9.9	53737	3	US-09-949-016-16157	Sequence 16157, A
C 250	228.2	10.0	1437	7	US-09-925-065A-694852	Sequence 694852, A	C 323	227	9.9	58837	5	US-09-982-091A-5	Sequence 5, Appli
C 251	228.2	10.0	60593	3	US-09-949-016-13779	Sequence 13779, A	C 324	227	9.9	183770	3	US-09-949-016-15494	Sequence 15494, A
C 252	228.2	10.0	63588	3	US-09-873-404-3	Sequence 3, Appli	C 325	226.8	9.9	648	7	US-09-925-065A-116042	Sequence 116042, A
C 253	228.2	10.0	63588	3	US-10-243-735-3	Sequence 3, Appli	C 326	226.8	9.9	2643	3	US-10-104-047-1923	Sequence 1923, Ap
C 254	228.2	10.0	63588	4	US-10-730-010-3	Sequence 3, Appli	C 327	226.8	9.9	7447	3	US-09-949-016-16540	Sequence 16540, A
C 255	228.2	10.0	84171	3	US-09-949-016-16356	Sequence 16356, A	C 328	226.8	9.9	12951	3	US-09-949-016-14075	Sequence 14075, A
C 256	228.2	10.0	173787	3	US-09-949-016-12542	Sequence 12542, A	C 329	226.8	9.9	24841	3	US-09-949-016-14009	Sequence 14009, A
C 257	228.2	10.0	173791	3	US-09-949-016-17302	Sequence 17302, A	C 330	226.8	9.9	110243	3	US-09-949-016-13698	Sequence 13698, A
C 258	228	10.0	601	3	US-09-949-016-66391	Sequence 66391, A	C 331	226.8	9.9	250958	3	US-09-949-016-16061	Sequence 16061, A
C 259	228	10.0	766	7	US-09-925-065A-957017	Sequence 957017, A	C 332	226.6	9.9	582	7	US-09-925-065A-878471	Sequence 878471, A
C 260	228	10.0	31318	3	US-09-949-016-12495	Sequence 12495, A	C 333	226.6	9.9	585	7	US-09-925-065A-257693	Sequence 257693, A
C 261	228	10.0	31318	3	US-09-949-016-15963	Sequence 15963, A	C 334	226.6	9.9	532	7	US-09-925-065A-785034	Sequence 785034, A
C 262	228	10.0	36907	3	US-09-949-016-12533	Sequence 12533, A	C 335	226.6	9.9	601	3	US-09-949-016-45775	Sequence 45775, A
C 263	228	10.0	36913	3	US-09-949-016-15585	Sequence 15585, A	C 336	226.6	9.9	601	3	US-09-949-002-3496	Sequence 3496, Ap
C 264	228	10.0	84761	3	US-09-949-016-11919	Sequence 11919, A	C 337	226.6	9.9	601	3	US-09-949-002-9468	Sequence 9468, Ap
C 265	228	10.0	84763	3	US-09-949-016-13914	Sequence 13914, A	C 338	226.6	9.9	54444	3	US-09-949-016-17344	Sequence 17344, A
C 266	228	10.0	128779	3	US-09-497-855A-38	Sequence 38, Appli	C 339	226.6	9.9	76118	3	US-09-949-016-15533	Sequence 15533, A
C 267	228	10.0	128779	5	US-10-081-327A-38	Sequence 38, Appli	C 340	226.6	9.9	83697	3	US-09-949-016-16040	Sequence 16040, A
C 268	227.8	10.0	24395	3	US-09-949-016-14758	Sequence 14758, A	C 341	226.6	9.9	135476	3	US-09-949-016-12611	Sequence 12611, A
C 269	227.8	10.0	50000	3	US-09-146-053-3	Sequence 3, Appli	C 342	226.6	9.9	135476	3	US-09-949-016-14413	Sequence 14413, A
C 270	227.8	10.0	103987	3	US-09-949-016-12513	Sequence 12513, A	C 343	226.6	9.9	155019	3	US-09-949-016-16029	Sequence 16029, A
C 271	227.8	10.0	103988	3	US-09-949-016-17050	Sequence 17050, A	C 344	226.6	9.9	190849	5	US-10-021-698A-706	Sequence 706, App
C 272	227.6	10.0	816	7	US-09-925-065A-249373	Sequence 249373, A	C 345	226.6	9.9	211528	5	US-10-021-698A-709	Sequence 709, App
C 273	227.6	10.0	17045	3	US-09-949-016-13681	Sequence 13681, A	C 346	226.6	9.9	212708	5	US-10-021-698A-708	Sequence 708, App
C 274	227.6	10.0	99014	4	US-09-880-107-3428	Sequence 3428, Ap	C 347	226.4	9.9	578	7	US-09-949-016-32489	Sequence 32489, A
C 275	227.6	10.0	110266	3	US-09-949-016-14913	Sequence 14913, A	C 348	226.4	9.9	601	3	US-09-949-016-171207	Sequence 171207, A
C 276	227.6	10.0	110266	3	US-09-949-016-14914	Sequence 14914, A	C 349	226.4	9.9	601	3	US-09-949-016-171337	Sequence 171337, A
C 277	227.6	10.0	110266	3	US-09-949-016-14915	Sequence 14915, A	C 350	226.4	9.9	601	3	US-09-949-016-185553	Sequence 185553, A
C 278	227.6	10.0	110266	3	US-09-949-016-14916	Sequence 14916, A	C 351	226.4	9.9	601	3	US-09-949-016-187410	Sequence 187410, A
C 279	227.6	10.0	110266	3	US-09-949-016-14917	Sequence 14917, A	C 352	226.4	9.9	801	7	US-09-925-065A-88626	Sequence 88626, A
C 280	227.6	10.0	110266	3	US-09-949-016-14918	Sequence 14918, A	C 353	226.4	9.9	801	7	US-09-925-065A-88626	Sequence 88626, A
C 281	227.6	10.0	110266	3	US-09-949-016-14919	Sequence 14919, A	C 354	226.4	9.9	2387	3	US-09-375-318-38	Sequence 38, Appli
C 282	227.6	10.0	110266	3	US-09-949-016-14920	Sequence 14920, A	C 355	226.4	9.9	10010	3	US-09-949-002-597	Sequence 597, App
C 283	227.6	10.0	110266	3	US-09-949-016-14921	Sequence 14921, A	C 356	226.4	9.9	10010	3	US-09-949-002-840	Sequence 840, App
C 284	227.6	10.0	110266	3	US-09-949-016-14922	Sequence 14922, A	C 357	226.4	9.9	23883	3	US-09-949-016-13726	Sequence 13726, A
C 285	227.6	10.0	132762	3	US-09-954-556-17	Sequence 17, Appli	C 358	226.4	9.9	28843	3	US-09-949-016-11812	Sequence 11812, A
C 286	227.6	10.0	189560	3	US-09-949-016-17202	Sequence 17202, A	C 359	226.4	9.9	28843	3	US-09-949-016-12712	Sequence 12712, A
C 287	227.6	10.0	300402	3	US-09-949-016-13632	Sequence 13632, A	C 360	226.4	9.9	28843	3	US-09-949-016-17158	Sequence 17158, A
C 288	227.6	10.0	421118	3	US-09-949-016-16297	Sequence 16297, A	C 361	226.4	9.9	28843	3	US-09-949-016-17159	Sequence 17159, A
C 289	227.4	10.0	601	3	US-09-949-016-185554	Sequence 185554, A	C 362	226.4	9.9	30480	5	US-09-339-352-15	Sequence 15, Appli
C 290	227.4	10.0	601	3	US-09-949-002-2638	Sequence 2638, Ap	C 363	226.4	9.9	43991	5	US-09-984-429-252	Sequence 252, App
C 291	227.4	10.0	1461	7	US-09-925-065A-680304	Sequence 680304, A	C 364	226.4	9.9	57875	3	US-09-949-016-13152	Sequence 13152, A
C 292	227.4	10.0	1988	3	US-10-104-047-1091	Sequence 1091, Ap	C 365	226.2	9.9	570	7	US-09-925-065A-561871	Sequence 561871, A
C 293	227.4	10.0	38368	3	US-09-949-016-12958	Sequence 12958, A	C 366	226.2	9.9	601	3	US-09-949-016-137032	Sequence 137032, A
C 294	227.4	10.0	53451	3	US-09-949-016-15859	Sequence 15859, A	C 367	226.2	9.9	677	7	US-09-925-065A-12236	Sequence 12236, A
C 295	227.4	10.0	54286	3	US-09-949-002-837	Sequence 837, App	C 368	226.2	9.9	1485	7	US-09-925-065A-700656	Sequence 700656, A
C 296	227.4	10.0	60304	3	US-09-949-016-11395	Sequence 11395, A	C 369	226.2	9.9	1968	7	US-09-925-065A-674359	Sequence 674359, A
C 297	227.4	10.0	60304	3	US-09-949-016-17264	Sequence 17264, A	C 370	226.2	9.9	3240	7	US-09-925-065A-704337	Sequence 704337, A
C 298	227.4	10.0	60304	3	US-09-949-016-17264	Sequence 17264, A	C 371	226.2	9.9	47781	3	US-09-949-016-16492	Sequence 16492, A
C 299	227.4	10.0	60955	3	US-09-949-002-642	Sequence 642, App	C 372	226.2	9.9	47781	3	US-09-949-016-16493	Sequence 16493, A
C 300	227.4	10.0	131978	3	US-09-949-016-13117	Sequence 13117, A	C 373	226.2	9.9	47781	3	US-09-949-016-16494	Sequence 16494, A
C 301	227.2	9.9	589	7	US-09-925-065A-920828	Sequence 920828, A	C 374	226.2	9.9	54986	3	US-09-949-016-16716	Sequence 16716, A
C 302	227.2	9.9	601	3	US-09-949-016-65995	Sequence 65995, A	C 375	226.2	9.9	74962	3	US-09-685-853A-3	Sequence 3, Appli
C 303	227.2	9.9	601	3	US-09-949-016-131801	Sequence 131801, A	C 376	226.2	9.9	171065	5	US-10-021-698A-695	Sequence 695, App
C 304	227.2	9.9	11939	3	US-09-949-016-13232	Sequence 13232, A	C 377	226.2	9.9	219964	3	US-09-949-016-15086	Sequence 15086, App
C 305	227.2	9.9	15454	3	US-09-949-016-16679	Sequence 16679, A	C 378	226	9.9	590	7	US-09-925-065A-389749	Sequence 389749, A
C 306	227.2	9.9	98708	3	US-09-949-016-16392	Sequence 16392, A	C 379	226	9.9	601	3	US-09-949-016-179611	Sequence 179611, A
C 307	227.2	9.9	154626	3	US-09-949-016-14000	Sequence 14000, A	C 380	226	9.9	601	3	US-09-949-016-193085	Sequence 193085, A
C 308	227	9.9	576	7	US-09-925-065A-116873	Sequence 116873, A	C 381	226	9.9	601	3	US-09-949-016-193178	Sequence 193178, A
C 309	227	9.9	601	3	US-09-949-016-33507	Sequence 33507, A	C 382	226	9.9	601	3	US-09-949-016-193271	Sequence 193271, A
C 310	227	9.9	601	3	US-09-949-016-42390	Sequence 42390, A	C 383	226	9.9	601	3	US-09-949-016-193364	Sequence 193364, A
C 311	227	9.9	601	3	US-09-949-016-128966	Sequence 128966, A	C 384	226	9.9	627	7	US-09-925-065A-845860	Sequence 845860, A
C 312	227	9.9	1461	7	US-09-925-065A-680305	Sequence 680305, A	C 385	226	9.9	628	7	US-09-925-065A-141463	Sequence 141463, A
C 313	227	9.9	1960	4	US-10-094-749-542	Sequence 542, App	C 386	226	9.9	628	7	US-09-925-065A-141464	Sequence 141464, A
C 314	227	9.9	13316	3	US-09-949-016-14651	Sequence 14651, A	C 387	226	9.9	628	7	US-09-925-065A-256895	Sequence 256895, A

388	226	9.9	630	7	US-09-925-065A-822191	Sequence 822191, A	461	225.4	9.9	156651	3	US-09-949-016-17349	Sequence 17349, A
389	226	9.9	632	7	US-09-925-065A-86568	Sequence 86568, A	C 462	225.4	9.9	194915	3	US-09-949-016-15584	Sequence 15584, A
390	226	9.9	801	7	US-09-925-065A-88625	Sequence 88625, A	C 463	225.4	9.9	209274	5	US-09-943-679A-3004	Sequence 3004, Ap
C 391	226	9.9	1008	7	US-09-925-065A-723903	Sequence 723903, A	C 464	225.4	9.9	247299	3	US-09-949-016-17590	Sequence 17590, A
C 392	226	9.9	1008	7	US-09-925-065A-723904	Sequence 723904, A	C 465	225.2	9.9	472	7	US-09-925-065A-45817	Sequence 45817, A
C 393	226	9.9	27916	3	US-09-949-016-15202	Sequence 15202, A	C 466	225.2	9.9	519	7	US-09-925-065A-857427	Sequence 857427, A
C 394	226	9.9	28592	3	US-09-949-002-806	Sequence 806, App	C 467	225.2	9.9	528	7	US-09-925-065A-850425	Sequence 850425, A
C 395	226	9.9	39960	5	US-09-339-352-7	Sequence 7, Appl	C 468	225.2	9.9	535	7	US-09-925-065A-857432	Sequence 857432, A
396	226	9.9	41612	3	US-09-949-016-12769	Sequence 12769, A	C 469	225.2	9.9	538	7	US-09-925-065A-834144	Sequence 834144, A
397	226	9.9	41639	3	US-09-949-016-12773	Sequence 12773, A	C 470	225.2	9.9	535	7	US-09-925-065A-345798	Sequence 345798, A
C 398	226	9.9	264358	3	US-09-949-016-15725	Sequence 15725, A	C 471	225.2	9.9	601	3	US-09-949-016-140678	Sequence 140678, A
399	225.8	9.9	539	7	US-09-925-065A-400001	Sequence 400001, A	C 472	225.2	9.9	601	3	US-09-949-016-182808	Sequence 182808, A
400	225.8	9.9	554	7	US-09-925-065A-583714	Sequence 583714, A	C 473	225.2	9.9	601	3	US-09-949-016-196229	Sequence 196229, A
401	225.8	9.9	576	7	US-09-925-065A-116871	Sequence 116871, A	C 474	225.2	9.9	608	7	US-09-925-065A-559667	Sequence 559667, A
402	225.8	9.9	576	7	US-09-925-065A-116872	Sequence 116872, A	C 475	225.2	9.9	678	7	US-09-925-065A-864955	Sequence 864955, A
403	225.8	9.9	601	3	US-09-949-016-204425	Sequence 204425, A	C 476	225.2	9.9	2177	5	US-10-294-229A-1	Sequence 1, Appl
404	225.8	9.9	601	3	US-09-949-016-204495	Sequence 204495, A	C 477	225.2	9.9	8297	3	US-09-949-016-14790	Sequence 14790, A
C 405	225.8	9.9	668	7	US-09-925-065A-91743	Sequence 91743, A	C 478	225.2	9.9	17086	3	US-09-949-016-13684	Sequence 13684, A
C 406	225.8	9.9	24553	3	US-09-949-016-16901	Sequence 16901, A	C 479	225.2	9.9	19389	3	US-09-949-016-15113	Sequence 15113, A
408	225.8	9.9	24984	3	US-09-949-016-14950	Sequence 14950, A	C 480	225.2	9.9	54245	3	US-09-949-016-17099	Sequence 17099, A
C 409	225.8	9.9	25131	3	US-09-949-016-12385	Sequence 12385, A	C 481	225.2	9.9	76563	3	US-09-949-016-12497	Sequence 12497, A
C 410	225.8	9.9	25131	3	US-09-949-016-13653	Sequence 13653, A	C 482	225.2	9.9	78269	3	US-09-949-016-15816	Sequence 15816, A
C 411	225.8	9.9	26433	3	US-09-949-016-18401	Sequence 18401, A	C 483	225.2	9.9	84839	3	US-09-949-016-13210	Sequence 13210, A
C 412	225.8	9.9	30456	3	US-09-949-016-14213	Sequence 14213, A	C 484	225.2	9.9	109925	3	US-09-949-016-17313	Sequence 17313, A
413	225.8	9.9	31797	3	US-09-949-016-17188	Sequence 17188, A	C 485	225.2	9.9	119762	3	US-09-949-016-15051	Sequence 15051, A
414	225.8	9.9	33578	3	US-09-949-016-15670	Sequence 15670, A	C 487	225.2	9.9	139257	3	US-09-920-671-11	Sequence 11, Appl
415	225.8	9.9	35465	5	US-10-030-937-56	Sequence 56, Appl	C 488	225.2	9.9	152486	3	US-09-949-016-12869	Sequence 12869, A
416	225.8	9.9	41132	3	US-09-949-016-12021	Sequence 12021, A	C 489	225.2	9.9	264206	3	US-09-949-016-12731	Sequence 12731, A
417	225.8	9.9	41136	3	US-09-949-016-13021	Sequence 13021, A	C 490	225.2	9.9	264304	3	US-09-949-016-13249	Sequence 13249, A
418	225.8	9.9	42381	3	US-09-949-016-12012	Sequence 12012, A	C 491	225.2	9.9	392000	3	US-10-027-983-11	Sequence 11, Appl
C 419	225.8	9.9	44378	3	US-09-949-016-12540	Sequence 12540, A	C 492	225.2	9.9	510	7	US-09-925-065A-258233	Sequence 258233, A
C 420	225.8	9.9	74527	3	US-09-949-016-12339	Sequence 12339, A	C 493	225.2	9.9	582	7	US-09-925-065A-787470	Sequence 787470, A
C 421	225.8	9.9	74528	3	US-09-949-016-13275	Sequence 13275, A	C 494	225.2	9.9	601	3	US-09-949-016-81260	Sequence 81260, A
C 422	225.8	9.9	165651	3	US-09-949-016-13032	Sequence 13032, A	C 495	225.2	9.9	601	3	US-09-949-016-131800	Sequence 131800, A
423	225.6	9.9	541	7	US-09-925-065A-127530	Sequence 127530, A	C 496	225.2	9.9	1698	7	US-09-925-065A-333396	Sequence 333396, A
424	225.6	9.9	601	3	US-09-949-016-32898	Sequence 32898, A	C 497	225.2	9.9	9454	3	US-09-949-016-12338	Sequence 12338, A
425	225.6	9.9	601	3	US-09-949-016-67276	Sequence 67276, A	C 498	225.2	9.9	9454	3	US-09-949-016-14650	Sequence 14650, A
C 426	225.6	9.9	624	7	US-09-925-065A-373313	Sequence 373313, A	C 499	225.2	9.9	9455	3	US-09-949-016-14099	Sequence 14099, A
C 427	225.6	9.9	627	7	US-09-925-065A-786968	Sequence 786968, A	C 500	225.2	9.9	22431	3	US-09-949-016-12612	Sequence 12612, A
C 428	225.6	9.9	693	7	US-09-925-065A-719234	Sequence 719234, A	C 501	225.2	9.9	24509	3	US-09-949-016-13687	Sequence 13687, A
C 430	225.6	9.9	2946	3	US-10-104-047-794	Sequence 794, App	C 502	225.2	9.9	28109	3	US-09-949-016-14329	Sequence 14329, A
C 431	225.6	9.9	17590	3	US-09-762-311-1	Sequence 1, Appl	C 503	225.2	9.9	54986	3	US-09-949-016-16716	Sequence 16716, A
C 432	225.6	9.9	29889	3	US-09-949-016-13682	Sequence 13682, A	C 504	225.2	9.9	82612	3	US-09-949-016-16823	Sequence 16823, A
C 433	225.6	9.9	43991	5	US-09-984-429-252	Sequence 252, App	C 505	225.2	9.9	82612	3	US-09-949-016-17292	Sequence 17292, A
C 434	225.6	9.9	53562	3	US-09-949-016-16286	Sequence 16286, A	C 506	225.2	9.9	145928	3	US-09-949-016-15444	Sequence 15444, A
C 435	225.4	9.9	101015	3	US-09-949-016-15981	Sequence 16981, A	C 507	225.2	9.9	134605	3	US-09-949-016-11894	Sequence 11894, A
C 436	225.4	9.9	424	7	US-09-925-065A-786430	Sequence 786430, A	C 508	225.2	9.9	260286	3	US-09-949-016-17037	Sequence 17037, A
C 437	225.4	9.9	601	3	US-09-949-016-80035	Sequence 80035, A	C 509	225.2	9.9	260286	3	US-09-949-016-12106	Sequence 12106, A
C 438	225.4	9.9	611	7	US-09-925-065A-373334	Sequence 373334, A	C 510	224.8	9.8	599	7	US-09-925-065A-763319	Sequence 763319, A
C 439	225.4	9.9	611	7	US-09-925-065A-373335	Sequence 373335, A	C 511	224.8	9.8	599	7	US-09-925-065A-763320	Sequence 763320, A
C 440	225.4	9.9	611	7	US-09-925-065A-373336	Sequence 373336, A	C 512	224.8	9.8	600	7	US-09-925-065A-765921	Sequence 765921, A
C 441	225.4	9.9	1184	7	US-09-925-065A-65816	Sequence 65816, A	C 513	224.8	9.8	600	7	US-09-925-065A-765922	Sequence 765922, A
C 442	225.4	9.9	7481	3	US-09-949-016-14492	Sequence 14492, A	C 514	224.8	9.8	601	3	US-09-949-016-193084	Sequence 193084, A
C 443	225.4	9.9	19650	3	US-09-819-989-3	Sequence 3, Appl	C 515	224.8	9.8	601	3	US-09-949-016-193177	Sequence 193177, A
C 444	225.4	9.9	19650	3	US-10-273-992-3	Sequence 3, Appl	C 516	224.8	9.8	601	3	US-09-949-016-193270	Sequence 193270, A
C 445	225.4	9.9	19650	3	US-10-681-222-3	Sequence 3, Appl	C 517	224.8	9.8	601	3	US-09-949-016-193363	Sequence 193363, A
C 446	225.4	9.9	20598	3	US-09-593-995-10	Sequence 10, Appl	C 518	224.8	9.8	606	7	US-09-925-065A-520953	Sequence 520953, A
C 447	225.4	9.9	20598	3	US-10-139-667-10	Sequence 10, Appl	C 519	224.8	9.8	608	7	US-09-925-065A-673158	Sequence 673158, A
C 448	225.4	9.9	29615	3	US-09-949-016-14590	Sequence 14590, A	C 520	224.8	9.8	9391	3	US-09-949-016-14299	Sequence 14299, A
C 449	225.4	9.9	32278	3	US-09-949-016-14575	Sequence 14575, A	C 521	224.8	9.8	9391	3	US-09-949-016-13216	Sequence 13216, A
C 450	225.4	9.9	34200	5	US-09-339-352-17	Sequence 17, Appl	C 522	224.8	9.8	12708	3	US-09-949-016-14877	Sequence 14877, A
C 451	225.4	9.9	72992	3	US-09-949-016-17592	Sequence 17592, A	C 523	224.8	9.8	19062	3	US-09-949-016-11921	Sequence 11921, A
452	225.4	9.9	90541	3	US-09-759-359A-3	Sequence 3, Appl	C 524	224.8	9.8	53452	3	US-09-949-016-13370	Sequence 13370, A
453	225.4	9.9	90541	3	US-10-207-973-3	Sequence 3, Appl	C 525	224.8	9.8	57299	3	US-09-949-016-12141	Sequence 12141, A
454	225.4	9.9	90541	5	US-10-799-676-3	Sequence 3, Appl	C 526	224.8	9.8	86716	3	US-09-949-016-17232	Sequence 17232, A
C 455	225.4	9.9	96845	3	US-09-949-016-13658	Sequence 13658, A	C 527	224.8	9.8	86716	3	US-09-949-016-17240	Sequence 17240, A
C 456	225.4	9.9	132205	5	US-10-185-047A-25	Sequence 25, Appl	C 528	224.8	9.8	86213	3	US-09-949-016-17241	Sequence 17241, A
457	225.4	9.9	141589	5	US-09-543-679A-2480	Sequence 2480, Ap	C 529	224.8	9.8	86213	3	US-09-949-016-17242	Sequence 17242, A
458	225.4	9.9	141589	5	US-09-543-679A-2694	Sequence 2694, Ap	C 530	224.8	9.8	86213	3	US-09-949-016-17243	Sequence 17243, A
459	225.4	9.9	141589	5	US-09-543-679A-2719	Sequence 2719, Ap	C 531	224.8	9.8	97423	3	US-09-949-016-12742	Sequence 12742, A
460	225.4	9.9	146982	5	US-09-543-679A-3009	Sequence 3009, Ap	C 532	224.8	9.8	97424	3	US-09-949-016-15576	Sequence 15576, A
							C 533	224.8	9.8				

C 680	223.6	9.8	90923	3	US-09-949-002-623	Sequence 623, App	C 753	223.2	9.8	160552	3	US-09-593-828-11	Sequence 11, Appl
C 681	223.6	9.8	90925	3	US-09-949-002-789	Sequence 789, App	C 754	223.2	9.8	160552	5	US-10-697-828-11	Sequence 11, Appl
C 682	223.6	9.8	363032	3	US-09-949-016-12415	Sequence 12415, A	C 755	223.2	9.8	174639	3	US-09-949-016-16509	Sequence 16509, A
C 683	223.6	9.8	363033	3	US-09-949-016-15754	Sequence 15754, A	C 756	223.2	9.8	177669	3	US-09-949-016-13713	Sequence 13713, A
C 684	223.4	9.8	600	7	US-09-925-065A-164539	Sequence 164539, A	C 757	223.2	9.8	187169	3	US-09-949-016-12776	Sequence 12776, A
C 685	223.4	9.8	601	3	US-09-949-016-31504	Sequence 31504, A	C 758	223.2	9.8	189560	3	US-09-949-016-17202	Sequence 17202, A
C 686	223.4	9.8	601	3	US-09-949-016-139083	Sequence 139083, A	C 759	223.2	9.8	191569	3	US-09-949-016-15940	Sequence 15940, A
C 687	223.4	9.8	601	3	US-09-949-016-179930	Sequence 179930, A	C 760	223.2	9.8	304533	3	US-09-949-016-15371	Sequence 15371, A
C 688	223.4	9.8	614	7	US-09-925-065A-322229	Sequence 322229, A	C 761	223.2	9.8	304533	3	US-09-949-016-15372	Sequence 15372, A
C 689	223.4	9.8	832	7	US-09-925-065A-918326	Sequence 918326, A	C 762	223	9.8	520	7	US-09-925-065A-497451	Sequence 497451, A
C 690	223.4	9.8	832	7	US-09-925-065A-918327	Sequence 918327, A	C 763	223	9.8	593	7	US-09-925-065A-324547	Sequence 324547, A
C 691	223.4	9.8	1191	7	US-09-925-065A-680687	Sequence 680687, A	C 764	223	9.8	584	7	US-09-925-065A-729387	Sequence 729387, A
C 692	223.4	9.8	26587	7	US-09-949-016-16636	Sequence 16636, A	C 765	223	9.8	588	7	US-09-925-065A-887368	Sequence 887368, A
C 693	223.4	9.8	31111	3	US-09-949-016-15628	Sequence 15628, A	C 766	223	9.8	601	3	US-09-949-016-66995	Sequence 66995, A
C 694	223.4	9.8	50109	3	US-09-949-016-14112	Sequence 14112, A	C 767	223	9.8	601	3	US-09-949-016-174706	Sequence 174706, A
C 695	223.4	9.8	57331	3	US-09-949-016-17277	Sequence 17277, A	C 768	223	9.8	603	7	US-09-925-065A-349602	Sequence 349602, A
C 696	223.4	9.8	75999	5	US-10-360-510-243	Sequence 243, App	C 769	223	9.8	629	7	US-09-925-065A-849048	Sequence 849048, A
C 697	223.4	9.8	78125	3	US-09-949-016-16006	Sequence 16006, A	C 770	223	9.8	635	7	US-09-925-065A-844042	Sequence 844042, A
C 698	223.4	9.8	125902	3	US-09-949-016-13715	Sequence 13715, A	C 771	223	9.8	645	7	US-09-925-065A-426544	Sequence 426544, A
C 699	223.4	9.8	166698	3	US-09-949-016-16038	Sequence 16038, A	C 772	223	9.8	790	7	US-09-925-065A-5393	Sequence 5393, App
C 700	223.4	9.8	178520	5	US-10-021-698A-701	Sequence 701, App	C 773	223	9.8	4916	3	US-09-949-016-13605	Sequence 13605, A
C 701	223.4	9.8	246230	3	US-09-949-016-17019	Sequence 17019, A	C 774	223	9.8	12113	3	US-09-949-016-15144	Sequence 15144, A
C 702	223.4	9.8	246230	3	US-09-949-016-17020	Sequence 17020, A	C 775	223	9.8	24221	3	US-09-949-016-14964	Sequence 14964, A
C 703	223.4	9.8	246230	3	US-09-949-016-17021	Sequence 17021, A	C 776	223	9.8	25097	5	US-10-021-698A-2263	Sequence 2263, App
C 704	223.4	9.8	246230	3	US-09-949-016-17022	Sequence 17022, A	C 777	223	9.8	48920	3	US-09-949-016-11954	Sequence 11954, A
C 705	223.4	9.8	636591	3	US-09-949-016-11808	Sequence 11808, A	C 778	223	9.8	55195	3	US-09-949-016-15854	Sequence 15854, A
C 706	223.4	9.8	636591	3	US-09-949-016-13388	Sequence 13388, A	C 779	223	9.8	66627	3	US-09-949-016-12630	Sequence 12630, A
C 707	223.2	9.8	552	7	US-09-925-065A-516235	Sequence 516235, A	C 780	223	9.8	66628	3	US-09-949-016-16112	Sequence 16112, A
C 708	223.2	9.8	568	7	US-09-925-065A-534797	Sequence 534797, A	C 781	223	9.8	84495	3	US-09-797-906-3	Sequence 3, Appl
C 709	223.2	9.8	581	7	US-09-925-065A-623735	Sequence 623735, A	C 782	223	9.8	84525	3	US-09-949-016-16678	Sequence 16678, A
C 710	223.2	9.8	606	7	US-09-925-065A-46908	Sequence 46908, A	C 783	223	9.8	99748	3	US-09-949-016-11990	Sequence 11990, A
C 711	223.2	9.8	612	7	US-09-925-065A-361599	Sequence 361599, A	C 784	223	9.8	99749	3	US-09-949-016-16518	Sequence 16518, A
C 712	223.2	9.8	620	7	US-09-925-065A-852810	Sequence 852810, A	C 785	223	9.8	106746	3	US-09-326-402C-1	Sequence 1, Appl
C 713	223.2	9.8	625	7	US-09-925-065A-813055	Sequence 813055, A	C 786	223	9.8	106746	3	US-09-326-402C-12	Sequence 12, Appl
C 714	223.2	9.8	639	7	US-09-925-065A-576431	Sequence 576431, A	C 787	223	9.8	119153	3	US-09-949-016-12378	Sequence 12378, A
C 715	223.2	9.8	649	7	US-09-925-065A-54073	Sequence 54073, A	C 788	223	9.8	142793	3	US-09-949-016-15127	Sequence 15127, A
C 716	223.2	9.8	2070	3	US-09-620-312D-958	Sequence 958, App	C 789	223	9.8	206433	3	US-09-949-016-13527	Sequence 13527, A
C 717	223.2	9.8	2649	3	US-09-925-065A-723891	Sequence 723891, A	C 790	223	9.8	254778	3	US-09-949-016-12417	Sequence 12417, A
C 718	223.2	9.8	7232	3	US-09-949-016-12580	Sequence 12580, A	C 791	222.8	9.8	474	7	US-09-925-065A-828503	Sequence 828503, A
C 719	223.2	9.8	7232	3	US-09-949-016-14265	Sequence 14265, A	C 792	222.8	9.8	553	7	US-09-925-065A-417396	Sequence 417396, A
C 720	223.2	9.8	13908	3	US-09-949-016-14265	Sequence 14265, A	C 793	222.8	9.8	601	7	US-09-949-016-119419	Sequence 119419, A
C 721	223.2	9.8	19965	5	US-10-103-295-384	Sequence 384, App	C 794	222.8	9.8	641	7	US-09-925-065A-47719	Sequence 47719, A
C 722	223.2	9.8	20420	3	US-10-103-295-385	Sequence 385, App	C 795	222.8	9.8	682	7	US-09-925-065A-48335	Sequence 48335, A
C 723	223.2	9.8	20902	3	US-09-949-016-12684	Sequence 12684, A	C 796	222.8	9.8	682	7	US-09-925-065A-48336	Sequence 48336, A
C 724	223.2	9.8	20908	3	US-09-949-016-14764	Sequence 14764, A	C 797	222.8	9.8	682	7	US-09-925-065A-48337	Sequence 48337, A
C 725	223.2	9.8	23501	3	US-09-949-016-17517	Sequence 17517, A	C 798	222.8	9.8	1138	7	US-09-925-065A-83681	Sequence 83681, A
C 726	223.2	9.8	24971	3	US-09-949-016-14444	Sequence 14444, A	C 799	222.8	9.8	1427	7	US-09-925-065A-675419	Sequence 675419, A
C 727	223.2	9.8	24972	3	US-09-949-016-15059	Sequence 15059, A	C 800	222.8	9.8	1427	7	US-09-925-065A-675420	Sequence 675420, A
C 728	223.2	9.8	30843	3	US-09-949-016-14487	Sequence 14487, A	C 801	222.8	9.8	2076	7	US-09-925-065A-686804	Sequence 686804, A
C 729	223.2	9.8	47403	3	US-09-949-016-15008	Sequence 15008, A	C 802	222.8	9.8	2905	7	US-09-925-065A-65364	Sequence 65364, A
C 730	223.2	9.8	49610	3	US-09-949-016-13459	Sequence 13459, A	C 803	222.8	9.8	24043	3	US-09-949-016-16104	Sequence 16104, A
C 731	223.2	9.8	64984	3	US-09-949-016-15254	Sequence 15254, A	C 804	222.8	9.8	36592	3	US-09-949-016-16313	Sequence 16313, A
C 732	223.2	9.8	78846	3	US-09-949-016-12396	Sequence 12396, A	C 805	222.8	9.8	38368	3	US-09-949-016-12958	Sequence 12958, A
C 733	223.2	9.8	78846	3	US-09-949-016-12791	Sequence 12791, A	C 806	222.8	9.8	50775	3	US-09-949-016-12858	Sequence 12858, A
C 734	223.2	9.8	78846	3	US-09-949-016-12792	Sequence 12792, A	C 807	222.8	9.8	50776	3	US-09-949-016-15438	Sequence 15438, A
C 735	223.2	9.8	78846	3	US-09-949-016-12793	Sequence 12793, A	C 808	222.8	9.8	106256	3	US-09-949-016-16858	Sequence 16858, A
C 736	223.2	9.8	78850	3	US-09-949-016-16013	Sequence 16013, A	C 809	222.8	9.8	107980	3	US-09-949-016-14370	Sequence 14370, A
C 737	223.2	9.8	78850	3	US-09-949-016-16014	Sequence 16014, A	C 810	222.8	9.8	110096	4	US-09-880-107-1542	Sequence 1542, App
C 738	223.2	9.8	78850	3	US-09-949-016-16015	Sequence 16015, A	C 811	222.8	9.8	131088	3	US-09-949-016-16240	Sequence 16240, A
C 739	223.2	9.8	78850	3	US-09-949-016-16016	Sequence 16016, A	C 812	222.8	9.8	151261	3	US-09-949-016-12674	Sequence 12674, A
C 740	223.2	9.8	78850	3	US-09-949-016-16201	Sequence 16201, A	C 813	222.8	9.8	151261	3	US-09-949-016-13242	Sequence 13242, A
C 741	223.2	9.8	78850	3	US-09-949-016-16202	Sequence 16202, A	C 814	222.8	9.8	818128	3	US-09-949-016-14546	Sequence 14546, A
C 742	223.2	9.8	78850	3	US-09-949-016-16203	Sequence 16203, A	C 815	222.8	9.8	818128	3	US-09-949-016-14547	Sequence 14547, A
C 743	223.2	9.8	78850	3	US-09-949-016-16204	Sequence 16204, A	C 816	222.8	9.8	818128	3	US-09-949-016-14548	Sequence 14548, A
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C 745	223.2	9.8	81001	5	US-10-121-034-1	Sequence 1, Appl	C 818	222.8	9.8	818128	3	US-09-949-016-14550	Sequence 14550, A
C 746	223.2	9.8	94142	3	US-09-949-016-16553	Sequence 16553, A	C 819	222.8	9.8	818128	3	US-09-949-016-14551	Sequence 14551, A
C 747	223.2	9.8	101981	3	US-09-949-016-13995	Sequence 13995, A	C 820	222.8	9.8	818128	3	US-09-949-016-14552	Sequence 14552, A
C 748	223.2	9.8	101982	3	US-09-949-016-12590	Sequence 12590, A	C 821	222.8	9.8	818128	3	US-09-949-016-14553	Sequence 14553, A
C 749	223.2	9.8	106315	3	US-09-949-016-16613	Sequence 16613, A	C 822	222.8	9.8	818128	3	US-09-949-016-14554	Sequence 14554, A
C 750	223.2	9.8	132205	5	US-10-185-047A-25	Sequence 25, Appl	C 823	222.8	9.8	818128	3	US-09-949-016-14555	Sequence 14555, A
C 751	223.2	9.8	137000	3	US-10-172-911-11	Sequence 11, Appl	C 824	222.8	9.8	818128	3	US-09-949-016-14556	Sequence 14556, A
C 752	223.2	9.8	143899	5	US-10-735-256-15	Sequence 15, Appl	C 825	222.8	9.8	818128	3	US-09-949-016-14557	Sequence 14557, A

C 826	222.8	9.8	818128	3	US-09-949-016-14558	Sequence 14558, A	C 899	222.2	9.7	601	3	US-09-949-002-6261	Sequence 6261, Ap
C 827	222.8	9.8	818128	3	US-09-949-016-14559	Sequence 14559, A	C 900	222.2	9.7	646	7	US-09-925-065A-500330	Sequence 500330,
C 828	222.8	9.8	818128	3	US-09-949-016-14560	Sequence 14560, A	C 901	222.2	9.7	841	8	PCT-US93-06251-80	Sequence 80, Appl
C 829	222.8	9.8	818128	3	US-09-949-016-14561	Sequence 14561, A	C 902	222.2	9.7	841	8	PCT-US93-06251-81	Sequence 81, Appl
C 830	222.8	9.8	818128	3	US-09-949-016-14562	Sequence 14562, A	C 903	222.2	9.7	878	7	US-09-925-065A-55287	Sequence 55287, A
C 831	222.8	9.8	818128	3	US-09-949-016-14563	Sequence 14563, A	C 904	222.2	9.7	1099	7	US-09-925-065A-75575	Sequence 75575, A
C 832	222.8	9.8	818128	3	US-09-949-016-14564	Sequence 14564, A	C 905	222.2	9.7	35688	3	US-09-949-016-16873	Sequence 16873, A
C 833	222.8	9.8	818128	3	US-09-949-016-14565	Sequence 14565, A	C 906	222.2	9.7	53769	3	US-09-949-016-17537	Sequence 17537, A
C 834	222.8	9.8	818128	3	US-09-949-016-14566	Sequence 14566, A	C 907	222.2	9.7	54878	3	US-09-949-016-12255	Sequence 12255, A
C 835	222.6	9.7	601	3	US-09-949-016-14567	Sequence 14567, A	C 908	222.2	9.7	62908	3	US-09-949-016-17554	Sequence 17554, A
C 836	222.6	9.7	601	3	US-09-949-016-152686	Sequence 52686, A	C 909	222.2	9.7	69062	3	US-09-949-016-13608	Sequence 13608, A
C 837	222.6	9.7	601	3	US-09-949-016-613387	Sequence 613387, A	C 910	222.2	9.7	69062	3	US-09-949-016-13609	Sequence 13609, A
C 838	222.6	9.7	601	3	US-09-949-016-121303	Sequence 121303, A	C 911	222.2	9.7	69687	3	US-09-949-016-12890	Sequence 12890, A
C 839	222.6	9.7	601	3	US-09-949-016-126049	Sequence 126049, A	C 912	222.2	9.7	77036	3	US-09-949-016-16156	Sequence 16156, A
C 840	222.6	9.7	601	3	US-09-949-016-177754	Sequence 177754, A	C 913	222.2	9.7	86127	3	US-09-949-016-12209	Sequence 12209, A
C 841	222.6	9.7	647	7	US-09-925-065A-304894	Sequence 304894, A	C 914	222.2	9.7	86128	3	US-09-949-016-15608	Sequence 15608, A
C 842	222.6	9.7	910	7	US-09-925-065A-710030	Sequence 710030, A	C 915	222.2	9.7	93398	3	US-09-949-016-14167	Sequence 14167, A
C 843	222.6	9.7	2477	3	US-10-104-047-969	Sequence 969, App	C 916	222.2	9.7	101558	3	US-09-949-016-12243	Sequence 12243, A
C 844	222.6	9.7	11746	5	US-10-103-298-387	Sequence 387, App	C 917	222.2	9.7	134434	3	US-09-949-016-17362	Sequence 17362, A
C 845	222.6	9.7	24993	3	US-09-949-016-12952	Sequence 12952, A	C 918	222.2	9.7	235452	3	US-09-949-016-13675	Sequence 13675, A
C 846	222.6	9.7	39960	5	US-09-339-352-7	Sequence 7, Appli	C 919	222	9.7	512	7	US-09-925-065A-155742	Sequence 69434, A
C 847	222.6	9.7	47284	3	US-09-949-016-17029	Sequence 17029, A	C 920	222	9.7	531	7	US-09-925-065A-69434	Sequence 69434, A
C 848	222.6	9.7	53737	3	US-09-949-016-16197	Sequence 16197, A	C 921	222	9.7	597	7	US-09-925-065A-887330	Sequence 887330,
C 849	222.6	9.7	56694	3	US-09-949-016-13568	Sequence 12568, A	C 922	222	9.7	597	7	US-09-925-065A-911878	Sequence 911878,
C 850	222.6	9.7	56702	3	US-09-949-016-13423	Sequence 15423, A	C 923	222	9.7	601	3	US-09-949-016-47164	Sequence 47164, A
C 851	222.6	9.7	80225	5	US-09-728-552A-4	Sequence 4, Appli	C 924	222	9.7	601	3	US-09-949-016-151861	Sequence 151861,
C 852	222.6	9.7	80246	3	US-09-078-294-4	Sequence 4, Appli	C 925	222	9.7	611	7	US-09-925-065A-850137	Sequence 850137,
C 853	222.6	9.7	80595	3	US-09-078-294-3	Sequence 3, Appli	C 926	222	9.7	613	7	US-09-925-065A-754442	Sequence 754442,
C 854	222.6	9.7	80595	5	US-09-728-552A-3	Sequence 3, Appli	C 927	222	9.7	621	7	US-09-925-065A-846357	Sequence 846357,
C 855	222.6	9.7	98302	3	US-09-949-016-16847	Sequence 16847, A	C 928	222	9.7	634	7	US-09-925-065A-830096	Sequence 830096,
C 856	222.6	9.7	128516	3	US-09-949-016-13501	Sequence 13501, A	C 929	222	9.7	699	7	US-09-925-065A-880171	Sequence 880171,
C 857	222.6	9.7	133157	3	US-09-949-016-12541	Sequence 12541, A	C 930	222	9.7	2828	7	US-09-925-065A-678983	Sequence 678983,
C 858	222.6	9.7	152393	3	US-09-949-016-14514	Sequence 14514, A	C 931	222	9.7	2828	7	US-09-925-065A-678985	Sequence 678985,
C 859	222.6	9.7	152393	3	US-09-949-016-14515	Sequence 14515, A	C 932	222	9.7	6417	3	US-09-949-016-16966	Sequence 16966, A
C 860	222.6	9.7	156894	3	US-09-949-016-12765	Sequence 12765, A	C 933	222	9.7	17996	3	US-09-949-016-16867	Sequence 16867, A
C 861	222.6	9.7	156894	3	US-09-949-016-12766	Sequence 12766, A	C 934	222	9.7	17996	3	US-09-949-016-16867	Sequence 16867, A
C 862	222.6	9.7	156895	3	US-09-949-016-16957	Sequence 16957, A	C 935	222	9.7	23781	3	US-09-949-016-13446	Sequence 13446, A
C 863	222.6	9.7	156895	3	US-09-949-016-16958	Sequence 16958, A	C 936	222	9.7	43086	3	US-09-949-016-13059	Sequence 13059, A
C 864	222.6	9.7	156895	3	US-09-949-016-16959	Sequence 16959, A	C 937	222	9.7	43086	3	US-09-949-016-13059	Sequence 13059, A
C 865	222.6	9.7	187580	3	US-09-949-016-13266	Sequence 13266, A	C 938	222	9.7	60376	3	US-09-949-016-12423	Sequence 12423, A
C 866	222.6	9.7	189268	5	US-10-021-698A-697	Sequence 697, App	C 939	222	9.7	70308	3	US-09-949-016-15601	Sequence 15601, A
C 867	222.6	9.7	194933	3	US-09-949-016-14172	Sequence 14172, A	C 940	222	9.7	76985	3	US-09-949-016-12416	Sequence 12416, A
C 868	222.6	9.7	346112	3	US-09-949-016-13165	Sequence 13165, A	C 941	222	9.7	76985	3	US-09-949-016-13120	Sequence 13120, A
C 869	222.4	9.7	601	3	US-09-949-016-22164	Sequence 22164, A	C 942	222	9.7	81384	3	US-09-949-016-12422	Sequence 12422, A
C 870	222.4	9.7	601	3	US-09-949-016-139175	Sequence 139175, A	C 943	222	9.7	113042	3	US-09-949-016-12343	Sequence 12343, A
C 871	222.4	9.7	601	3	US-09-949-016-139669	Sequence 139669, A	C 944	222	9.7	113042	3	US-09-949-016-15246	Sequence 15246, A
C 872	222.4	9.7	601	3	US-09-949-016-150942	Sequence 150942, A	C 945	222	9.7	133358	3	US-09-949-016-16964	Sequence 16964, A
C 873	222.4	9.7	613	7	US-09-925-065A-825281	Sequence 825281, A	C 946	222	9.7	133360	3	US-09-949-016-12651	Sequence 12651, A
C 874	222.4	9.7	639	7	US-09-925-065A-92802	Sequence 92802, A	C 947	222	9.7	162025	3	US-09-834-700-13	Sequence 13, Appl
C 875	222.4	9.7	766	5	US-10-021-698A-428	Sequence 428, App	C 948	222	9.7	162025	3	US-09-834-700-14	Sequence 14, Appl
C 876	222.4	9.7	11494	3	US-09-949-016-13347	Sequence 13347, A	C 949	222	9.7	162025	3	US-09-834-700-17	Sequence 17, Appl
C 877	222.4	9.7	18679	3	US-09-949-016-13443	Sequence 13443, A	C 950	222	9.7	162025	3	US-09-834-700-18	Sequence 18, Appl
C 878	222.4	9.7	26867	3	US-09-949-016-16332	Sequence 16332, A	C 951	222	9.7	199945	3	US-09-949-016-15436	Sequence 15436, A
C 879	222.4	9.7	26867	3	US-09-949-016-16333	Sequence 16333, A	C 952	221.8	9.7	508	7	US-09-925-065A-884576	Sequence 884576,
C 880	222.4	9.7	34414	3	US-09-949-016-16330	Sequence 12330, A	C 953	221.8	9.7	508	7	US-09-925-065A-884577	Sequence 884577,
C 881	222.4	9.7	34414	3	US-09-949-016-16157	Sequence 16157, A	C 954	221.8	9.7	555	7	US-09-925-065A-791692	Sequence 791692,
C 882	222.4	9.7	35256	3	US-09-949-016-11991	Sequence 11991, A	C 955	221.8	9.7	594	7	US-09-925-065A-436087	Sequence 436087,
C 883	222.4	9.7	35707	3	US-09-949-016-17120	Sequence 17120, A	C 956	221.8	9.7	601	3	US-09-949-016-27651	Sequence 27651, A
C 884	222.4	9.7	43463	3	US-09-949-016-16341	Sequence 16341, A	C 957	221.8	9.7	601	3	US-09-949-016-63845	Sequence 63845, A
C 885	222.4	9.7	44653	3	US-09-949-016-11944	Sequence 11944, A	C 958	221.8	9.7	601	3	US-09-949-016-63920	Sequence 63920, A
C 886	222.4	9.7	44653	3	US-09-949-016-15690	Sequence 15690, A	C 959	221.8	9.7	601	3	US-09-949-016-65931	Sequence 65931, A
C 887	222.4	9.7	49848	3	US-09-949-016-15675	Sequence 15675, A	C 960	221.8	9.7	601	3	US-09-949-016-158182	Sequence 158182,
C 888	222.4	9.7	51773	3	US-09-949-016-16002	Sequence 16002, A	C 961	221.8	9.7	601	3	US-09-949-016-160721	Sequence 160721,
C 889	222.4	9.7	52711	3	US-09-949-016-12224	Sequence 12224, A	C 962	221.8	9.7	601	3	US-09-949-016-178594	Sequence 178594,
C 890	222.4	9.7	52865	3	US-09-949-016-15618	Sequence 15618, A	C 963	221.8	9.7	601	3	US-09-949-016-199161	Sequence 199161,
C 891	222.4	9.7	72602	3	US-09-949-016-14385	Sequence 14385, A	C 964	221.8	9.7	601	3	US-09-949-002-3495	Sequence 3495, Ap
C 892	222.4	9.7	190849	5	US-10-021-698A-706	Sequence 706, App	C 965	221.8	9.7	601	3	US-09-949-002-9467	Sequence 9467, Ap
C 893	222.4	9.7	264665	3	US-09-949-016-13747	Sequence 13747, A	C 966	221.8	9.7	603	7	US-09-925-065A-349601	Sequence 349601,
C 894	222.4	9.7	275110	3	US-09-949-016-12706	Sequence 12706, A	C 967	221.8	9.7	618	7	US-09-925-065A-81044	Sequence 81044, A
C 895	222.4	9.7	275110	3	US-09-949-016-16070	Sequence 16070, A	C 968	221.8	9.7	1115	7	US-09-925-065A-688168	Sequence 688168,
C 896	222.2	9.7	561	7	US-09-925-065A-280839	Sequence 280839, A	C 969	221.8	9.7	1806	7	US-09-925-065A-726395	Sequence 726395,
C 897	222.2	9.7	569	7	US-09-925-065A-945440	Sequence 945440, A	C 970	221.8	9.7	13617	3	US-09-949-002-811	Sequence 811, App
C 898	222.2	9.7	576	7	US-09-925-065A-431198	Sequence 431198, A	C 971	221.8	9.7	14205	3	US-09-949-016-16196	Sequence 16196, A

972	221.8	9.7	14243	3	US-09-949-002-626	Sequence 626, App	c1045	221.4	9.7	15222	3	US-09-949-016-11916	Sequence 11916, A
c 973	221.8	9.7	15402	3	US-09-949-016-12868	Sequence 12868, A	c1046	221.4	9.7	15223	3	US-09-949-016-15982	Sequence 15982, A
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c 976	221.8	9.7	22124	3	US-09-949-016-14666	Sequence 14666, A	1049	221.4	9.7	40546	3	US-09-949-016-12847	Sequence 12847, A
c 977	221.8	9.7	41677	3	US-09-949-002-668	Sequence 668, App	1050	221.4	9.7	50073	3	US-09-949-016-16026	Sequence 16026, A
c 978	221.8	9.7	75378	3	US-09-949-016-17140	Sequence 17140, A	c1051	221.4	9.7	57859	3	US-09-949-016-12334	Sequence 12334, A
c 979	221.8	9.7	84425	3	US-09-949-016-17402	Sequence 17402, A	c1052	221.4	9.7	57859	3	US-09-949-016-14657	Sequence 14657, A
c 980	221.8	9.7	102520	3	US-09-949-016-17367	Sequence 17367, A	c1053	221.4	9.7	57859	3	US-09-949-016-14658	Sequence 14658, A
c 981	221.8	9.7	102526	3	US-09-949-016-12448	Sequence 12448, A	c1054	221.4	9.7	59319	3	US-09-949-016-16115	Sequence 16115, A
c 982	221.8	9.7	119594	3	US-09-949-016-12080	Sequence 12080, A	1055	221.4	9.7	83708	3	US-09-949-016-17207	Sequence 17207, A
c 983	221.8	9.7	119601	3	US-09-949-016-15952	Sequence 15952, A	1056	221.4	9.7	133278	3	US-09-949-016-12524	Sequence 12524, A
c 984	221.8	9.7	151088	3	US-09-949-016-16240	Sequence 16240, A	c1057	221.4	9.7	135030	3	US-09-949-016-14896	Sequence 14896, A
c 985	221.6	9.7	469	7	US-09-925-065A-799777	Sequence 799777, App	c1058	221.4	9.7	254964	3	US-09-949-016-12583	Sequence 12583, A
c 986	221.6	9.7	474	7	US-09-925-065A-792523	Sequence 792523, App	c1059	221.4	9.7	254964	3	US-09-949-016-17392	Sequence 17392, A
c 987	221.6	9.7	552	7	US-09-925-065A-357738	Sequence 357738, App	c1060	221.4	9.7	678533	3	US-09-949-016-14577	Sequence 14577, A
c 988	221.6	9.7	601	3	US-09-949-016-87763	Sequence 87763, A	c1061	221.4	9.7	678533	3	US-09-949-016-14578	Sequence 14578, A
c 989	221.6	9.7	601	3	US-09-949-016-87764	Sequence 87764, A	c1062	221.2	9.7	501	7	US-09-925-065A-799758	Sequence 799758, A
c 990	221.6	9.7	601	3	US-09-949-016-135168	Sequence 135168, App	c1063	221.2	9.7	508	7	US-09-925-065A-741605	Sequence 741605, A
c 991	221.6	9.7	629	7	US-09-925-065A-576432	Sequence 576432, App	1064	221.2	9.7	508	7	US-09-925-065A-787319	Sequence 787319, A
c 992	221.6	9.7	1426	3	US-09-925-065A-12448	Sequence 12448, A	1065	221.2	9.7	561	7	US-09-925-065A-502735	Sequence 502735, A
c 993	221.6	9.7	2092	7	US-09-925-065A-710753	Sequence 710753, App	c1066	221.2	9.7	573	7	US-09-925-065A-833297	Sequence 833297, A
c 994	221.6	9.7	2345	5	US-10-108-260A-112	Sequence 112, App	1067	221.2	9.7	581	7	US-09-925-065A-318711	Sequence 318711, A
c 995	221.6	9.7	2405	3	US-10-104-047-1452	Sequence 1452, App	c1068	221.2	9.7	601	3	US-09-949-016-182224	Sequence 182224, A
c 996	221.6	9.7	2436	7	US-09-925-065A-670010	Sequence 670010, App	c1069	221.2	9.7	601	3	US-09-949-016-189339	Sequence 189339, A
c 997	221.6	9.7	2555	7	US-09-925-065A-700387	Sequence 700387, App	1070	221.2	9.7	629	7	US-09-925-065A-810014	Sequence 810014, A
c 998	221.6	9.7	2555	7	US-09-925-065A-700388	Sequence 700388, App	1071	221.2	9.7	641	7	US-09-925-065A-47720	Sequence 47720, A
c 999	221.6	9.7	2836	7	US-09-925-065A-698795	Sequence 698795, App	c1072	221.2	9.7	688	7	US-09-925-065A-35460	Sequence 35460, A
c1000	221.6	9.7	10857	3	US-09-949-016-14880	Sequence 14880, A	c1073	221.2	9.7	843	7	US-09-925-065A-722490	Sequence 722490, A
1001	221.6	9.7	11665	3	US-09-949-016-12446	Sequence 12446, A	1074	221.2	9.7	1048	7	US-09-925-065A-37593	Sequence 37593, A
c1002	221.6	9.7	11665	3	US-09-949-016-16500	Sequence 16500, A	1075	221.2	9.7	1340	7	US-09-925-065A-81066	Sequence 81066, A
c1003	221.6	9.7	13193	3	US-09-949-016-17515	Sequence 17515, A	c1076	221.2	9.7	1867	3	US-08-943-731-111	Sequence 111, App
c1004	221.6	9.7	14079	3	US-09-949-016-11993	Sequence 11993, A	c1077	221.2	9.7	2133	7	US-09-925-065A-78615	Sequence 78615, A
c1005	221.6	9.7	19806	3	US-09-740-028A-3	Sequence 3, Appli	1078	221.2	9.7	8429	3	US-09-949-016-14483	Sequence 14483, A
1006	221.6	9.7	19806	3	US-10-118-037-3	Sequence 3, Appli	1079	221.2	9.7	15116	3	US-09-949-016-12354	Sequence 12354, A
c1007	221.6	9.7	19806	3	US-10-924-785-3	Sequence 3, Appli	1080	221.2	9.7	15117	3	US-09-949-016-16260	Sequence 16260, A
c1008	221.6	9.7	22888	5	US-09-949-016-14659	Sequence 14659, A	c1081	221.2	9.7	24183	3	US-08-943-731-3	Sequence 3, Appli
1009	221.6	9.7	25428	3	US-09-949-016-17161	Sequence 17161, A	c1082	221.2	9.7	25951	3	US-09-949-016-16194	Sequence 16194, A
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1012	221.6	9.7	49389	3	US-09-949-016-13630	Sequence 13630, A	c1085	221.2	9.7	50810	3	Sequence 16039, A	Sequence 16039, A
c1013	221.6	9.7	50518	3	US-09-949-016-12315	Sequence 12315, A	1086	221.2	9.7	54033	3	Sequence 12091, A	Sequence 12091, A
c1014	221.6	9.7	58162	3	US-09-949-016-16289	Sequence 16289, A	1087	221.2	9.7	54033	3	Sequence 14325, A	Sequence 14325, A
c1015	221.6	9.7	63982	3	US-09-949-016-16769	Sequence 16769, A	1088	221.2	9.7	57638	3	Sequence 17000, A	Sequence 17000, A
c1016	221.6	9.7	71879	3	US-09-949-016-17465	Sequence 17465, A	1089	221.2	9.7	60194	3	Sequence 656, App	Sequence 656, App
1017	221.6	9.7	101951	3	US-09-949-016-15648	Sequence 15648, A	1090	221.2	9.7	60195	3	Sequence 697, App	Sequence 697, App
1018	221.6	9.7	107980	3	US-09-949-016-14370	Sequence 14370, A	c1091	221.2	9.7	135192	3	Sequence 14120, A	Sequence 14120, A
1019	221.6	9.7	138693	3	US-09-949-016-16724	Sequence 16724, A	1092	221.2	9.7	239527	3	Sequence 15980, A	Sequence 15980, A
c1020	221.6	9.7	276687	3	US-09-949-016-13840	Sequence 13840, A	c1093	221.2	9.7	278866	3	Sequence 13922, A	Sequence 13922, A
c1021	221.4	9.7	536	7	US-09-925-065A-890306	Sequence 890306, App	c1094	221.2	9.7	278866	3	Sequence 13923, A	Sequence 13923, A
1022	221.4	9.7	598	7	US-09-925-065A-839297	Sequence 839297, App	c1095	221.2	9.7	278866	3	Sequence 13924, A	Sequence 13924, A
c1023	221.4	9.7	601	3	US-09-949-016-51669	Sequence 51669, A	c1096	221.2	9.7	278866	3	Sequence 13925, A	Sequence 13925, A
c1024	221.4	9.7	601	3	US-09-949-016-51670	Sequence 51670, A	c1097	221.2	9.7	278866	3	Sequence 13926, A	Sequence 13926, A
c1025	221.4	9.7	601	3	US-09-949-016-149747	Sequence 149747, App	c1098	221.2	9.7	278866	3	Sequence 14699, A	Sequence 14699, A
c1026	221.4	9.7	601	3	US-09-949-016-149748	Sequence 149748, App	c1099	221.2	9.7	278866	3	Sequence 14700, A	Sequence 14700, A
c1027	221.4	9.7	601	3	US-09-949-016-179931	Sequence 179931, App	c1100	221.2	9.7	278866	3	Sequence 14701, A	Sequence 14701, A
c1028	221.4	9.7	601	3	US-09-949-016-179931	Sequence 179931, App	c1101	221.2	9.7	278866	3	Sequence 14702, A	Sequence 14702, A
1029	221.4	9.7	618	7	US-09-949-016-183483	Sequence 183483, App	c1102	221.2	9.7	278866	3	Sequence 14703, A	Sequence 14703, A
c1030	221.4	9.7	618	7	US-09-925-065A-836532	Sequence 836532, App	1103	221.2	9.7	321022	3	Sequence 11852, A	Sequence 11852, A
c1031	221.4	9.7	623	7	US-09-925-065A-816909	Sequence 816909, App	c1104	221.2	9.7	321022	3	Sequence 14166, A	Sequence 14166, A
c1032	221.4	9.7	633	7	US-09-925-065A-723304	Sequence 723304, App	c1105	221.2	9.7	565	7	US-09-925-065A-414376	Sequence 414376, A
c1033	221.4	9.7	647	7	US-09-925-065A-304893	Sequence 304893, App	c1106	221	9.7	600	7	US-09-925-065A-858611	Sequence 858611, A
c1034	221.4	9.7	2383	7	US-09-925-065A-552108	Sequence 552108, App	c1107	221	9.7	601	3	US-09-949-016-32490	Sequence 32490, A
c1035	221.4	9.7	2383	7	US-09-925-065A-552109	Sequence 552109, App	1108	221	9.7	601	3	Sequence 55384, A	Sequence 55384, A
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c1037	221.4	9.7	5173	3	US-09-949-016-13985	Sequence 13985, A	c1110	221	9.7	601	3	Sequence 125475, A	Sequence 125475, A
c1038	221.4	9.7	10751	3	US-09-949-016-12097	Sequence 12097, A	c1111	221	9.7	601	3	US-09-949-016-125476	Sequence 125476, A
c1039	221.4	9.7	10751	3	US-09-949-016-13486	Sequence 13486, A	1112	221	9.7	601	3	US-09-949-016-138588	Sequence 138588, A
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1041	221.4	9.7	12482	3	US-09-512-563C-25	Sequence 25, Appli	1114	221	9.7	605	7	US-09-925-065A-842773	Sequence 842773, A
1042	221.4	9.7	12482	3	US-10-060-607-25	Sequence 25, Appli	c1115	221	9.7	617	7	US-09-925-065A-49035	Sequence 49035, A
1043	221.4	9.7	12482	5	US-10-270-877-25	Sequence 25, Appli	c1116	221	9.7	826	7	US-09-925-065A-722461	Sequence 722461, A
1044	221.4	9.7	12482	5	US-10-270-837-25	Sequence 25, Appli	1117	221	9.7	864	7	US-09-925-065A-82967	Sequence 82967, A

c1118	221	9.7	874	7	US-09-925-065A-83475	Sequence 83475, A	1191	220.8	9.7	209210	3	US-09-949-016-15094	Sequence 15094, A
c1119	221	9.7	878	7	US-09-925-065A-55288	Sequence 55288, A	c1192	220.8	9.7	223471	3	US-09-949-016-12387	Sequence 12387, A
c1120	221	9.7	1038	7	US-09-925-065A-726984	Sequence 726984, A	c1193	220.8	9.7	223471	3	US-09-949-016-12724	Sequence 12724, A
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c1122	221	9.7	1107	7	US-09-925-065A-715884	Sequence 715884, A	1195	220.6	9.7	543	7	US-09-925-065A-486784	Sequence 486784, A
c1123	221	9.7	1168	7	US-09-925-065A-45033	Sequence 45033, A	c1196	220.6	9.7	557	7	US-09-925-065A-177024	Sequence 177024, A
c1124	221	9.7	1421	7	US-09-925-065A-667547	Sequence 667547, A	c1197	220.6	9.7	576	7	US-09-925-065A-431197	Sequence 431197, A
c1125	221	9.7	1421	7	US-09-925-065A-667548	Sequence 667548, A	c1198	220.6	9.7	586	7	US-09-925-065A-175723	Sequence 175723, A
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1128	221	9.7	1670	7	US-09-925-065A-702197	Sequence 702197, A	1201	220.6	9.7	601	3	US-09-949-016-35250	Sequence 35250, A
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c1130	221	9.7	2182	7	US-09-925-065A-698956	Sequence 698956, A	c1203	220.6	9.7	601	3	US-09-949-016-57969	Sequence 57969, A
c1131	221	9.7	2561	3	US-09-270-542-101	Sequence 101, App	1204	220.6	9.7	601	3	US-09-949-016-63173	Sequence 63173, A
c1132	221	9.7	2561	3	US-09-270-542-119	Sequence 119, App	c1205	220.6	9.7	601	3	US-09-949-016-91445	Sequence 91445, A
c1133	221	9.7	5957	5	US-10-342-887-252	Sequence 252, App	c1206	220.6	9.7	601	3	US-09-949-016-125477	Sequence 125477, A
c1134	221	9.7	11982	3	US-09-949-016-17084	Sequence 17084, A	1207	220.6	9.7	601	3	US-09-949-016-140123	Sequence 140123, A
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1136	221	9.7	15024	3	US-09-949-016-15704	Sequence 15704, A	1209	220.6	9.7	601	3	US-09-949-016-156812	Sequence 156812, A
1137	221	9.7	18891	3	US-09-949-016-16523	Sequence 16523, A	c1210	220.6	9.7	601	3	US-09-949-002-3305	Sequence 3305, Ap
1138	221	9.7	22480	5	US-08-630-629B-43	Sequence 43, Appl	c1211	220.6	9.7	601	3	US-09-949-002-7764	Sequence 7764, Ap
1139	221	9.7	22481	3	US-08-367-841A-43	Sequence 43, Appl	c1212	220.6	9.7	646	7	US-09-925-065A-500329	Sequence 500329, A
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1142	221	9.7	22484	3	US-09-875-114-2	Sequence 2, Appl	c1215	220.6	9.7	1421	7	US-09-925-065A-667545	Sequence 667545, A
1143	221	9.7	22484	4	US-09-880-107-3341	Sequence 3341, Ap	c1216	220.6	9.7	1421	7	US-09-925-065A-667546	Sequence 667546, A
1144	221	9.7	25260	3	US-09-949-016-11985	Sequence 11985, A	c1217	220.6	9.7	2034	5	US-09-973-278-872	Sequence 872, App
1145	221	9.7	25260	3	US-09-949-016-12907	Sequence 12907, A	c1218	220.6	9.7	2167	7	US-09-925-065A-88279	Sequence 88279, A
1146	221	9.7	25263	3	US-09-949-016-11876	Sequence 11876, A	c1219	220.6	9.7	2167	7	US-09-925-065A-88281	Sequence 88281, A
c1147	221	9.7	25266	3	US-09-949-002-739	Sequence 739, App	1220	220.6	9.7	23907	3	US-09-949-016-15329	Sequence 15329, A
c1148	221	9.7	29742	3	US-09-949-016-15650	Sequence 15650, A	1221	220.6	9.7	27780	3	US-09-949-016-12013	Sequence 12013, A
c1149	221	9.7	32654	3	US-09-801-191A-3	Sequence 3, Appl	1222	220.6	9.7	27791	3	US-09-949-016-17498	Sequence 17498, A
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1151	221	9.7	33624	3	US-09-949-016-15301	Sequence 15301, A	1224	220.6	9.7	38252	3	US-09-949-016-13570	Sequence 13570, A
1152	221	9.7	37710	3	US-09-949-016-15761	Sequence 15761, A	c1225	220.6	9.7	47493	3	US-09-949-016-13241	Sequence 13241, A
1153	221	9.7	37712	3	US-09-949-016-12692	Sequence 12692, A	1226	220.6	9.7	84132	3	US-09-949-016-16241	Sequence 16241, A
c1154	221	9.7	38944	3	US-09-949-002-615	Sequence 615, App	c1227	220.6	9.7	85854	3	US-09-949-016-12908	Sequence 12908, A
c1155	221	9.7	51905	3	US-09-949-002-667	Sequence 667, App	1228	220.6	9.7	112114	3	US-09-949-016-17292	Sequence 17292, A
c1156	221	9.7	51905	3	US-09-949-002-781	Sequence 781, App	c1229	220.6	9.7	149543	3	US-09-949-016-15947	Sequence 15947, A
c1157	221	9.7	70770	3	US-09-949-016-16938	Sequence 16938, A	1230	220.6	9.7	154605	3	US-09-949-016-11894	Sequence 11894, A
1158	221	9.7	74424	5	US-10-773-678A-153	Sequence 153, App	1231	220.6	9.7	187916	3	US-09-949-016-12980	Sequence 12980, A
c1159	221	9.7	81927	3	US-09-949-016-15623	Sequence 15623, A	1232	220.6	9.7	202111	3	US-09-949-016-13877	Sequence 13877, A
c1160	221	9.7	97195	3	US-09-949-016-12212	Sequence 12212, A	c1233	220.4	9.6	601	3	US-09-949-016-22674	Sequence 22674, A
c1161	221	9.7	97196	3	US-09-949-016-12212	Sequence 12212, A	c1234	220.4	9.6	601	3	US-09-949-016-29409	Sequence 29409, A
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c1163	221	9.7	143155	3	US-09-949-016-11925	Sequence 11925, A	c1236	220.4	9.6	601	3	US-09-949-016-29411	Sequence 29411, A
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c1165	221	9.7	143173	3	US-09-949-016-14513	Sequence 14513, A	c1238	220.4	9.6	601	3	US-09-949-016-89013	Sequence 89013, A
c1166	221	9.7	165698	3	US-09-949-016-16038	Sequence 16038, A	1239	220.4	9.6	601	3	US-09-949-016-143723	Sequence 143723, A
c1167	221	9.7	231129	3	US-09-949-016-16110	Sequence 16110, A	c1240	220.4	9.6	601	3	US-09-949-016-158257	Sequence 158257, A
1168	221	9.7	255679	3	US-09-949-016-17189	Sequence 17189, A	c1241	220.4	9.6	601	3	US-09-949-016-158258	Sequence 158258, A
c1169	221	9.7	262293	3	US-09-949-016-11934	Sequence 11934, A	c1242	220.4	9.6	601	3	US-09-949-016-158259	Sequence 158259, A
c1170	220.8	9.7	532	7	US-09-925-065A-825849	Sequence 825849, A	c1243	220.4	9.6	601	3	US-09-949-016-172718	Sequence 172718, A
1171	220.8	9.7	565	7	US-09-925-065A-161603	Sequence 161603, A	1244	220.4	9.6	601	3	US-09-949-016-186879	Sequence 186879, A
c1172	220.8	9.7	572	7	US-09-925-065A-305458	Sequence 305458, A	c1245	220.4	9.6	605	7	US-09-925-065A-526564	Sequence 526564, A
c1173	220.8	9.7	601	3	US-09-949-016-65816	Sequence 65816, A	1246	220.4	9.6	624	7	US-09-925-065A-207796	Sequence 207796, A
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1175	220.8	9.7	601	3	US-09-949-016-143724	Sequence 143724, A	1248	220.4	9.6	636	7	US-09-925-065A-956896	Sequence 956896, A
1176	220.8	9.7	601	3	US-09-949-016-159210	Sequence 159210, A	1249	220.4	9.6	638	7	US-09-925-065A-939006	Sequence 939006, A
c1177	220.8	9.7	601	3	US-09-949-016-172989	Sequence 172989, A	1250	220.4	9.6	638	7	US-09-925-065A-954627	Sequence 954627, A
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1179	220.8	9.7	681	7	US-09-925-065A-824516	Sequence 824516, A	1252	220.4	9.6	608	7	US-09-925-065A-921710	Sequence 921710, A
1180	220.8	9.7	682	7	US-09-925-065A-827685	Sequence 827685, A	c1253	220.4	9.6	1009	7	US-09-925-065A-13903	Sequence 13903, Ap
1181	220.8	9.7	1009	7	US-09-925-065A-80000	Sequence 80000, A	c1254	220.4	9.6	1015	7	US-09-925-065A-31286	Sequence 31286, A
1182	220.8	9.7	2227	5	US-10-210-120-87	Sequence 87, Appl	c1255	220.4	9.6	1443	7	US-09-925-065A-64449	Sequence 64449, A
c1183	220.8	9.7	41106	3	US-09-949-016-15796	Sequence 15796, A	c1256	220.4	9.6	1443	7	US-09-925-065A-64450	Sequence 64450, A
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c1185	220.8	9.7	96739	3	US-09-949-016-15606	Sequence 15606, A	1258	220.4	9.6	12797	3	US-09-949-016-16798	Sequence 16798, A
1186	220.8	9.7	99014	4	US-09-880-107-3428	Sequence 3428, Ap	c1259	220.4	9.6	171327	2	US-07-906-871-15	Sequence 15, Appl
1187	220.8	9.7	102053	3	US-09-949-016-13025	Sequence 13025, A	c1260	220.4	9.6	22089	3	US-09-949-016-16890	Sequence 16890, A
1188	220.8	9.7	205044	3	US-09-949-016-15851	Sequence 15851, A	c1261	220.4	9.6	26587	3	US-09-949-016-16636	Sequence 16636, A
c1189	220.8	9.7	205044	3	US-09-949-016-15852	Sequence 15852, A	c1262	220.4	9.6	29485	3	US-09-785-381-6	Sequence 6, Appl
c1190	220.8	9.7	205044	3	US-09-949-016-15853	Sequence 15853, A	c1263	220.4	9.6	32010	3	US-09-949-016-13127	Sequence 13127, A

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c1265	220.4	9.6	34548	3	US-09-949-016-16124	Sequence 16124, A	1338	220	9.6	601	3	US-09-949-016-51235	Sequence 51235, A
c1266	220.4	9.6	36611	3	US-09-949-016-17287	Sequence 17287, A	1339	220	9.6	601	3	US-09-949-016-63315	Sequence 63315, A
c1267	220.4	9.6	37215	3	US-09-949-016-15526	Sequence 15526, A	1340	220	9.6	601	3	US-09-949-016-115352	Sequence 115352, A
c1268	220.4	9.6	45249	3	US-09-949-016-13228	Sequence 13228, A	c1341	220	9.6	601	3	US-09-949-016-140482	Sequence 140482, A
c1269	220.4	9.6	46319	3	US-09-949-016-12526	Sequence 12526, A	c1342	220	9.6	601	3	US-09-949-016-162142	Sequence 162142, A
c1270	220.4	9.6	46323	3	US-09-949-016-13267	Sequence 13267, A	c1343	220	9.6	601	3	US-09-949-016-178888	Sequence 178888, A
c1271	220.4	9.6	76553	3	US-09-949-016-13432	Sequence 13432, A	c1344	220	9.6	621	7	US-09-925-065A-353663	Sequence 353663, A
c1272	220.4	9.6	85850	3	US-09-949-016-13424	Sequence 13424, A	c1345	220	9.6	644	7	US-09-925-065A-929015	Sequence 929015, A
c1273	220.4	9.6	87734	3	US-09-949-016-17521	Sequence 17521, A	c1346	220	9.6	1048	7	US-09-925-065A-37590	Sequence 37590, A
c1274	220.4	9.6	90541	3	US-09-759-359A-3	Sequence 3, Appli	c1347	220	9.6	1048	7	US-09-925-065A-37592	Sequence 37592, A
c1275	220.4	9.6	90541	3	US-10-207-973-3	Sequence 3, Appli	c1348	220	9.6	1048	7	US-09-925-065A-37594	Sequence 37594, A
c1276	220.4	9.6	90541	5	US-10-799-676-3	Sequence 3, Appli	c1349	220	9.6	1048	7	US-09-925-065A-37595	Sequence 37595, A
c1277	220.4	9.6	150032	3	US-09-949-016-14321	Sequence 14321, A	c1350	220	9.6	1470	7	US-09-925-065A-690838	Sequence 690838, A
c1278	220.4	9.6	156651	3	US-09-949-016-17349	Sequence 17349, A	c1351	220	9.6	1470	7	US-09-925-065A-690839	Sequence 690839, A
c1279	220.4	9.6	193169	3	US-09-949-016-15091	Sequence 15091, A	c1352	220	9.6	1470	7	US-09-925-065A-690840	Sequence 690840, A
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c1289	220.2	9.6	601	3	US-09-949-016-166861	Sequence 166861, A	c1362	220	9.6	57933	3	US-09-949-002-822	Sequence 822, App
c1290	220.2	9.6	619	7	US-09-925-065A-651578	Sequence 651578, A	c1363	220	9.6	63783	3	US-09-949-016-13576	Sequence 13576, A
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RESULT 2

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 ; GENERAL INFORMATION:
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 ; APPLICANT: Wood, William
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 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
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 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
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 ; PRIOR APPLICATION NUMBER: 09/216,021
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 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
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 ; PRIOR FILING DATE: June 22, 1999
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 ; PRIOR FILING DATE: September 15, 1999
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 ; PRIOR FILING DATE: No. 6734288ember 30, 1999
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 ; PRIOR FILING DATE: No. 6734288ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
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 ; PRIOR FILING DATE: March 2, 2000
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 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
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 ; PRIOR FILING DATE: December 1, 2000
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 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 82
 ; LENGTH: 2284
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-944-457-82

Query Match 100.0%; Score 2284; DB 3; Length 2284;
 Best Local Similarity 100.0%; Pred. No. 0;
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Qy	181	GATTATCCTTGACCTTTGAAGACCAAACTGAAATTTAAATTTAAATTTAAATTTAAATTT	240
Db	181	GATTATCCTTGACCTTTGAAGACCAAACTGAAATTTAAATTTAAATTTAAATTTAAATTT	240
Qy	241	GAAGGAGCTTGACCTTTGAAGACCAAACTGAAATTTAAATTTAAATTTAAATTTAAATTT	300
Db	241	GAAGGAGCTTGACCTTTGAAGACCAAACTGAAATTTAAATTTAAATTTAAATTTAAATTT	300
Qy	301	AGTCAGAAATTCCTCAAAAAGAGCTAGAAAGATTTGCTGACATCACTGATCTCTCTT	360
Db	301	AGTCAGAAATTCCTCAAAAAGAGCTAGAAAGATTTGCTGACATCACTGATCTCTCTT	360
Qy	361	TCTAAGGAGCTAGGAGCAATGAGCCGCTATATATCTCACTCAAGAGCTGATTAAT	420
Db	361	TCTAAGGAGCTAGGAGCAATGAGCCGCTATATATCTCACTCAAGAGCTGATTAAT	420
Qy	421	TCTTGTCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAATCTTGTATCTTTCGAC	480
Db	421	TCTTGTCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAATCTTGTATCTTTCGAC	480
Qy	481	ACTCGAAAAACAGCTAGACCAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC	540
Db	481	ACTCGAAAAACAGCTAGACCAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC	540

481 ACTGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGTCCCAACGGAAGCC 540
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541 TGTCCATTGAAACACAGCAAAAGGACTTATGAGTTACAGGATATATACAGATTTTCCATCT 600
601 TTGACACAGAAATTTGCAAGCAAGAGTTACCCAGGAAGATTTCTCTTTACATGCGCAA 660
601 TTGACACAGAAATTTGCAAGCAAGAGTTACCCAGGAAGATTTCTCTTTACATGCGCAA 660
661 TTTTCAACAGCAGTCACTCCCTAGCCCATCATCACACAGATTTATTCAAAGCCCAACCGAT 720
661 TTTTCAACAGCAGTCACTCCCTAGCCCATCATCACACAGATTTATTCAAAGCCCAACCGAT 720
721 ATCTCATGAGAGACACACTTTCTCAGAAAGTTTGGATCTCTCAGATCACCTGGGAAACTA 780
721 ATCTCATGAGAGACACACTTTCTCAGAAAGTTTGGATCTCTCAGATCACCTGGGAAACTA 780
781 TTTAAGATGGATGAAGCAAGTGCCAGCTCTCTTGTCTTATAAGGAAAAAGGCCAATTTCTCAG 840
781 TTTAAGATGGATGAAGCAAGTGCCAGCTCTCTTGTCTTATAAGGAAAAAGGCCAATTTCTCAG 840
841 AGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
841 AGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
901 CTCCTCAGCTACGGTGGCAGTTGCTCTCCACATACCACTCGGCTACTTCCAAAGCCCGCC 960
901 CTCCTCAGCTACGGTGGCAGTTGCTCTCCACATACCACTCGGCTACTTCCAAAGCCCGCC 960
961 ACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020
961 ACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020
1021 ACCAGAGCTCCACCTGTAACCACTGTCTCTCAGCTCCAGCCCTCCAGCCCTCATTTCTACA 1080
1021 ACCAGAGCTCCACCTGTAACCACTGTCTCTCAGCTCCAGCCCTCCAGCCCTCATTTCTACA 1080
1081 GTTTTTCACAGGGCTCGGCTACACTCCAAAGCAATGGCTACAACAGCAGTCTTGACTACC 1140
1081 GTTTTTCACAGGGCTCGGCTACACTCCAAAGCAATGGCTACAACAGCAGTCTTGACTACC 1140
1141 ACCTTTCAGCAGCTACCGACTCGAAAGGAGCTTAGAAACCATACCGTTTACAGAAATC 1200
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1321 AGTTCTCTCCAGGCGCAGTGTTCAGAAAAATCAGTACGGCTTCCATTTGAAAAATGSCCTT 1380
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1381 CTTATCGGGTCCCTGCTCTTTGTGTGCTCTGTTCTGGTGATAGCCCTCGTCTCGGCT 1440
1441 AGAATCTTTCGAATCACTCCGACGGAACGTTACTCAAGACTGGATTTATTTGATCAAT 1500
1441 AGAATCTTTCGAATCACTCCGACGGAACGTTACTCAAGACTGGATTTATTTGATCAAT 1500
1501 GGGATCTATGTGACATCTAAGGATGGAATCGGTGCTCTTAATTCATTTAGTAACAG 1560
1501 GGGATCTATGTGACATCTAAGGATGGAATCGGTGCTCTTAATTCATTTAGTAACAG 1560
1561 AAGCCCCAAATGCAATGAGTTTCTGCTGACTTGTGCTAGTCTTGTAGCAGGAGGTTGATTTGA 1620
1561 AAGCCCCAAATGCAATGAGTTTCTGCTGACTTGTGCTAGTCTTGTAGCAGGAGGTTGATTTGA 1620

1621 AGACAGAAAAATGCCCCCTTCTGCTTCTCTTTTCTTTTGGAGACAGAGTCTTGTCTGT 1680
1621 AGACAGAAAAATGCCCCCTTCTGCTTCTCTTTTCTTTTGGAGACAGAGTCTTGTCTGT 1680
1681 TTGCCAGAGCTGAGTGACAGTACGATCTCGCTCTCACCGCAACTCCGCTCTCTGG 1740
1681 TTGCCAGAGCTGAGTGACAGTACGATCTCGCTCTCACCGCAACTCCGCTCTCTGG 1740
1741 GTTCAAGCGATTTCTCTGCTCAGCCTCTTAAGTATCTGGGATTTACAGGATGTGCCACC 1800
1741 GTTCAAGCGATTTCTCTGCTCAGCCTCTTAAGTATCTGGGATTTACAGGATGTGCCACC 1800
1801 ACACCTGGGATTTTGTATTTTGTAGTAGAGAGGGGTTTCCACATGTGGTCAAGCTG 1860
1801 ACACCTGGGATTTTGTATTTTGTAGTAGAGAGGGGTTTCCACATGTGGTCAAGCTG 1860
1861 GTCTCAAACTCTGACCTAGTATCCACCTCTCGGCTCTCCAAAGTGTGGGATTTACA 1920
1861 GTCTCAAACTCTGACCTAGTATCCACCTCTCGGCTCTCCAAAGTGTGGGATTTACA 1920
1921 GGCATGAGCCACCAACAGCTGGCCCCCTTCTGTTTATTTGTTGTTTGAAGGAATGA 1980
1921 GGCATGAGCCACCAACAGCTGGCCCCCTTCTGTTTATTTGTTGTTTGAAGGAATGA 1980
1981 AGTGGGAACCAAAATAGTAAATTTGGGTAATCTGCTCTAAATAATATAGCTAAAAACAA 2040
1981 AGTGGGAACCAAAATAGTAAATTTGGGTAATCTGCTCTAAATAATATAGCTAAAAACAA 2040
2041 AGCTCTATGTAAGTAATAAGTATTAATGCCATATAATTTCAAAATTTCAACTGGCTTT 2100
2041 AGCTCTATGTAAGTAATAAGTATTAATGCCATATAATTTCAAAATTTCAACTGGCTTT 2100
2101 TATGCAAGAAACAGGTTTAGGACATCTAGGTTCCAAATTCATTCATTTCTGGTTCAGA 2160
2101 TATGCAAGAAACAGGTTTAGGACATCTAGGTTCCAAATTCATTCATTTCTGGTTCAGA 2160
2161 TAAAAACAATGTTTATATCAATTTCTTAATGGAATTTCTTTTCTTTTATATGATTCCT 2220
2161 TAAAAACAATGTTTATATCAATTTCTTAATGGAATTTCTTTTCTTTTATATGATTCCT 2220
2221 TTTAACTTTATTCAGATAGTTCCTTCCAAATTAATAATTTGAATAATCTTTGTTAC 2280
2221 TTTAACTTTATTCAGATAGTTCCTTCCAAATTAATAATTTGAATAATCTTTGTTAC 2280
2281 TCAA 2284
2281 TCAA 2284

RESULT 3

US-09-945-584-82
; Sequence 82, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,584
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/966,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. 6908993ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. 6908993ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 82
LENGTH: 2284
TYPE: DNA
ORGANISM: Homo Sapien
US-09-945-584-82

Query Match 100.0%; Score 2284; DB 3; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGGGAGCATCCGCTGGCGGTCCTCGCGAGACCCCGCGCGGATTCGCGGGTCTTCCCGC	60
DB	1	GGGGAGCATCCGCTGGCGGTCCTCGCGAGACCCCGCGCGGATTCGCGGGTCTTCCCGC	60
QY	61	GGGCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGTCTCTCGAC	120
DB	61	GGGCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGTCTCTCGAC	120
QY	121	GCCAGAGAGAAATCTCATCATCTGTGCGAGCTTCTTAAAGCAAATAAGACGAGGGAG	180
DB	121	GCCAGAGAGAAATCTCATCATCTGTGCGAGCTTCTTAAAGCAAATAAGACGAGGGAG	180
QY	181	GATTATCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATTTCTTCGGGGGA	240
DB	181	GATTATCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATTTCTTCGGGGGA	240
QY	241	GAAGGAGCTTGACTTACACTTTGGTAAATAATTGGCTTCTGACACTAAGGCTGTCTGCT	300
DB	241	GAAGGAGCTTGACTTACACTTTGGTAAATAATTGGCTTCTGACACTAAGGCTGTCTGCT	300
QY	301	AGTCAGAAATGGCTCAAAAAGAGTCTAGAAGATTTGTCATTTGACATCCAGTCACTCTT	360
DB	301	AGTCAGAAATGGCTCAAAAAGAGTCTAGAAGATTTGTCATTTGACATCCAGTCACTCTT	360
QY	361	TCTAAGGGAATCAGAGGCAATGAGCCGCTATATACCTCAACTCAAGAAGCTGATTAAT	420
DB	361	TCTAAGGGAATCAGAGGCAATGAGCCGCTATATACCTCAACTCAAGAAGCTGATTAAT	420
QY	421	TCTTGCTGTTTCAACAAAAACATATCAGGGGACAAAGCATGTAACCTTGATCATCTTCAC	480
DB	421	TCTTGCTGTTTCAACAAAAACATATCAGGGGACAAAGCATGTAACCTTGATCATCTTCAC	480
QY	481	ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGCTCCCAACGAGGAAGCC	540
DB	481	ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGCTCCCAACGAGGAAGCC	540
QY	541	TGTCATTTGAAACACAGCAAAAGGACTTATGAGTTACAGGATAATACAGATTTTCCATCT	600
DB	541	TGTCATTTGAAACACAGCAAAAGGACTTATGAGTTACAGGATAATACAGATTTTCCATCT	600
QY	601	TTGACCAAGAAATTTGCCAAGCCAGAGCTTACCCAGGAAGATTTCTCTTACATGGCCAA	660
DB	601	TTGACCAAGAAATTTGCCAAGCCAGAGCTTACCCAGGAAGATTTCTCTTACATGGCCAA	660
QY	661	TTTTTCAACAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATCAAGGCCACCCGAT	720
DB	661	TTTTTCAACAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATCAAGGCCACCCGAT	720
QY	721	ATCTCATGGAGAGACACATTTTCTCAGAAAGTTGGATCTCTCAGATCACTCGAGAACTA	780
DB	721	ATCTCATGGAGAGACACATTTTCTCAGAAAGTTGGATCTCTCAGATCACTCGAGAACTA	780
QY	781	TTTTAAGATGATGAAGCAAGTGCCAGCTCTTCTGCTTATAGGAAAGGCCATTTCTCAG	840
DB	781	TTTTAAGATGATGAAGCAAGTGCCAGCTCTTCTGCTTATAGGAAAGGCCATTTCTCAG	840

QY 841 AGTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
DB 841 AGTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
QY 901 CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCTACTCCAAAGCCGCC 960
DB 901 CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCTACTCCAAAGCCGCC 960
QY 961 ACCCTTTTACCCACCAATGCTTCAGTGACACCTTTCTGGGACTTCCAGCCACAGCTGGCC 1020
DB 961 ACCCTTTTACCCACCAATGCTTCAGTGACACCTTTCTGGGACTTCCAGCCACAGCTGGCC 1020
QY 1021 ACCAGCTCCACTGTAAACACTGTCTCTCAGCTCCAGCCCTCATTTCTAC 1080
DB 1021 ACCAGCTCCACTGTAAACACTGTCTCTCAGCTCCAGCCCTCATTTCTAC 1080
QY 1081 GTTTTACAGGGCTGGGCTACCTCCAAAGCAATGCTCAACAGCAGTCTGACTACC 1140
DB 1081 GTTTTACAGGGCTGGGCTACCTCCAAAGCAATGCTCAACAGCAGTCTGACTACC 1140
QY 1141 ACCTTTTACGGCAGCTCGGACTCGAAAGGAGCTTGAACACCATACCGTTTACAGAAATC 1200
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QY 1201 TCCAACTTAATTTGAACACAGGGAATGTGTATAACCCCTACTGCACTTTCTATGTCAAAT 1260
DB 1201 TCCAACTTAATTTGAACACAGGGAATGTGTATAACCCCTACTGCACTTTCTATGTCAAAT 1260
QY 1261 GTGGAGCTTCCACTATGAATAAACTGCTTCTGGGAAGGTAGGAGGCGCAGTCCAGGC 1320
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DB 1321 AGTTCTCCAGGCGAGTGTTCAGAAATCAGTACGGCCTTCCATTTGAAAAATGGCTT 1380
QY 1381 CTATCGGGTCCCTGCTCTTTGGTGTCTCTGCTGCTGATAGGCTCGCTCCCTGGGT 1440
DB 1381 CTATCGGGTCCCTGCTCTTTGGTGTCTCTGCTGCTGATAGGCTCGCTCCCTGGGT 1440
QY 1441 AGAATCCTTTTGGAAATCCTCCGAGGAAAGTGTACTCAAGACTGGATTTTATGATCAAT 1500
DB 1441 AGAATCCTTTTGGAAATCCTCCGAGGAAAGTGTACTCAAGACTGGATTTTATGATCAAT 1500
QY 1501 GGGATCTATGTGACATCTAAGGATGAACTCGGTGCTCTTAATTCATTTAGTAAACAG 1560
DB 1501 GGGATCTATGTGACATCTAAGGATGAACTCGGTGCTCTTAATTCATTTAGTAAACAG 1560
QY 1561 AAGCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTGTATTTGA 1620
DB 1561 AAGCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTGTATTTGA 1620
QY 1621 AGACAGAAATGCCCCCTTCTGCTTCTTTTGGAGACAGAGTCTTGCTCTG 1680
DB 1621 AGACAGAAATGCCCCCTTCTGCTTCTTTTGGAGACAGAGTCTTGCTCTG 1680
QY 1681 TTGCCAGGCTGGAGTGCAGTACAGCATCTCGGCTCTCACGCAACTCGCTCCCTCG 1740
DB 1681 TTGCCAGGCTGGAGTGCAGTACAGCATCTCGGCTCTCACGCAACTCGCTCCCTCG 1740
QY 1741 GTTCAAGGATTTCTCTGCTCCTCAGCTTCTAAGTATCTGGATTAACAGGATGTGCCACC 1800
DB 1741 GTTCAAGGATTTCTCTGCTCCTCAGCTTCTAAGTATCTGGATTAACAGGATGTGCCACC 1800
QY 1801 ACACCTGGGTGATTTTGTATTTTGTAGTACAGAGCGGGTTTCAACATGTTGGTCAAGCTG 1860
DB 1801 ACACCTGGGTGATTTTGTATTTTGTAGTACAGAGCGGGTTTCAACATGTTGGTCAAGCTG 1860
QY 1861 GTCTCAAACTCCTGACCTAGTATGATCCACCTCTCCGGCTCCCAAGTGTGGGATTAACA 1920
DB 1861 GTCTCAAACTCCTGACCTAGTATGATCCACCTCTCCGGCTCCCAAGTGTGGGATTAACA 1920
QY 1921 GGCAATGAGCCACCACAGCTGSCCCCTCTCTGTTTATGTTGTTTGTGAGAGGAATGA 1980

DB 1921 GGCAATGAGCCACCACAGCTGSCCCCTCTCTGTTTATGTTTGTGAGAGGAATGA 1980
QY 1981 AGTGGGAACCAAAATTAGTAAATTTTGGGTAATCTGTCTCTAAATATATTAGCTAAAAACAA 2040
DB 1981 AGTGGGAACCAAAATTAGTAAATTTTGGGTAATCTGTCTCTAAATATATTAGCTAAAAACAA 2040
QY 2041 AGCTCTATGTAAAGTAATAAAGTATAATTTGCCATATAAATTTCAAAATTTCAACTGGCTTT 2100
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DB 2101 TATGCAAGAAACACAGGTTTAGGACATCTAGTTCCTCAATTTCTTTGGTTCACAGA 2160
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DB 2281 TCAA 2284

RESULT 4

US-09-991-181-514
; Sequence 514, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

:	PRIOR APPLICATION NUMBER:	60/089598
:	PRIOR FILING DATE:	1998-06-17
:	PRIOR APPLICATION NUMBER:	60/089599
:	PRIOR FILING DATE:	1998-06-17
:	PRIOR APPLICATION NUMBER:	60/089600
:	PRIOR FILING DATE:	1998-06-17
:	PRIOR APPLICATION NUMBER:	60/089653
:	PRIOR FILING DATE:	1998-06-17
:	PRIOR APPLICATION NUMBER:	60/089801
:	PRIOR FILING DATE:	1998-06-18
:	PRIOR APPLICATION NUMBER:	60/089907
:	PRIOR FILING DATE:	1998-06-18
:	PRIOR APPLICATION NUMBER:	60/089908
:	PRIOR FILING DATE:	1998-06-18
:	PRIOR APPLICATION NUMBER:	60/089947
:	PRIOR FILING DATE:	1998-06-19
:	PRIOR APPLICATION NUMBER:	60/089948
:	PRIOR FILING DATE:	1998-06-19
:	PRIOR APPLICATION NUMBER:	60/089955
:	PRIOR FILING DATE:	1998-06-19
:	PRIOR APPLICATION NUMBER:	60/090246
:	PRIOR FILING DATE:	1998-06-22
:	PRIOR APPLICATION NUMBER:	60/090252
:	PRIOR FILING DATE:	1998-06-22
:	PRIOR APPLICATION NUMBER:	60/090254
:	PRIOR FILING DATE:	1998-06-22
:	PRIOR APPLICATION NUMBER:	60/090349
:	PRIOR FILING DATE:	1998-06-23
:	PRIOR APPLICATION NUMBER:	60/090355
:	PRIOR FILING DATE:	1998-06-23
:	PRIOR APPLICATION NUMBER:	60/090429
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090431
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090435
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090444
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090445
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090472
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090535
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090540
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090542
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090557
:	PRIOR FILING DATE:	1998-06-24
:	PRIOR APPLICATION NUMBER:	60/090676
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090678
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090690
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090694
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090695
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090696
:	PRIOR FILING DATE:	1998-06-25
:	PRIOR APPLICATION NUMBER:	60/090862
:	PRIOR FILING DATE:	1998-06-26
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:	PRIOR APPLICATION NUMBER:	60/091360
:	PRIOR FILING DATE:	1998-07-01
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:	PRIOR FILING DATE:	1998-07-01
:	PRIOR APPLICATION NUMBER:	60/091519

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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 3; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCGCGGACAGAGCTGTCTCGACCTTGGATGGCAGCGGGGCGCGGGTCTCTCGAC 120

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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088030
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; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252

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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990,444
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 3; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 2281 TCAA 2284

Db 2281 TCAA 2284

RESULT 7

US-09-945-587-82
 : Sequence 82, Application US/09945587
 : Patent No. 6936254
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin
 : APPLICANT: Botstein, David
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Gerritsen, Mary
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul
 : APPLICANT: Grimaldi, Christopher
 : APPLICANT: Gurney, Austin
 : APPLICANT: Hillan, Kenneth
 : APPLICANT: Kljavin, Ivar
 : APPLICANT: Napier, Mary
 : APPLICANT: Roy, Margaret
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Wood, William
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P2548P1C1
 : CURRENT APPLICATION NUMBER: US/09/945,587
 : CURRENT FILING DATE: 2001-09-26
 : PRIOR APPLICATION NUMBER: 09/866,028
 : PRIOR FILING DATE: 2001-05-25
 : PRIOR APPLICATION NUMBER: 60/067,411
 : PRIOR FILING DATE: December 3, 1997
 : PRIOR APPLICATION NUMBER: 60/069,334
 : PRIOR FILING DATE: December 11, 1997
 : PRIOR APPLICATION NUMBER: 60/069,335
 : PRIOR FILING DATE: December 11, 1997
 : PRIOR APPLICATION NUMBER: 60/069,278
 : PRIOR FILING DATE: December 11, 1997
 : PRIOR APPLICATION NUMBER: 60/069,425
 : PRIOR FILING DATE: December 12, 1997
 : PRIOR APPLICATION NUMBER: 60/069,696
 : PRIOR FILING DATE: December 16, 1997
 : PRIOR APPLICATION NUMBER: 60/069,694
 : PRIOR FILING DATE: December 16, 1997
 : PRIOR APPLICATION NUMBER: 60/069,702
 : PRIOR FILING DATE: December 16, 1997
 : PRIOR APPLICATION NUMBER: 60/069,870
 : PRIOR FILING DATE: December 17, 1997
 : PRIOR APPLICATION NUMBER: 60/069,873
 : PRIOR FILING DATE: December 17, 1997
 : PRIOR APPLICATION NUMBER: 60/068,017
 : PRIOR FILING DATE: December 18, 1997
 : PRIOR APPLICATION NUMBER: 60/070,440
 : PRIOR FILING DATE: January 5, 1998
 : PRIOR APPLICATION NUMBER: 60/074,086
 : PRIOR FILING DATE: February 9, 1998
 : PRIOR APPLICATION NUMBER: 60/074,092
 : PRIOR FILING DATE: February 9, 1998
 : PRIOR APPLICATION NUMBER: 60/075,945
 : PRIOR FILING DATE: February 25, 1998
 : PRIOR APPLICATION NUMBER: 60/112,850
 : PRIOR FILING DATE: December 16, 1998
 : PRIOR APPLICATION NUMBER: 60/113,296
 : PRIOR FILING DATE: December 22, 1998
 : PRIOR APPLICATION NUMBER: 60/146,222
 : PRIOR FILING DATE: July 28, 1999
 : PRIOR APPLICATION NUMBER: PCT/US98/19330
 : PRIOR FILING DATE: September 16, 1998
 : PRIOR APPLICATION NUMBER: PCT/US98/25108
 : PRIOR FILING DATE: December 1, 1998
 : PRIOR APPLICATION NUMBER: 09/216,021

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; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
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; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-945-587-82

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

US-09-997-333-514
; Sequence 514, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 3; Length 2284;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	GGGCGGAGAGAGTGTCTCGACCTGGATGGAGAGGGGCGCGGGTCTCTCGAC	120
Qy	121	GCCAGAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACTAAGACAGAGGAG	180
Db	121	GCCAGAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACTAAGACAGAGGAG	180
Qy	181	GATTATCTTTGACCTTTGAAGACCAAACTAAATTTAAATTTTCTTCGGGGA	240
Db	181	GATTATCTTTGACCTTTGAAGACCAAACTAAATTTAAATTTTCTTCGGGGA	240
Qy	241	GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCT	300
Db	241	GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCT	300
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Db	301	AGTCAGAAATTCCTCAAAAAGAGTCTAGAGAGTGTGTCATTGACATCCAGTCATCT	360
Qy	361	TCTAAGGGAATCAGAGGCAATGAGCCCGTATATCTTCAACTCAAGAGAGCTGATTAAT	420
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Qy	421	TCTTGCTGTTCAACAAAAAATATCATGAGGGAACAAAGCATGTAACTTGATGATCTTCGAC	480
Db	421	TCTTGCTGTTCAACAAAAAATATCATGAGGGAACAAAGCATGTAACTTGATGATCTTCGAC	480

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APPLICANT: Paoni, Nicholas F.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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DB	961	ACCTTTCTACCCACCACCAATGCTTCAGTGACACACTTTCTGGGACTTCCAGGACACAGCTGGCC	1020		
QY	1021	ACCACAGCTCCACTGTATAACCACTGTCACTTTCAGCCTCCACGACCTCATTTCTACA	1080		
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QY	1321	AGTTCTCCAGGAGAGTGTTCAGAAATCAGTACGGCTTCCATTTGAAAATGGCTT	1380		
DB	1321	AGTTCTCCAGGAGAGTGTTCAGAAATCAGTACGGCTTCCATTTGAAAATGGCTT	1380		
QY	1381	CTTATCGGCTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCTCGTCTCTCTGGGT	1440		
DB	1381	CTTATCGGCTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCTCGTCTCTCTGGGT	1440		
QY	1441	AGAACTCTTTTGGAAATCACTCCGAGGAAACGTTTACTCAAGACTGGATTTATTCAT	1500		
DB	1441	AGAACTCTTTTGGAAATCACTCCGAGGAAACGTTTACTCAAGACTGGATTTATTCAT	1500		
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DB	1501	GGGATCTATGTGACATCTAAGGATGGAACTCGGTGTCTTAAATTCATTTAGTAAACAG	1560		

QY 1561 AAGCCAAATGCAATGAGTCTTCTGCTGACTTCTGCTAGTCTTTAGCAGAGAGTTGTATTTTGA 1620
Db 1561 AAGCCAAATGCAATGAGTCTTCTGCTGACTTCTGCTAGTCTTTAGCAGAGAGTTGTATTTTGA 1620
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QY 1861 GTCTCAAACTCTGACCTAGTGTATCCACCTCTCTCGGCTCTCCAAAGTGTGGGATTACA 1920
Db 1861 GTCTCAAACTCTGACCTAGTGTATCCACCTCTCTCGGCTCTCCAAAGTGTGGGATTACA 1920
QY 1921 GGCATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTGTTTGGAGAGGAATGA 1980
Db 1921 GGCATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTGTTTGGAGAGGAATGA 1980
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QY 2221 TTAATACTTATCCAGATGATGTTCTTCCAAATTAATTTTCAATAAATCTTTTGTTC 2280
Db 2221 TTAATACTTATCCAGATGATGTTCTTCCAAATTAATTTTCAATAAATCTTTTGTTC 2280
QY 2281 TCAA 2284
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RESULT 10

US-09-989-735-514
; Sequence 514, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 11

US-09-989-726-514

; Sequence 514, Application US/09989726

; Patent No. 7018811

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/092182			
PRIOR FILING DATE: 1998-07-09			
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QY	241	GAAGGAGCTTGACTTACACTTTGGTAAATTTGCTTCTGACACTAAAGGCTGTCTGCT	300
DB	241	GAAGGAGCTTGACTTACACTTTGGTAAATTTGCTTCTGACACTAAAGGCTGTCTGCT	300
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QY	601	TTGACCAAGAAATTTGCCAAGCAAGAGTTACCCAGCAAGATTTCTCTTACATGGGCCAA	660
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QY	841	AGTTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGGC	900
DB	841	AGTTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGGC	900
QY	901	CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCTACTTCCAAAGCCGCC	960
DB	901	CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCTACTTCCAAAGCCGCC	960
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QY	1021	ACCACAGCTCCACTGTAACCACTGCTCACTCTCAGCTCCACAGCCTCATTTCTACA	1080
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QY	1321	AGTTTCTCCAGGSCAGTGTTCAGAAATACAGTACCGGCTTCCATTTGAAAAATGGCTT	1380
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QY	1381	CTTATCGGGTCTGCTCTTGTGTTCTGTTCTGTTGATAGGCTCGTCTCTCTGGGT	1440
DB	1381	CTTATCGGGTCTGCTCTTGTGTTCTGTTCTGTTGATAGGCTCGTCTCTCTGGGT	1440
QY	1441	AGAACTCTTTCGGAATCACTCCGAGGAAGCTTACTCAAGACTGGATTTATTTGATCAAT	1500
DB	1441	AGAACTCTTTCGGAATCACTCCGAGGAAGCTTACTCAAGACTGGATTTATTTGATCAAT	1500
QY	1501	GGGATCTATGTGACATCTAAGGATGGAATCGGCTGTCTTAAATTCATTTAGTAACCG	1560
DB	1501	GGGATCTATGTGACATCTAAGGATGGAATCGGCTGTCTTAAATTCATTTAGTAACCG	1560
QY	1561	AAGCCCAAAATGCAATGATTTCTGCTGATCTGTAGTCTTACAGGAGGTTGATTTTGA	1620
DB	1561	AAGCCCAAAATGCAATGATTTCTGCTGATCTGTAGTCTTACAGGAGGTTGATTTTGA	1620

Db 1561 AAGCCAAATGCAATGAGTTTCTGTGCTGACTTGTCTAGCTTCTAGCAGGAGTGTGATTTTGA 1620
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Db 1621 AGACAGAAAAAGCCCCCTCTGCTTCTCTTTTGTGGAGACAGAGTCTTGTCTG 1680
Qy 1681 TTGCCAGGTGAGTGCAGTACGATCTCGGCTCTCACCGCAACCTCCGCTCCTCG 1740
Db 1681 TTGCCAGGTGAGTGCAGTACGATCTCGGCTCTCACCGCAACCTCCGCTCCTCG 1740
Qy 1741 GTTCAAGCGATTCTCTGCTCAGCTCTCTAGTATCTGGATTACAGGATGTCGCACC 1800
Db 1741 GTTCAAGCGATTCTCTGCTCAGCTCTCTAGTATCTGGATTACAGGATGTCGCACC 1800
Qy 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGAGACGGGGTTTACCAATGTTGTCAGGCTG 1860
Db 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGAGACGGGGTTTACCAATGTTGTCAGGCTG 1860
Qy 1861 GTCTCAAACTCTGACCTAGTATGATCCACCTCTCGGCTCTCCAAAGTGTGGATTACA 1920
Db 1861 GTCTCAAACTCTGACCTAGTATGATCCACCTCTCGGCTCTCCAAAGTGTGGATTACA 1920
Qy 1921 GGCAATGAGCCACACAGCTGGCCCTCTCTGTTTATGTTTGTGTTTGTAGAGGAATGA 1980
Db 1921 GGCAATGAGCCACACAGCTGGCCCTCTCTGTTTATGTTTGTGTTTGTAGAGGAATGA 1980
Qy 1981 AGTGGGAACCAAAATTAGTAAATTTGGGTAATCTGTCTCTAAATATTAGCTAAACAA 2040
Db 1981 AGTGGGAACCAAAATTAGTAAATTTGGGTAATCTGTCTCTAAATATTAGCTAAACAA 2040
Qy 2041 AGCTCTATGTAAGTAATAAGTATTAATTGGCCATATAAATTTCAAATTTCAACTGGCTTT 2100
Db 2041 AGCTCTATGTAAGTAATAAGTATTAATTGGCCATATAAATTTCAAATTTCAACTGGCTTT 2100
Qy 2101 TATGCAAGAAACAGCTTAGGACATCTAGTTCCTCAATTCATTCACATTTCTGGTTCAGA 2160
Db 2101 TATGCAAGAAACAGCTTAGGACATCTAGTTCCTCAATTCATTCACATTTCTGGTTCAGA 2160
Qy 2161 TAAATCAACTGTTTATATCAATTTCTAATGATTTGCTTTTCTTTTATATGATTCCT 2220
Db 2161 TAAATCAACTGTTTATATCAATTTCTAATGATTTGCTTTTCTTTTATATGATTCCT 2220
Qy 2221 TTAATCTTATTCAGATGATGTCCTTCAATTAATAATTTGAATAAATCTTTTGTTC 2280
Db 2221 TTAATCTTATTCAGATGATGTCCTTCAATTAATAATTTGAATAAATCTTTTGTTC 2280
Qy 2281 TCAA 2284
Db 2281 TCAA 2284

RESULT 12

US-09-944-884-82
; Sequence 82, Application US/09944884
; Patent No. 7018837
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,884
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-884-82

Query Match 100.0%; Score 2284; DB 5; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGAGCATCCGCTGCGGCTCTCGCGAGACCCCGCGCGGATTCGCGGTCCTTCGCG 60
Db 1 GCGGAGCATCCGCTGCGGCTCTCGCGAGACCCCGCGCGGATTCGCGGTCCTTCGCG 60
Qy 61 GCGCGGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGCGCGGGGTCTCTCGAC 120
Db 61 GCGCGGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGCGCGGGGTCTCTCGAC 120
Qy 121 GCCAGAGAGAAATCTCATCATCTGTGCGCTTCTTAAAGCAAACTAAGACAGAGGAG 180
Db 121 GCCAGAGAGAAATCTCATCATCTGTGCGCTTCTTAAAGCAAACTAAGACAGAGGAG 180
Qy 181 GATTATCTTGACCTTTGAAGACCAAACTTAAACTGAAATTTAAATTTCTTCGGGGA 240
Db 181 GATTATCTTGACCTTTGAAGACCAAACTTAAACTGAAATTTAAATTTCTTCGGGGA 240
Qy 241 GAAGGAGCTTGACTTACACTTTGGTAAATTAATTTGCTTCTGACACTAAGGCTGTCT 300
Db 241 GAAGGAGCTTGACTTACACTTTGGTAAATTAATTTGCTTCTGACACTAAGGCTGTCT 300
Qy 301 AGTCAGAAATTCCTCAAAAAGAGTCTAGAAAGATGTTGCTCAATTCATCCAGTCACTCT 360
Db 301 AGTCAGAAATTCCTCAAAAAGAGTCTAGAAAGATGTTGCTCAATTCATCCAGTCACTCT 360
Qy 361 TCTAAGGGAATCAGAGCAATGAGCCGTATATATCTCAACTCAAGAGACTGATTAAT 420
Db 361 TCTAAGGGAATCAGAGCAATGAGCCGTATATATCTCAACTCAAGAGACTGATTAAT 420
Qy 421 TCTTGTCTGTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGTATGATCTTCGAC 480
Db 421 TCTTGTCTGTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGTATGATCTTCGAC 480
Qy 481 ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGCTCCCAACGAGGAAGCC 540
Db 481 ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGCTCCCAACGAGGAAGCC 540
Qy 541 TGTCCATTTGAAACAGCAAAAGAGCTTATGAGTTACAGGATTAATAAGATTTTCCATCT 600
Db 541 TGTCCATTTGAAACAGCAAAAGAGCTTATGAGTTACAGGATTAATAAGATTTTCCATCT 600
Qy 601 TTGACCAAGAAATTTGCCAGCCAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAA 660
Db 601 TTGACCAAGAAATTTGCCAGCCAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAA 660
Qy 661 TTTTTCACAGCAGTCACTCCCTAGCCCATCATCACACAGATTAATTCAGAGCCCAACGAT 720
Db 661 TTTTTCACAGCAGTCACTCCCTAGCCCATCATCACACAGATTAATTCAGAGCCCAACGAT 720
Qy 721 ATCTCATGGAGACACACTTTTCTCAGAAGTTGGATTCCTCAGATCACTCGAGAAACTA 780
Db 721 ATCTCATGGAGACACACTTTTCTCAGAAGTTGGATTCCTCAGATCACTCGAGAAACTA 780
Qy 781 TTTAAGATGATGAAGCAAGTGCAGCTCTGCTTATTAAGGAAAAAGGCCATTTCTCAG 840
Db 781 TTTAAGATGATGAAGCAAGTGCAGCTCTGCTTATTAAGGAAAAAGGCCATTTCTCAG 840

QY 841 AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
DB 841 AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGG 900
QY 901 CTCACAGCTACGGTGGCAGTGTCTCTCACATACCACTCGGCTACTCCAAAGCCCGC 960
DB 901 CTCACAGCTACGGTGGCAGTGTCTCTCACATACCACTCGGCTACTCCAAAGCCCGC 960
QY 961 ACCCTTCTACCCACCAATGCTTCTAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020
DB 961 ACCCTTCTACCCACCAATGCTTCTAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020
QY 1021 ACACAGCTCCACCTGTATACCACTGTCTCTAGGCTTCCACGACCCCTCATTTCTACA 1080
DB 1021 ACACAGCTCCACCTGTATACCACTGTCTCTAGGCTTCCACGACCCCTCATTTCTACA 1080
QY 1081 GTTTTACAGGGCTGGGCTACCTCCAGCAATGGCTACACAGCAGTCTGACTACC 1140
DB 1081 GTTTTACAGGGCTGGGCTACCTCCAGCAATGGCTACACAGCAGTCTGACTACC 1140
QY 1141 ACCTTTCAGGCACCTACGAGCTCGAAGGCAGCTTAGAAACCATACCGTTTACAGAAATC 1200
DB 1141 ACCTTTCAGGCACCTACGAGCTCGAAGGCAGCTTAGAAACCATACCGTTTACAGAAATC 1200
QY 1201 TCAACTTAACCTTTGAACACAGGGAATGTATACCCCTACTGCACTTTCTATGTCAAAT 1260
DB 1201 TCAACTTAACCTTTGAACACAGGGAATGTATACCCCTACTGCACTTTCTATGTCAAAT 1260
QY 1261 GTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGTAGGAGGCCAGTCCAGGC 1320
DB 1261 GTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGTAGGAGGCCAGTCCAGGC 1320
QY 1321 AGTTCTCTCCAGGCGAGTGTCCAGAAATCAGTACGGCTTCCATTTGAAAAATGGCTT 1380
DB 1321 AGTTCTCTCCAGGCGAGTGTCCAGAAATCAGTACGGCTTCCATTTGAAAAATGGCTT 1380
QY 1381 CTTATCGGGTCCCTGCTCTTTGGTGCTCTTCTGGTGATAGGCTCGCTCTCTGGGT 1440
DB 1381 CTTATCGGGTCCCTGCTCTTTGGTGCTCTTCTGGTGATAGGCTCGCTCTCTGGGT 1440
QY 1441 AGAATCCTTTGGAATCAGTCCGAGGAAACGTTACTCAAGACTGGAATTTATTTGATCAAT 1500
DB 1441 AGAATCCTTTGGAATCAGTCCGAGGAAACGTTACTCAAGACTGGAATTTATTTGATCAAT 1500
QY 1501 GGGATCTATGTGACACTAAGGATGGAATCGGTGTCTTAATTCATTTAGTAACAG 1560
DB 1501 GGGATCTATGTGACACTAAGGATGGAATCGGTGTCTTAATTCATTTAGTAACAG 1560
QY 1561 AAGCCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTTAGCAGGAGGTGTATTGTA 1620
DB 1561 AAGCCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTTAGCAGGAGGTGTATTGTA 1620
QY 1621 AGACAGAAATGCGCCCTCTGCTTCTCTTTTCTTTTGGAGACAGAGTCTGTCTG 1680
DB 1621 AGACAGAAATGCGCCCTCTGCTTCTCTTTTCTTTTGGAGACAGAGTCTGTCTG 1680
QY 1681 TTGCCAGGCTGAGTGACAGTCTCGGCTCTACCGCACTCGCTCTCTG 1740
DB 1681 TTGCCAGGCTGAGTGACAGTCTCGGCTCTACCGCACTCGCTCTCTG 1740
QY 1741 GTTCAAGCGATTTCTCTGCTCAGCTCTCAAGTATCTGGGATTAACAGGATGTGCCACC 1800
DB 1741 GTTCAAGCGATTTCTCTGCTCAGCTCTCAAGTATCTGGGATTAACAGGATGTGCCACC 1800
QY 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGAGCGGGTTTCAACATGTTGGTCAAGCTG 1860
DB 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGAGCGGGTTTCAACATGTTGGTCAAGCTG 1860
QY 1861 GTCTCAAACTCCTGACCTAGTATCAACCTCTCTCGGCTTCCAAAGTCTGGGATTACA 1920
DB 1861 GTCTCAAACTCCTGACCTAGTATCAACCTCTCTCGGCTTCCAAAGTCTGGGATTACA 1920
QY 1921 GGATGATGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGTAGAGGAATGA 1980

DB 1921 GGATGATGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGTAGAGGAATGA 1980
QY 1981 AGTGGGAACCAATTAGGTAATTTTGGGTAATCTGTCTCTTAAATATTTAGCTAAAAACAA 2040
DB 1981 AGTGGGAACCAATTAGGTAATTTTGGGTAATCTGTCTCTTAAATATTTAGCTAAAAACAA 2040
QY 2041 AGCTCTATGTAAAGTAATAAAGTATATTCGCCATATAAATTTCAAAATTCAACTGGCTTT 2100
DB 2041 AGCTCTATGTAAAGTAATAAAGTATATTCGCCATATAAATTTCAAAATTCAACTGGCTTT 2100
QY 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCATTTCTTGGTTCAGA 2160
DB 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCATTTCTTGGTTCAGA 2160
QY 2161 TAAATCAACTGTTTATATCAATTTCTTAATGGAATTTCTTTTATATGATTCCT 2220
DB 2161 TAAATCAACTGTTTATATCAATTTCTTAATGGAATTTCTTTTATATGATTCCT 2220
QY 2221 TTAACCTTATTCAGATGATTCCTTCCAAATTAATTTGAATAAATCTTTTGTATC 2280
DB 2221 TTAACCTTATTCAGATGATTCCTTCCAAATTAATTTGAATAAATCTTTTGTATC 2280
QY 2281 TCAA 2284
DB 2281 TCAA 2284

RESULT 13

US-09-997-514-514
; Sequence 514, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

1	PRIOR FILING DATE: 1998-02-25	
2	PRIOR APPLICATION NUMBER: 60/078910	
3	PRIOR FILING DATE: 1998-03-20	
4	PRIOR APPLICATION NUMBER: 60/083322	
5	PRIOR FILING DATE: 1998-04-28	
6	PRIOR APPLICATION NUMBER: 60/084600	
7	PRIOR FILING DATE: 1998-05-07	
8	PRIOR APPLICATION NUMBER: 60/087106	
9	PRIOR FILING DATE: 1998-05-28	
10	PRIOR APPLICATION NUMBER: 60/087607	
11	PRIOR FILING DATE: 1998-06-02	
12	PRIOR APPLICATION NUMBER: 60/087609	
13	PRIOR FILING DATE: 1998-06-02	
14	PRIOR APPLICATION NUMBER: 60/087759	
15	PRIOR FILING DATE: 1998-06-02	
16	PRIOR APPLICATION NUMBER: 60/087827	
17	PRIOR FILING DATE: 1998-06-03	
18	PRIOR APPLICATION NUMBER: 60/088021	
19	PRIOR FILING DATE: 1998-06-04	
20	PRIOR APPLICATION NUMBER: 60/088025	
21	PRIOR FILING DATE: 1998-06-04	
22	PRIOR APPLICATION NUMBER: 60/088026	
23	PRIOR FILING DATE: 1998-06-04	
24	PRIOR APPLICATION NUMBER: 60/088030	
25	PRIOR FILING DATE: 1998-06-04	
26	PRIOR APPLICATION NUMBER: 60/088033	
27	PRIOR FILING DATE: 1998-06-04	
28	PRIOR APPLICATION NUMBER: 60/088029	
29	PRIOR FILING DATE: 1998-06-04	
30	PRIOR APPLICATION NUMBER: 60/088326	
31	PRIOR FILING DATE: 1998-06-04	
32	PRIOR APPLICATION NUMBER: 60/088167	
33	PRIOR FILING DATE: 1998-06-05	
34	PRIOR APPLICATION NUMBER: 60/088202	
35	PRIOR FILING DATE: 1998-06-05	
36	PRIOR APPLICATION NUMBER: 60/088212	
37	PRIOR FILING DATE: 1998-06-05	
38	PRIOR APPLICATION NUMBER: 60/088217	
39	PRIOR FILING DATE: 1998-06-05	
40	PRIOR APPLICATION NUMBER: 60/088655	
41	PRIOR FILING DATE: 1998-06-09	
42	PRIOR APPLICATION NUMBER: 60/088734	
43	PRIOR FILING DATE: 1998-06-10	
44	PRIOR APPLICATION NUMBER: 60/088738	
45	PRIOR FILING DATE: 1998-06-10	
46	PRIOR APPLICATION NUMBER: 60/088742	
47	PRIOR FILING DATE: 1998-06-10	
48	PRIOR APPLICATION NUMBER: 60/088810	
49	PRIOR FILING DATE: 1998-06-10	
50	PRIOR APPLICATION NUMBER: 60/088824	
51	PRIOR FILING DATE: 1998-06-10	
52	PRIOR APPLICATION NUMBER: 60/088826	
53	PRIOR FILING DATE: 1998-06-10	
54	PRIOR APPLICATION NUMBER: 60/088858	
55	PRIOR FILING DATE: 1998-06-11	
56	PRIOR APPLICATION NUMBER: 60/088861	
57	PRIOR FILING DATE: 1998-06-11	
58	PRIOR APPLICATION NUMBER: 60/088876	
59	PRIOR FILING DATE: 1998-06-11	
60	PRIOR APPLICATION NUMBER: 60/089105	
61	PRIOR FILING DATE: 1998-06-12	
62	PRIOR APPLICATION NUMBER: 60/089440	
63	PRIOR FILING DATE: 1998-06-16	
64	PRIOR APPLICATION NUMBER: 60/089512	
65	PRIOR FILING DATE: 1998-06-16	
66	PRIOR APPLICATION NUMBER: 60/089514	
67	PRIOR FILING DATE: 1998-06-16	
68	PRIOR APPLICATION NUMBER: 60/089532	
69	PRIOR FILING DATE: 1998-06-17	
70	PRIOR APPLICATION NUMBER: 60/089538	
71	PRIOR FILING DATE: 1998-06-17	

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 5; Length 2284;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGGAGCATCCGCTGGGCTCTCGCGAGACCCCGCGGGATTCCGCGGTCCTCCCGC	60
DB	1	GGGAGCATCCGCTGGGCTCTCGCGAGACCCCGCGGGATTCCGCGGTCCTCCCGC	60
QY	61	GGGCGGCACAGAGCTGTCTCGCACCTGGATGGCAGCGGGCGCGGGTCTCTCGAC	120
DB	61	GGGCGGCACAGAGCTGTCTCGCACCTGGATGGCAGCGGGCGCGGGTCTCTCGAC	120
QY	121	GCCAGAGAAATCTCATCTGTGCGAGCTTCTTTAAAGCAAACTAAGACAGAGGAG	180
DB	121	GCCAGAGAAATCTCATCTGTGCGAGCTTCTTTAAAGCAAACTAAGACAGAGGAG	180
QY	181	GAATTATCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCGGGGA	240
DB	181	GAATTATCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCGGGGA	240
QY	241	GAAGGAGCTTGACTTTACACTTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCT	300
DB	241	GAAGGAGCTTGACTTTACACTTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCT	300
QY	301	AGTCAGAAATGGCTCAAAAGAGCTAGAGAGTGTGTGCTATTGACATCCAGTCACTCTT	360
DB	301	AGTCAGAAATGGCTCAAAAGAGCTAGAGAGTGTGTGCTATTGACATCCAGTCACTCTT	360
QY	361	TCTAAGGGAATCAGAGCAATGAGCCGCTATATCTTCAACTCAAGAGACTGCAATTAAT	420
DB	361	TCTAAGGGAATCAGAGCAATGAGCCGCTATATCTTCAACTCAAGAGACTGCAATTAAT	420
QY	421	TCTTGCTGTTCACAAACATATCAGGGGCAAGAGATGTAATTTGATGATCTTCGAC	480
DB	421	TCTTGCTGTTCACAAACATATCAGGGGCAAGAGATGTAATTTGATGATCTTCGAC	480
QY	481	ACTCGAAAAACAGCTAGACAAACCAACTGCTACTATTTTCTGTCCCAACGAGGAAGCC	540
DB	481	ACTCGAAAAACAGCTAGACAAACCAACTGCTACTATTTTCTGTCCCAACGAGGAAGCC	540
QY	541	TGTCCATTGAAACACAGAAAGACTTATGAGTTACAGGATAATTAAGATTTTCCATCT	600
DB	541	TGTCCATTGAAACACAGAAAGACTTATGAGTTACAGGATAATTAAGATTTTCCATCT	600
QY	601	TTGACAGAAATTTGCCAAGCCAGAGTTACCCCGAGAGATTTCTCTTACATGGCCAA	660
DB	601	TTGACAGAAATTTGCCAAGCCAGAGTTACCCCGAGAGATTTCTCTTACATGGCCAA	660
QY	661	TTTTTCAAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATTCAAAGCCACCGAT	720
DB	661	TTTTTCAAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATTCAAAGCCACCGAT	720
QY	721	ATCTCATGGAGAGACACTTTTCTCAGAGTTTGGATTCCTCAGATCACTGGGAAACTA	780
DB	721	ATCTCATGGAGAGACACTTTTCTCAGAGTTTGGATTCCTCAGATCACTGGGAAACTA	780
QY	781	TTTTAAGATGATGAAGCAAGTGGCCAGCTCTTGTCTTATTAAGAAAGGCCATTTCTCAG	840
DB	781	TTTTAAGATGATGAAGCAAGTGGCCAGCTCTTGTCTTATTAAGAAAGGCCATTTCTCAG	840
QY	841	AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATTTGAGTGCG	900

DB	841	AGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAATTTGAGTGCG	900
QY	901	CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCTACTTCCAAAGCCGCC	960
DB	901	CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCTACTTCCAAAGCCGCC	960
QY	961	ACCTTTTACCCACCAATGTTTCTCAGTGACACCTTCTGGAGCTTCCAGGCACTGCGC	1020
DB	961	ACCTTTTACCCACCAATGTTTCTCAGTGACACCTTCTGGAGCTTCCAGGCACTGCGC	1020
QY	1021	ACCACAGCTCCACTGTAAACACTGTCTCAGCTCCACAGCCTCCACAGCCTCATTTCTACA	1080
DB	1021	ACCACAGCTCCACTGTAAACACTGTCTCAGCTCCACAGCCTCCACAGCCTCATTTCTACA	1080
QY	1081	GTTTTACAGGGCTGGGCTACACTCAAGCAATGCTTACCAAGCAGTCTCTGACTACC	1140
DB	1081	GTTTTACAGGGCTGGGCTACACTCAAGCAATGCTTACCAAGCAGTCTCTGACTACC	1140
QY	1141	ACCTTTTACGGCCTACCGACTCGAAAGGAGCTTGAAGAACCTACCGTTTACAGAAATC	1200
DB	1141	ACCTTTTACGGCCTACCGACTCGAAAGGAGCTTGAAGAACCTACCGTTTACAGAAATC	1200
QY	1201	TCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTACTGCACTTCTATGTCAAT	1260
DB	1201	TCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTACTGCACTTCTATGTCAAT	1260
QY	1261	GTGGAGCTTCCACTATGAATAAACTGCTTCTGGGAAGGTAGGAGGCGAGTCCAGGC	1320
DB	1261	GTGGAGCTTCCACTATGAATAAACTGCTTCTGGGAAGGTAGGAGGCGAGTCCAGGC	1320
QY	1321	AGTTCTCTCCAGGCGAGTGTTCAGAAATCAGTACGCGCTTCCATTTGAAAAATGGCTT	1380
DB	1321	AGTTCTCTCCAGGCGAGTGTTCAGAAATCAGTACGCGCTTCCATTTGAAAAATGGCTT	1380
QY	1381	CTTATCGGGTCCCTGCTCTTTTGGTGTCTGTCTCTGTTGATAGGCTCTCTCTGSGT	1440
DB	1381	CTTATCGGGTCCCTGCTCTTTTGGTGTCTGTCTCTGTTGATAGGCTCTCTCTGSGT	1440
QY	1441	AGAACTCTTTCGGAATCACTCCGAGGAAACGTTTACTCAAGACTGGATTTATTTGATCAAT	1500
DB	1441	AGAACTCTTTCGGAATCACTCCGAGGAAACGTTTACTCAAGACTGGATTTATTTGATCAAT	1500
QY	1501	GGGATCTATGTGACATCTAAGGATGGAATCGGCTGTCTTAAATTCATTTAGTAACAG	1560
DB	1501	GGGATCTATGTGACATCTAAGGATGGAATCGGCTGTCTTAAATTCATTTAGTAACAG	1560
QY	1561	AAGCCAAATGCAATGATTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTGATTTGA	1620
DB	1561	AAGCCAAATGCAATGATTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTGATTTGA	1620
QY	1621	AGACAGGAAATGCCCTTCTGCTTCTTCTTTTCTGAGACAGAGTCTTCTCTG	1680
DB	1621	AGACAGGAAATGCCCTTCTGCTTCTTCTTTTCTGAGACAGAGTCTTCTCTG	1680
QY	1681	TTGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCGCAACCTCGCTCTCTGG	1740
DB	1681	TTGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCGCAACCTCGCTCTCTGG	1740
QY	1741	GTTCAAGGATTTCTTGGCTCAGCTCTTAAGTATCTGGGATTTACAGGATGTGCCACC	1800
DB	1741	GTTCAAGGATTTCTTGGCTCAGCTCTTAAGTATCTGGGATTTACAGGATGTGCCACC	1800
QY	1801	ACACTGGGATTTTGTATTTTAGTAGAGCGGGTTTCAACATGTTGGTCAAGGCTG	1860
DB	1801	ACACTGGGATTTTGTATTTTAGTAGAGCGGGTTTCAACATGTTGGTCAAGGCTG	1860
QY	1861	GTCTCAAACTCTCAGCTTAGTATCCACTCTCGGCTCTCCAAAGTCTGGGATTTACA	1920
DB	1861	GTCTCAAACTCTCAGCTTAGTATCCACTCTCGGCTCTCCAAAGTCTGGGATTTACA	1920
QY	1921	GGCATGAGCCACCAAGCTGGCCCCCTTCTGTTTATGTTTGGTTTGGAGAGGAATGA	1980
DB	1921	GGCATGAGCCACCAAGCTGGCCCCCTTCTGTTTATGTTTGGTTTGGAGAGGAATGA	1980

Db 1921 GGCAAGGACCCACAGCTGGCCCTTCGTCTTATGTTTGGTTTGGTGAAGGAATGA 1980
QY 1981 AGTGGAAACCAATAGGTAAATTTTGGGTAATCTGTCTCTAAATATATAGCTAAAAACAA 2040
Db 1981 AGTGGAAACCAATAGGTAAATTTTGGGTAATCTGTCTCTAAATATATAGCTAAAAACAA 2040
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RESULT 14

US-09-989-728-514

; Sequence 514, Application US/09989728

; Patent No. 7029873

; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

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; APPLICANT: Eaton, Dan L.

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; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C72

; CURRENT APPLICATION NUMBER: US/09/989,728

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; PRIOR APPLICATION NUMBER: 60/049787

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; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

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; PRIOR FILING DATE: 1998-07-07
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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95	2284	100.0	2284	9	US-10-677-471-82
96	2284	100.0	2284	9	US-10-677-669-82
97	2284	100.0	2284	10	US-10-735-014-82
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332	235.2	10.3	62386	16	US-10-940-774-12823	Sequence 12823, A	405	234.8	10.3	188346	26	US-11-443-428A-735321	Sequence 735321, A
333	235.2	10.3	238417	11	US-10-461-862-98	Sequence 98, App	406	234.8	10.3	188366	26	US-11-443-428A-735309	Sequence 735309, A
334	235	10.3	601	16	US-10-940-774-94321	Sequence 94321, A	407	234.8	10.3	188378	26	US-11-443-428A-735294	Sequence 735294, A
335	235	10.3	601	16	US-10-940-774-94322	Sequence 94322, A	408	234.8	10.3	188384	26	US-11-443-428A-735294	Sequence 735294, A
336	235	10.3	625	4	US-09-925-065A-808258	Sequence 808258, A	409	234.8	10.3	188385	26	US-11-443-428A-735305	Sequence 735305, A
337	235	10.3	625	5	US-09-925-065A-808258	Sequence 808258, A	410	234.8	10.3	188385	26	US-11-443-428A-735301	Sequence 735301, A
338	235	10.3	11173	3	US-09-898-556A-10	Sequence 10, App	411	234.8	10.3	188421	26	US-11-443-428A-735297	Sequence 735297, A
339	235	10.3	11173	9	US-10-772-542-10	Sequence 10, App	412	234.8	10.3	188424	26	US-11-443-428A-735319	Sequence 735319, A
340	235	10.3	13619	16	US-10-990-328-96937	Sequence 96937, A	413	234.8	10.3	188427	26	US-11-443-428A-735295	Sequence 735295, A
341	235	10.3	24177	16	US-10-990-328-96937	Sequence 96937, A	414	234.8	10.3	188448	26	US-11-443-428A-735322	Sequence 735322, A
342	235	10.3	76838	23	US-10-033-056A-37312	Sequence 37312, A	415	234.8	10.3	188467	26	US-11-443-428A-735318	Sequence 735318, A
343	235	10.3	128034	8	US-10-282-174-186	Sequence 186, App	416	234.8	10.3	188529	26	US-11-443-428A-735296	Sequence 735296, A
344	235	10.3	128034	8	US-10-282-174-187	Sequence 187, App	417	234.8	10.3	188529	26	US-11-443-428A-735296	Sequence 735296, A
345	235	10.3	128034	10	US-10-600-009-186	Sequence 186, App	418	234.8	10.3	188548	26	US-11-443-428A-735292	Sequence 735292, A
346	235	10.3	202100	8	US-10-600-009-187	Sequence 187, App	419	234.8	10.3	400438	15	US-10-796-280-13229	Sequence 12229, A
347	235	10.3	202100	8	US-10-282-174-484	Sequence 484, App	420	234.8	10.3	400438	16	US-10-796-280-13229	Sequence 8717, App
348	235	10.3	202100	13	US-10-600-009-484	Sequence 484, App	421	234.6	10.3	597	4	US-09-925-065A-823703	Sequence 823703, A
349	234.8	10.3	994	13	US-10-301-480-54433	Sequence 54433, A	422	234.6	10.3	597	5	US-09-925-065A-823703	Sequence 823703, A
350	234.8	10.3	994	13	US-10-301-480-1207842	Sequence 1207842, A	423	234.6	10.3	639	4	US-09-925-065A-863172	Sequence 863172, A
351	234.8	10.3	5872	26	US-11-443-428A-313692	Sequence 313692, A	424	234.6	10.3	639	5	US-09-925-065A-863172	Sequence 863172, A
352	234.8	10.3	5952	26	US-11-443-428A-313690	Sequence 313690, A	425	234.6	10.3	13624	16	US-10-990-328-94132	Sequence 94132, A
353	234.8	10.3	6491	26	US-11-443-428A-313691	Sequence 313691, A	426	234.6	10.3	33830	16	US-10-990-328-95071	Sequence 95071, A
354	234.8	10.3	7085	26	US-11-443-428A-313688	Sequence 313688, A	427	234.6	10.3	60550	16	US-10-990-328-96238	Sequence 96238, A
355	234.8	10.3	7250	26	US-11-443-428A-313687	Sequence 313687, A	428	234.6	10.3	146361	16	US-10-990-328-93202	Sequence 93202, A
356	234.8	10.3	7252	26	US-11-443-428A-313682	Sequence 313682, A	429	234.4	10.3	169495	20	US-11-121-086-61	Sequence 61, Appl
357	234.8	10.3	7252	26	US-11-443-428A-313683	Sequence 313683, A	430	234.4	10.3	462586	11	US-10-476-264-420	Sequence 420, App
358	234.8	10.3	7252	26	US-11-443-428A-313684	Sequence 313684, A	431	234.2	10.3	993	13	US-10-301-480-600145	Sequence 600145, A
359	234.8	10.3	7269	26	US-11-443-428A-313679	Sequence 313679, A	432	234.2	10.3	993	13	US-10-301-480-1213554	Sequence 1213554, A
360	234.8	10.3	7278	26	US-11-443-428A-313680	Sequence 313680, A	433	234.2	10.3	9819	16	US-10-940-774-14050	Sequence 14050, A
361	234.8	10.3	7306	26	US-11-443-428A-313678	Sequence 313678, A	434	234.2	10.3	58212	16	US-10-940-774-15697	Sequence 15697, A
362	234.8	10.3	7306	26	US-11-443-428A-313678	Sequence 313678, A	435	234.2	10.3	13970	15	US-10-105-299-9643	Sequence 9643, App
363	234.8	10.3	31277	7	US-11-443-428A-313685	Sequence 313685, A	436	234.2	10.3	13970	15	US-10-868-184-7492	Sequence 7492, App
364	234.8	10.3	32351	16	US-10-087-192-1510	Sequence 1510, App	437	234.2	10.3	29331	23	US-11-033-056A-36084	Sequence 36084, A
365	234.8	10.3	187583	26	US-10-990-328-93698	Sequence 93698, A	438	234.2	10.3	50836	16	US-10-940-774-16722	Sequence 16722, A
366	234.8	10.3	187664	26	US-11-443-428A-735343	Sequence 735343, A	439	234.2	10.3	67228	16	US-10-990-328-94343	Sequence 94343, A
367	234.8	10.3	187679	26	US-11-443-428A-735342	Sequence 735342, A	440	234.2	10.3	127369	7	US-10-087-192-238	Sequence 238, App
368	234.8	10.3	187746	26	US-11-443-428A-735330	Sequence 735330, A	441	234.2	10.3	128978	10	US-10-775-169-345	Sequence 345, App
369	234.8	10.3	187760	26	US-11-443-428A-735316	Sequence 735316, A	442	234.2	10.3	128978	11	US-10-775-169-345	Sequence 345, App
370	234.8	10.3	187779	26	US-11-443-428A-735290	Sequence 735290, A	443	234.2	10.3	128978	16	US-10-567-867-1791	Sequence 1791, App
371	234.8	10.3	187827	26	US-11-443-428A-735304	Sequence 735304, A	444	234.2	10.3	128978	21	US-11-266-748A-61436	Sequence 61436, A
372	234.8	10.3	187842	26	US-11-443-428A-735329	Sequence 735329, A	445	234.2	10.3	128978	22	US-11-378-923-6	Sequence 6, Appl
373	234.8	10.3	187842	26	US-11-443-428A-735341	Sequence 735341, A	446	234.2	10.3	232641	16	US-10-990-328-93650	Sequence 93650, A
374	234.8	10.3	187860	26	US-11-443-428A-735291	Sequence 735291, A	447	234	10.2	24239	3	US-10-940-774-15452	Sequence 15452, A
375	234.8	10.3	187923	26	US-11-443-428A-735303	Sequence 735303, A	448	234	10.2	31871	3	US-09-764-847-1403	Sequence 1403, App
376	234.8	10.3	187923	26	US-11-443-428A-735315	Sequence 735315, A	449	234	10.2	31871	7	US-10-092-154-1403	Sequence 1403, App
377	234.8	10.3	188005	26	US-11-443-428A-735328	Sequence 735328, A	450	234	10.2	86361	9	US-10-741-601-5702	Sequence 5702, App
378	234.8	10.3	188013	26	US-11-443-428A-735338	Sequence 735338, A	451	234	10.2	86361	10	US-10-741-600-17803	Sequence 17803, A
379	234.8	10.3	188056	26	US-11-443-428A-735339	Sequence 735339, A	452	234	10.2	86361	11	US-10-995-561-13364	Sequence 13364, A
380	234.8	10.3	188086	26	US-11-443-428A-735302	Sequence 735302, A	453	234	10.2	143389	20	US-11-112-908-30	Sequence 30, Appl
381	234.8	10.3	188094	26	US-11-443-428A-735312	Sequence 735312, A	454	234	10.2	150314	20	US-11-112-908-24	Sequence 24, Appl
382	234.8	10.3	188134	26	US-11-443-428A-735337	Sequence 735337, A	455	234	10.2	220895	11	US-10-775-169-78	Sequence 78, Appl
383	234.8	10.3	188134	26	US-11-443-428A-735313	Sequence 735313, A	456	234	10.2	220895	10	US-10-756-149-723	Sequence 723, App
384	234.8	10.3	188140	26	US-11-443-428A-735333	Sequence 735333, A	457	234	10.2	220895	11	US-10-775-169-88	Sequence 88, Appl
385	234.8	10.3	188158	26	US-11-443-428A-735340	Sequence 735340, A	458	234	10.2	312453	23	US-11-033-056A-36041	Sequence 36041, A
386	234.8	10.3	188176	26	US-11-443-428A-735325	Sequence 735325, A	459	233.8	10.2	601	16	US-10-940-774-18060	Sequence 18060, A
387	234.8	10.3	188177	26	US-11-443-428A-735325	Sequence 735325, A	460	233.8	10.2	601	16	US-10-940-774-197087	Sequence 197087, A
388	234.8	10.3	188177	26	US-11-443-428A-735336	Sequence 735336, A	461	233.8	10.2	2300	27	US-11-636-385-29032	Sequence 29032, A
389	234.8	10.3	188215	26	US-11-443-428A-735311	Sequence 735311, A	462	233.8	10.2	7001	9	US-10-304-116-15	Sequence 15, Appl
390	234.8	10.3	188219	26	US-11-443-428A-735326	Sequence 735326, A	463	233.8	10.2	25284	16	US-10-990-328-93630	Sequence 93630, A

C 464	233.8	10.2	103665	12	US-10-330-773-680	Sequence 680, App	C 537	232.6	10.2	816	13	US-10-301-480-1172444	Sequence 1172444,
C 465	233.8	10.2	103665	14	US-10-540-898-680	Sequence 680, App	C 538	232.6	10.2	16573	16	US-10-940-774-11764	Sequence 11764, A
C 466	233.8	10.2	104073	23	US-11-033-056A-37679	Sequence 37679, A	C 539	232.6	10.2	17370	16	US-10-940-774-11731	Sequence 11731, A
C 467	233.8	10.2	104073	25	US-11-033-056A-37958	Sequence 37958, A	C 540	232.6	10.2	35336	16	US-10-990-328-98148	Sequence 98148, A
C 468	233.8	10.2	824376	25	US-11-066-316A-9906	Sequence 9906, App	C 541	232.6	10.2	36360	11	US-10-995-561-13498	Sequence 13498, A
C 469	233.6	10.2	34260	16	US-10-990-328-93427	Sequence 93427, A	C 542	232.6	10.2	36360	15	US-10-796-280-12589	Sequence 12589, A
C 470	233.6	10.2	68445	15	US-10-796-280-12493	Sequence 12493, A	C 543	232.6	10.2	36360	16	US-10-990-328-95949	Sequence 95949, A
C 471	233.6	10.2	76573	15	US-10-767-471-10718	Sequence 10718, A	C 544	232.6	10.2	43537	16	US-10-990-328-98109	Sequence 98109, A
C 472	233.6	10.2	161052	16	US-10-990-328-97674	Sequence 97674, A	C 545	232.6	10.2	74881	16	US-10-940-774-15545	Sequence 15545, A
C 473	233.6	10.2	160552	10	US-10-697-828-11	Sequence 11, Appl	C 546	232.6	10.2	74914	16	US-10-940-774-12286	Sequence 12286, A
C 474	233.6	10.2	168516	20	US-11-121-086-3	Sequence 3, Appl	C 547	232.6	10.2	100301	9	US-10-450-826-83	Sequence 83, Appl
C 475	233.4	10.2	832	13	US-10-301-480-545764	Sequence 545764, A	C 548	232.6	10.2	100301	10	US-10-723-860-3574	Sequence 3574, App
C 476	233.4	10.2	832	13	US-10-301-480-1159173	Sequence 1159173, A	C 549	232.6	10.2	238526	23	US-11-033-056A-37739	Sequence 37739, A
C 477	233.4	10.2	2330	27	US-10-990-328-97765	Sequence 97765, A	C 550	232.6	10.2	238526	23	US-11-033-056A-37740	Sequence 37740, A
C 478	233.4	10.2	19739	16	US-10-990-328-97775	Sequence 97775, A	C 551	232.6	10.2	238526	23	US-11-033-056A-38776	Sequence 38776, A
C 479	233.4	10.2	22728	16	US-10-940-774-11795	Sequence 11795, A	C 552	232.6	10.2	238579	23	US-11-033-056A-35686	Sequence 35686, A
C 480	233.4	10.2	32278	16	US-10-940-774-14575	Sequence 14575, A	C 553	232.6	10.2	238579	23	US-11-033-056A-35687	Sequence 35687, A
C 481	233.4	10.2	215281	15	US-10-767-471-10745	Sequence 10745, A	C 554	232.6	10.2	238579	23	US-11-033-056A-38766	Sequence 38766, A
C 482	233.4	10.2	232234	16	US-10-990-328-93684	Sequence 93684, A	C 555	232.6	10.2	246230	16	US-10-940-774-17019	Sequence 17019, A
C 483	233.4	10.2	2132949	23	US-11-033-056A-38500	Sequence 38500, A	C 556	232.6	10.2	246230	16	US-10-940-774-17020	Sequence 17020, A
C 484	233.2	10.2	1701	3	US-09-728-552-9	Sequence 9, Appl	C 557	232.6	10.2	246230	16	US-10-940-774-17021	Sequence 17021, A
C 485	233.2	10.2	1701	27	US-11-641-626-9	Sequence 9, Appl	C 558	232.6	10.2	246230	16	US-10-940-774-17022	Sequence 17022, A
C 486	233.2	10.2	2300	27	US-11-636-385-10226	Sequence 10226, A	C 559	232.6	10.2	281370	23	US-11-033-056A-36547	Sequence 36547, A
C 487	233.2	10.2	2300	27	US-11-636-385-23182	Sequence 25182, A	C 560	232.4	10.2	28475	15	US-11-443-428A-628165	Sequence 628165, A
C 488	233.2	10.2	173602	20	US-10-210-556-27	Sequence 27, Appl	C 561	232.4	10.2	28475	15	US-10-767-471-10766	Sequence 10766, A
C 489	233.2	10.2	176001	9	US-10-210-556-27	Sequence 27, Appl	C 562	232.4	10.2	31385	16	US-10-940-774-13310	Sequence 13310, A
C 490	233.2	10.2	180531	21	US-11-114-798-57	Sequence 57, Appl	C 563	232.4	10.2	31385	16	US-10-940-774-12358	Sequence 12358, A
C 491	233.2	10.2	185035	11	US-10-723-860-3104	Sequence 3104, App	C 564	232.4	10.2	74853	16	US-10-990-328-98074	Sequence 98074, A
C 492	233.2	10.2	185035	11	US-10-756-149-2896	Sequence 2896, App	C 565	232.4	10.2	90380	16	US-10-990-328-97546	Sequence 97546, A
C 493	233.2	10.2	185035	14	US-10-470-050-281	Sequence 281, App	C 566	232.4	10.2	100525	23	US-11-033-056A-35916	Sequence 35916, A
C 494	233.2	10.2	185035	21	US-11-266-748A-59932	Sequence 59932, A	C 567	232.4	10.2	150248	20	US-11-033-056A-36438	Sequence 36438, A
C 495	233.2	10.2	186739	9	US-10-210-556-19	Sequence 19, Appl	C 568	232.4	10.2	171427	23	US-11-112-908-60	Sequence 60, Appl
C 496	233	10.2	597	4	US-09-925-065A-751915	Sequence 751915, A	C 569	232.4	10.2	184665	21	US-11-266-748A-32088	Sequence 32088, A
C 497	233	10.2	597	4	US-09-925-065A-751915	Sequence 751915, A	C 570	232.4	10.2	217214	16	US-10-990-328-94062	Sequence 94062, A
C 498	233	10.2	597	5	US-09-925-065A-751915	Sequence 751915, A	C 571	232.4	10.2	293046	16	US-10-990-328-94327	Sequence 94327, A
C 499	233	10.2	597	5	US-09-925-065A-751915	Sequence 751915, A	C 572	232.4	10.2	293046	16	US-10-990-328-97181	Sequence 97181, A
C 500	233	10.2	1329	26	US-11-443-428A-665898	Sequence 665898, A	C 573	232.4	10.2	389627	11	US-10-504-689-3	Sequence 3, Appl
C 501	233	10.2	5633	15	US-10-105-299-13373	Sequence 13373, A	C 574	232.4	10.2	402850	9	US-09-844-653-5	Sequence 5, Appl
C 502	233	10.2	5633	16	US-10-868-184-11222	Sequence 11222, A	C 575	232.4	10.2	405660	9	US-10-322-696-82	Sequence 82, Appl
C 503	233	10.2	68610	15	US-10-796-280-12467	Sequence 12467, A	C 576	232.4	10.2	408438	14	US-10-669-920-1277	Sequence 1277, App
C 504	233	10.2	68610	16	US-10-796-307-8843	Sequence 8843, App	C 577	232.4	10.2	4647455	14	US-10-641-321-205	Sequence 205, App
C 505	233	10.2	256493	7	US-10-087-192-1000	Sequence 1000, App	C 578	232.2	10.2	605	4	US-09-925-065A-878037	Sequence 878037, A
C 506	233	10.2	1184710	15	US-10-796-280-12394	Sequence 12394, A	C 579	232.2	10.2	605	5	US-09-925-065A-878037	Sequence 878037, A
C 507	232.8	10.2	601	16	US-10-940-774-45773	Sequence 45773, A	C 580	232.2	10.2	607	4	US-09-925-065A-873360	Sequence 873360, A
C 508	232.8	10.2	601	16	US-10-940-774-45774	Sequence 45774, A	C 581	232.2	10.2	607	5	US-09-925-065A-873360	Sequence 873360, A
C 509	232.8	10.2	797	8	US-10-027-632-127789	Sequence 127789, A	C 582	232.2	10.2	614	4	US-09-925-065A-878367	Sequence 878367, A
C 510	232.8	10.2	797	8	US-10-027-632-127789	Sequence 127789, A	C 583	232.2	10.2	614	5	US-09-925-065A-878367	Sequence 878367, A
C 511	232.8	10.2	78568	16	US-10-990-328-96022	Sequence 96022, A	C 584	232.2	10.2	2300	27	US-11-636-385-17771	Sequence 17771, A
C 512	232.8	10.2	109472	16	US-10-990-328-98005	Sequence 98005, A	C 585	232.2	10.2	12878	16	US-10-990-328-97194	Sequence 97194, A
C 513	232.8	10.2	121160	12	US-10-330-773-847	Sequence 847, App	C 586	232.2	10.2	12960	23	US-11-033-056A-38495	Sequence 38495, A
C 514	232.8	10.2	121160	14	US-10-540-898-847	Sequence 847, App	C 587	232.2	10.2	18008	23	US-10-940-774-13291	Sequence 13291, A
C 515	232.8	10.2	136017	16	US-10-990-328-93377	Sequence 93377, A	C 588	232.2	10.2	26878	16	US-10-990-328-97667	Sequence 97667, A
C 516	232.8	10.2	138627	12	US-10-330-773-159	Sequence 159, App	C 589	232.2	10.2	31451	16	US-10-990-328-97757	Sequence 97757, A
C 517	232.8	10.2	138627	14	US-10-540-898-159	Sequence 159, App	C 590	232.2	10.2	60463	16	US-10-990-328-94067	Sequence 94067, A
C 518	232.8	10.2	211148	16	US-10-990-328-94673	Sequence 94673, A	C 591	232.2	10.2	60463	16	US-10-990-328-95083	Sequence 95083, A
C 519	232.8	10.2	430700	23	US-11-033-056A-37994	Sequence 37994, A	C 592	232.2	10.2	68004	16	US-10-990-328-95083	Sequence 95083, A
C 520	232.6	10.2	461	10	US-10-357-930-49228	Sequence 49228, A	C 593	232.2	10.2	78568	15	US-10-767-471-10897	Sequence 10897, A
C 521	232.6	10.2	601	16	US-10-940-774-87766	Sequence 87766, A	C 594	232.2	10.2	488	4	US-09-925-065A-850388	Sequence 850388, A
C 522	232.6	10.2	624	7	US-10-027-632-78403	Sequence 78403, A	C 595	232.2	10.2	488	5	US-09-925-065A-850388	Sequence 850388, A
C 523	232.6	10.2	624	7	US-10-027-632-78404	Sequence 78404, A	C 596	232.2	10.2	489	4	US-09-925-065A-842830	Sequence 842830, A
C 524	232.6	10.2	624	7	US-10-027-632-78405	Sequence 78405, A	C 597	232.2	10.2	489	5	US-09-925-065A-842830	Sequence 842830, A
C 525	232.6	10.2	624	7	US-10-027-632-78406	Sequence 78406, A	C 598	232.2	10.2	984	13	US-10-301-480-537929	Sequence 537929, A
C 526	232.6	10.2	624	7	US-10-027-632-78407	Sequence 78407, A	C 599	232.2	10.2	984	13	US-10-301-480-1151338	Sequence 1151338, A
C 527	232.6	10.2	624	7	US-10-027-632-78408	Sequence 78408, A	C 600	232.2	10.2	994	13	US-10-301-480-586474	Sequence 586474, A
C 528	232.6	10.2	624	8	US-10-027-632-78409	Sequence 78409, A	C 601	232.2	10.2	994	13	US-10-301-480-119883	Sequence 119883, A
C 529	232.6	10.2	624	8	US-10-027-632-78404	Sequence 78404, A	C 602	232.2	10.2	15366	3	US-09-764-860-1057	Sequence 1057, App
C 530	232.6	10.2	624	8	US-10-027-632-78405	Sequence 78405, A	C 603	232.2	10.2	15366	8	US-10-074-095-1057	Sequence 1057, App
C 531	232.6	10.2	624	8	US-10-027-632-78406	Sequence 78406, A	C 604	232.2	10.2	15366	8	US-10-212-872-1057	Sequence 1057, App
C 532	232.6	10.2	624	8	US-10-027-632-78407	Sequence 78407, A	C 605	232.2	10.2	23410	23	US-11-033-056A-37244	Sequence 37244, A
C 533	232.6	10.2	624	8	US-10-027-632-78408	Sequence 78408, A	C 606	232.2	10.2	53046	23	US-11-033-056A-38464	Sequence 38464, A
C 534	232.6	10.2	765	7	US-10-027-632-173966	Sequence 173966, A	C 607	232.2	10.2	63885	16	US-10-990-328-96682	Sequence 96682, A
C 535	232.6	10.2	765	8	US-10-027-632-173966	Sequence 173966, A	C 608	232.2	10.2	126552	20	US-11-121-086-1	Sequence 1, Appl
C 536	232.6	10.2	816	13	US-10-301-480-559035	Sequence 559035, A	C 609	232.2	10.2	162510	16	US-10-990-328-97157	Sequence 97157, A

c 610	232	10.2	170245	9	US-10-717-597-322	Sequence 322, App	683	231.4	10.1	1463	4	US-09-925-065A-678834	Sequence 678834,
c 611	232	10.2	191684	20	US-11-121-086-2	Sequence 2, Appli	684	231.4	10.1	1463	5	US-09-925-065A-678834	Sequence 678834,
c 612	232	10.2	194275	23	US-11-033-056A-37687	Sequence 37687, A	685	231.4	10.1	18218	23	US-11-033-056A-36208	Sequence 36208, A
c 613	232	10.2	194275	23	US-11-033-056A-37689	Sequence 37689, A	686	231.4	10.1	18700	16	US-10-940-774-13140	Sequence 13140, A
c 614	232	10.2	260209	8	US-10-265-071-23	Sequence 23, Appl	687	231.4	10.1	28054	16	US-10-990-328-97317	Sequence 97317, A
c 615	232	10.2	260209	8	US-10-025-966A-23	Sequence 23, Appl	688	231.4	10.1	31489	16	US-10-990-328-95215	Sequence 95215, A
c 616	232	10.2	260209	11	US-10-933-025-23	Sequence 23, Appl	689	231.4	10.1	32124	16	US-10-990-328-93448	Sequence 93448, A
c 617	232	10.2	260209	21	US-11-219-360-23	Sequence 23, Appl	690	231.4	10.1	39451	9	US-10-322-281-554	Sequence 554, App
c 618	232	10.2	300351	16	US-10-990-328-96853	Sequence 96853, A	691	231.4	10.1	39451	14	US-10-539-228-554	Sequence 554, App
c 619	232	10.2	385460	23	US-11-033-056A-36444	Sequence 36444, A	692	231.4	10.1	44244	16	US-10-940-774-11743	Sequence 11743, A
c 620	232	10.2	482767	23	US-11-033-056A-38391	Sequence 38391, A	693	231.4	10.1	44244	16	US-10-940-774-11743	Sequence 11743, A
c 621	232	10.2	486468	23	US-11-033-056A-35962	Sequence 35962, A	694	231.4	10.1	48490	16	US-10-990-328-94910	Sequence 94910, A
c 622	231.8	10.1	596	13	US-10-301-480-14081	Sequence 14081, A	695	231.4	10.1	52410	16	US-10-990-328-97453	Sequence 97453, A
c 623	231.8	10.1	596	13	US-10-301-480-14081	Sequence 14081, A	696	231.4	10.1	52410	16	US-10-990-328-97453	Sequence 97453, A
c 624	231.8	10.1	601	23	US-10-301-480-627490	Sequence 627490, A	697	231.4	10.1	58014	16	US-10-990-328-94333	Sequence 94333, A
c 625	231.8	10.1	601	23	US-11-033-545-6961	Sequence 6961, Ap	698	231.4	10.1	66641	16	US-10-990-328-94333	Sequence 94333, A
c 626	231.8	10.1	970	5	US-09-925-065A-727962	Sequence 727962,	699	231.4	10.1	87648	16	US-10-940-774-13655	Sequence 13655, A
c 627	231.8	10.1	970	5	US-09-925-065A-727962	Sequence 727962,	699	231.4	10.1	87648	16	US-10-940-774-13655	Sequence 13655, A
c 628	231.8	10.1	998	13	US-10-301-480-587769	Sequence 587769,	700	231.4	10.1	104245	9	US-10-160-807-4	Sequence 4, Appli
c 629	231.8	10.1	10000	22	US-11-375-359-258	Sequence 258, App	701	231.4	10.1	104245	9	US-10-655-847-4	Sequence 4, Appli
c 630	231.8	10.1	18396	23	US-11-033-545-763	Sequence 763, App	702	231.4	10.1	114693	10	US-10-473-392-3	Sequence 3, Appli
c 631	231.8	10.1	18700	16	US-10-940-774-13140	Sequence 13140, A	703	231.4	10.1	147700	11	US-10-723-681-3	Sequence 3, Appli
c 632	231.8	10.1	57038	11	US-10-287-436A-646	Sequence 646, App	704	231.4	10.1	147700	11	US-10-857-780-3	Sequence 785, App
c 633	231.8	10.1	83016	23	US-11-033-056A-35589	Sequence 35589, A	705	231.4	10.1	154091	17	US-10-674-575-785	Sequence 322, App
c 634	231.8	10.1	83016	23	US-11-033-056A-36123	Sequence 36123, A	706	231.4	10.1	170245	9	US-10-717-597-322	Sequence 32, App
c 635	231.8	10.1	83016	23	US-11-033-056A-37409	Sequence 37409, A	707	231.4	10.1	170245	9	US-10-717-597-322	Sequence 32, App
c 636	231.8	10.1	83016	23	US-11-033-056A-37463	Sequence 37463, A	708	231.4	10.1	171162	20	US-11-112-908-38	Sequence 38, Appl
c 637	231.8	10.1	92794	11	US-10-287-436A-708	Sequence 708, App	709	231.4	10.1	171162	20	US-11-112-908-38	Sequence 38, Appl
c 638	231.8	10.1	207433	8	US-10-277-216-5	Sequence 5, Appli	710	231.4	10.1	202814	25	US-11-066-316A-23494	Sequence 23494, A
c 639	231.8	10.1	207433	9	US-10-126-022-5	Sequence 5, Appli	711	231.4	10.1	202814	25	US-11-066-316A-23494	Sequence 23494, A
c 640	231.8	10.1	251909	23	US-11-405-322-1	Sequence 1, Appli	712	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 641	231.8	10.1	256164	21	US-11-266-748A-60910	Sequence 60910, A	713	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 642	231.6	10.1	394191	13	US-10-506-549-3	Sequence 3, Appli	714	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 643	231.6	10.1	461	10	US-10-357-930-19427	Sequence 19427, A	715	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 644	231.6	10.1	737	13	US-10-301-480-580734	Sequence 580734, A	716	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 645	231.6	10.1	737	13	US-10-301-480-580734	Sequence 580734, A	717	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 646	231.6	10.1	2271	26	US-11-443-428A-299112	Sequence 299112, A	718	231.4	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 647	231.6	10.1	2300	27	US-11-636-385-42069	Sequence 42069, A	719	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 648	231.6	10.1	2381	26	US-11-443-428A-299111	Sequence 299111, A	720	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 649	231.6	10.1	3158	26	US-11-443-428A-299105	Sequence 299105, A	721	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 650	231.6	10.1	3230	26	US-11-443-428A-299110	Sequence 299110, A	722	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 651	231.6	10.1	3301	26	US-11-443-428A-299107	Sequence 299107, A	723	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 652	231.6	10.1	3310	26	US-11-443-428A-299108	Sequence 299108, A	724	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 653	231.6	10.1	3364	26	US-11-443-428A-299104	Sequence 299104, A	725	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 654	231.6	10.1	3408	26	US-11-443-428A-299109	Sequence 299109, A	726	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 655	231.6	10.1	3464	26	US-11-443-428A-299106	Sequence 299106, A	727	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 656	231.6	10.1	17932	16	US-10-990-328-97852	Sequence 97852, A	728	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 657	231.6	10.1	23748	3	US-09-764-891-7917	Sequence 7917, Ap	729	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 658	231.6	10.1	25376	16	US-10-990-328-96948	Sequence 96948, A	730	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 659	231.6	10.1	39140	16	US-10-990-328-95630	Sequence 95630, A	731	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 660	231.6	10.1	40951	16	US-10-940-774-15845	Sequence 15845, A	732	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 661	231.6	10.1	45299	16	US-10-940-774-12465	Sequence 12465, A	733	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 662	231.6	10.1	45300	16	US-10-940-774-13045	Sequence 13045, A	734	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 663	231.6	10.1	48185	23	US-11-033-056A-36768	Sequence 36768, A	735	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 664	231.6	10.1	54711	16	US-10-940-774-17439	Sequence 17439, A	736	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 665	231.6	10.1	58289	16	US-10-990-328-94348	Sequence 94348, A	737	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 666	231.6	10.1	6815	23	US-11-033-056A-36425	Sequence 36425, A	738	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 667	231.6	10.1	75159	15	US-10-796-280-12543	Sequence 12543, A	739	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 668	231.6	10.1	75159	15	US-10-990-328-97698	Sequence 97698, A	740	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 669	231.6	10.1	105045	23	US-11-033-545-663	Sequence 663, App	741	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 670	231.6	10.1	107045	23	US-11-033-545-772	Sequence 772, App	742	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 671	231.6	10.1	118923	16	US-10-940-774-13227	Sequence 13227, A	743	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 672	231.6	10.1	148037	25	US-11-066-316A-9911	Sequence 9911, Ap	744	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 673	231.6	10.1	164702	10	US-10-484-577-658	Sequence 658, App	745	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 674	231.6	10.1	210748	23	US-11-033-056A-36345	Sequence 36345, A	746	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 675	231.6	10.1	239879	16	US-10-990-328-93921	Sequence 93921, A	747	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 676	231.6	10.1	304533	16	US-10-940-774-15371	Sequence 15371, A	748	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 677	231.6	10.1	304533	16	US-10-940-774-15372	Sequence 15372, A	749	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 678	231.6	10.1	601	23	US-11-033-545-6962	Sequence 6962, Ap	750	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 679	231.4	10.1	970	5	US-09-925-065A-727961	Sequence 727961, A	751	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 680	231.4	10.1	970	5	US-09-925-065A-727961	Sequence 727961, A	752	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 681	231.4	10.1	996	13	US-10-301-480-594154	Sequence 594154, A	753	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 682	231.4	10.1	996	13	US-10-301-480-1207563	Sequence 1207563, A	754	231.2	10.1	262814	16	US-10-990-328-97221	Sequence 97221, A
c 683	231.4	10.1	996	13	US-10-301-480-12								

c 756	231	10.1	116644	16	US-10-990-328-96120	Sequence 96120, A	c 829	230.2	10.1	1000	21	US-11-266-748A-344371	Sequence 344371, A
c 757	231	10.1	126001	20	US-10-175-492-13	Sequence 13, Appl	c 830	230.2	10.1	1427	4	US-09-925-065A-726021	Sequence 726021, A
c 758	231	10.1	176503	8	US-11-121-086-53	Sequence 53, Appl	c 831	230.2	10.1	1427	5	US-09-925-065A-726021	Sequence 726021, A
c 759	231	10.1	197645	16	US-10-990-328-96919	Sequence 96919, A	c 832	230.2	10.1	1721	7	US-10-027-632-97145	Sequence 97145, A
c 760	231	10.1	224235	16	US-10-990-328-97252	Sequence 97252, A	c 833	230.2	10.1	1721	8	US-10-027-632-97145	Sequence 97145, A
c 761	231	10.1	261381	23	US-11-033-056A-37874	Sequence 37874, A	c 834	230.2	10.1	2291	21	US-11-266-748A-31369	Sequence 31369, A
c 762	230.8	10.1	679	4	US-09-925-065A-532787	Sequence 532787, A	c 835	230.2	10.1	2291	23	US-11-371-354-11097	Sequence 11097, A
c 763	230.8	10.1	679	5	US-09-925-065A-532787	Sequence 532787, A	c 836	230.2	10.1	2300	27	US-11-636-385-12508	Sequence 12508, A
c 764	230.8	10.1	875	7	US-10-027-632-169472	Sequence 169472, A	c 837	230.2	10.1	2300	27	US-11-636-385-12508	Sequence 12508, A
c 765	230.8	10.1	875	8	US-10-027-632-169472	Sequence 169472, A	c 838	230.2	10.1	6777	8	US-10-376-566-10	Sequence 10, Appl
c 766	230.8	10.1	2300	27	US-11-636-385-35266	Sequence 35266, A	c 839	230.2	10.1	10281	16	US-10-940-774-15812	Sequence 15812, A
c 767	230.8	10.1	17628	16	US-10-940-774-16718	Sequence 16718, A	c 840	230.2	10.1	10465	16	US-10-940-774-13136	Sequence 13136, A
c 768	230.8	10.1	22135	16	US-10-990-328-96594	Sequence 96594, A	c 841	230.2	10.1	13286	13	US-10-517-441-113	Sequence 113, Appl
c 769	230.8	10.1	40859	16	US-10-990-328-96594	Sequence 96594, A	c 842	230.2	10.1	14670	16	US-10-741-600-17749	Sequence 17749, A
c 770	230.8	10.1	45091	16	US-10-990-328-95100	Sequence 95100, A	c 843	230.2	10.1	17901	16	US-10-990-328-97628	Sequence 97628, A
c 771	230.8	10.1	71879	16	US-10-990-328-95100	Sequence 95100, A	c 844	230.2	10.1	18097	10	US-10-741-600-17981	Sequence 17981, A
c 772	230.8	10.1	71879	9	US-10-940-774-17465	Sequence 17465, A	c 845	230.2	10.1	18895	10	US-10-741-600-17750	Sequence 17750, A
c 773	230.8	10.1	87878	15	US-10-052-482-82	Sequence 82, Appl	c 846	230.2	10.1	22131	16	US-10-990-328-94882	Sequence 94882, A
c 774	230.8	10.1	87878	15	US-10-035-832-1094	Sequence 1094, Appl	c 847	230.2	10.1	22131	16	US-10-990-328-94882	Sequence 94882, A
c 775	230.8	10.1	127369	22	US-11-330-726-82	Sequence 82, Appl	c 848	230.2	10.1	26059	15	US-10-105-299-10406	Sequence 10406, A
c 776	230.8	10.1	127369	16	US-10-990-328-93789	Sequence 93789, A	c 849	230.2	10.1	26059	16	US-10-868-184-8255	Sequence 8255, Appl
c 777	230.8	10.1	285569	23	US-11-033-056A-38757	Sequence 38757, A	c 850	230.2	10.1	26665	22	US-11-073-360-1599	Sequence 1599, Appl
c 778	230.8	10.1	418196	23	US-11-033-056A-37368	Sequence 37368, A	c 851	230.2	10.1	66916	9	US-10-741-601-5708	Sequence 5708, Appl
c 779	230.8	10.1	418196	23	US-11-033-056A-37414	Sequence 37414, A	c 852	230.2	10.1	66916	11	US-10-741-600-17810	Sequence 17810, A
c 780	230.8	10.1	479168	16	US-10-990-328-97660	Sequence 97660, A	c 853	230.2	10.1	66916	11	US-10-995-561-13374	Sequence 13374, A
c 781	230.6	10.1	601	16	US-10-940-774-68606	Sequence 68606, A	c 854	230.2	10.1	66916	16	US-10-990-328-93218	Sequence 93218, A
c 782	230.6	10.1	616	4	US-09-925-065A-931112	Sequence 931112, A	c 855	230.2	10.1	86168	16	US-10-990-328-95490	Sequence 95490, A
c 783	230.6	10.1	616	5	US-09-925-065A-931112	Sequence 931112, A	c 856	230.2	10.1	102541	16	US-10-990-328-96643	Sequence 96643, A
c 784	230.6	10.1	806	13	US-10-301-480-560813	Sequence 560813, A	c 857	230.2	10.1	113000	8	US-10-376-566-16	Sequence 16, Appl
c 785	230.6	10.1	806	13	US-10-301-480-560813	Sequence 560813, A	c 858	230.2	10.1	114503	16	US-10-990-328-94201	Sequence 94201, A
c 786	230.6	10.1	2300	27	US-11-636-385-316	Sequence 316, Appl	c 859	230.2	10.1	188056	21	US-11-120-923-1	Sequence 1, Appl
c 787	230.6	10.1	2300	27	US-11-636-385-10727	Sequence 10727, A	c 860	230.2	10.1	188056	21	US-11-121-086-54	Sequence 54, Appl
c 788	230.6	10.1	2300	27	US-11-636-385-19804	Sequence 19804, A	c 861	230.2	10.1	202814	10	US-10-719-993-6812	Sequence 6812, Appl
c 789	230.6	10.1	2300	27	US-11-636-385-35371	Sequence 35371, A	c 862	230.2	10.1	202814	16	US-10-990-328-97440	Sequence 97440, A
c 790	230.6	10.1	14863	23	US-11-033-056A-37210	Sequence 37210, A	c 863	230.2	10.1	246826	23	US-11-033-056A-37194	Sequence 37194, A
c 791	230.6	10.1	17498	3	US-09-764-860-798	Sequence 798, Appl	c 864	230.2	10.1	246826	23	US-11-033-056A-37195	Sequence 37195, A
c 792	230.6	10.1	17498	8	US-10-074-095-798	Sequence 798, Appl	c 865	230.2	10.1	246826	23	US-11-033-056A-37195	Sequence 37195, A
c 793	230.6	10.1	20090	23	US-11-033-056A-37933	Sequence 37933, A	c 866	230.2	10.1	230040	10	US-10-850-586-3	Sequence 3, Appl
c 794	230.6	10.1	24005	16	US-10-940-774-13758	Sequence 13758, A	c 867	230.2	10.1	230040	10	US-10-850-586-3	Sequence 3, Appl
c 795	230.6	10.1	25859	16	US-10-940-774-15052	Sequence 15052, A	c 868	230.2	10.1	325791	4	US-09-768-185A-1	Sequence 1, Appl
c 796	230.6	10.1	26509	16	US-10-990-328-94126	Sequence 94126, A	c 869	230.2	10.1	32704	23	US-11-033-056A-36747	Sequence 36747, A
c 797	230.6	10.1	29490	16	US-10-990-328-97394	Sequence 97394, A	c 870	230.2	10.1	32704	23	US-11-033-056A-37600	Sequence 37600, A
c 798	230.6	10.1	30381	16	US-10-990-328-95595	Sequence 95595, A	c 871	230.2	10.1	405740	23	US-10-796-307-8716	Sequence 8716, Appl
c 799	230.6	10.1	69920	15	US-10-767-471-10739	Sequence 10739, A	c 872	230.2	10.1	408997	23	US-11-033-056A-36439	Sequence 36439, A
c 800	230.6	10.1	69920	16	US-10-990-328-95794	Sequence 95794, A	c 873	230.2	10.1	524169	23	US-11-033-056A-36660	Sequence 36660, A
c 801	230.6	10.1	86141	15	US-10-796-280-12292	Sequence 12292, A	c 874	230	10.1	955	7	US-10-037-270-228	Sequence 228, Appl
c 802	230.6	10.1	87001	10	US-10-741-600-17792	Sequence 17792, A	c 875	230	10.1	955	8	US-10-117-722-228	Sequence 228, Appl
c 803	230.6	10.1	89171	16	US-10-990-328-95720	Sequence 95720, A	c 876	230	10.1	955	11	US-10-122-851-228	Sequence 228, Appl
c 804	230.6	10.1	95597	16	US-10-990-328-95297	Sequence 95297, A	c 877	230	10.1	2300	27	US-11-636-385-27569	Sequence 27569, A
c 805	230.6	10.1	102993	23	US-11-033-056A-37458	Sequence 37458, A	c 878	230	10.1	2300	27	US-11-636-385-43081	Sequence 43081, A
c 806	230.6	10.1	130877	9	US-10-322-281-54	Sequence 54, Appl	c 879	230	10.1	17146	3	US-09-764-877-3850	Sequence 3850, Appl
c 807	230.6	10.1	130877	14	US-10-539-228-54	Sequence 54, Appl	c 880	230	10.1	17146	8	US-10-242-515-3850	Sequence 3850, Appl
c 808	230.6	10.1	177531	10	US-10-484-577-660	Sequence 660, Appl	c 881	230	10.1	25708	16	US-10-990-328-94068	Sequence 94068, A
c 809	230.6	10.1	215595	16	US-10-990-328-94061	Sequence 94061, A	c 882	230	10.1	30568	3	US-09-764-877-3851	Sequence 3851, Appl
c 810	230.6	10.1	295669	23	US-11-033-056A-38457	Sequence 38457, A	c 883	230	10.1	30568	3	US-10-242-515-3851	Sequence 3851, Appl
c 811	230.4	10.1	601	16	US-10-940-774-120458	Sequence 120458, A	c 884	230	10.1	40512	16	US-10-940-774-16612	Sequence 16612, A
c 812	230.4	10.1	601	16	US-10-940-774-120458	Sequence 120458, A	c 885	230	10.1	45720	16	US-10-990-328-94980	Sequence 94980, A
c 813	230.4	10.1	631	4	US-09-925-065A-499794	Sequence 499794, A	c 886	230	10.1	88645	23	US-11-417-450-38	Sequence 38, Appl
c 814	230.4	10.1	631	5	US-09-925-065A-499794	Sequence 499794, A	c 887	230	10.1	88645	23	US-11-417-450-38	Sequence 38, Appl
c 815	230.4	10.1	2000	27	US-11-266-748A-202568	Sequence 202568, A	c 888	230	10.1	165213	23	US-11-033-056A-37169	Sequence 37169, A
c 816	230.4	10.1	2300	27	US-11-636-385-4145	Sequence 4145, Appl	c 889	230	10.1	183704	23	US-11-033-056A-37170	Sequence 37170, A
c 817	230.4	10.1	12993	16	US-10-990-328-93372	Sequence 93372, A	c 890	230	10.1	193636	23	US-11-417-450-36	Sequence 36, Appl
c 818	230.4	10.1	24268	16	US-10-100-683-13305	Sequence 13305, A	c 891	230	10.1	242923	16	US-10-990-328-96176	Sequence 96176, A
c 819	230.4	10.1	24268	16	US-10-100-683-13305	Sequence 13305, A	c 892	229.8	10.1	489	4	US-09-925-065A-469133	Sequence 469133, A
c 820	230.2	10.1	334385	16	US-10-990-328-96323	Sequence 96323, A	c 893	229.8	10.1	489	5	US-09-925-065A-469133	Sequence 469133, A
c 821	230.2	10.1	574	13	US-10-301-480-49061	Sequence 49061, A	c 894	229.8	10.1	578	7	US-10-027-632-289745	Sequence 289745, A
c 822	230.2	10.1	574	13	US-10-301-480-49061	Sequence 49061, A	c 895	229.8	10.1	578	8	US-10-027-632-289745	Sequence 289745, A
c 823	230.2	10.1	628	13	US-10-301-480-545191	Sequence 545191, A	c 896	229.8	10.1	591	4	US-09-925-065A-526304	Sequence 526304, A
c 824	230.2	10.1	628	13	US-10-301-480-545191	Sequence 545191, A	c 897	229.8	10.1	591	5	US-09-925-065A-526304	Sequence 526304, A
c 825	230.2	10.1	986	13	US-10-301-480-59168	Sequence 59168, A	c 898	229.8	10.1	619	5	US-09-925-065A-536042	Sequence 536042, A
c 826	230.2	10.1	986	13	US-10-301-480-59168	Sequence 59168, A	c 899	229.8	10.1	619	5	US-09-925-065A-536042	Sequence 536042, A
c 827	230.2	10.1	1000	21	US-11-266-748A-224259	Sequence 224259, A	c 900	229.8	10.1	2300	27	US-11-636-385-20755	Sequence 20755, A
c 828	230.2	10.1	1000	21	US-11-266-748A-292942	Sequence 292942, A	c 901	229.8	10.1	14670	11	US-10-995-561-13328	Sequence 13328, A

C 902	229.8	10.1	18097	11	US-10-995-561-13486	Sequence 13486, A	975	229.4	10.0	576	13	US-10-301-480-1014615	Sequence 1014615,
C 903	229.8	10.1	18895	11	US-10-995-561-13329	Sequence 13329, A	976	229.4	10.0	576	13	US-10-301-480-1014616	Sequence 1014616,
C 904	229.8	10.1	24590	16	US-10-990-328-96793	Sequence 96793, A	C 977	229.4	10.0	578	7	US-10-027-632-289743	Sequence 289743,
C 905	229.8	10.1	31737	14	US-10-219-051B-13986	Sequence 13986, A	C 978	229.4	10.0	578	7	US-10-027-632-289744	Sequence 289744,
C 906	229.8	10.1	31737	14	US-10-219-051B-13986	Sequence 13986, A	C 979	229.4	10.0	578	8	US-10-027-632-289743	Sequence 289743,
C 907	229.8	10.1	38206	16	US-10-940-774-15527	Sequence 15527, A	C 980	229.4	10.0	578	8	US-10-027-632-289744	Sequence 289744,
C 908	229.8	10.1	46215	10	US-10-741-600-17973	Sequence 17973, A	C 981	229.4	10.0	619	4	US-09-925-065A-536043	Sequence 536043,
C 909	229.8	10.1	46215	11	US-10-995-561-13483	Sequence 13483, A	C 982	229.4	10.0	619	5	US-09-925-065A-536043	Sequence 536043,
C 910	229.8	10.1	46215	15	US-10-995-561-13483	Sequence 13483, A	C 983	229.4	10.0	619	5	US-09-925-065A-536043	Sequence 536043,
C 911	229.8	10.1	66972	7	US-10-087-192-556	Sequence 556, App	C 984	229.4	10.0	713	4	US-09-925-065A-93712	Sequence 93712, A
C 912	229.8	10.1	75007	9	US-10-741-601-5612	Sequence 5612, App	C 985	229.4	10.0	713	4	US-09-925-065A-93712	Sequence 93712, A
C 913	229.8	10.1	75007	10	US-10-741-600-17556	Sequence 17556, A	C 986	229.4	10.0	713	13	US-10-301-480-194954	Sequence 194954,
C 914	229.8	10.1	75007	11	US-10-995-561-13194	Sequence 13194, A	C 987	229.4	10.0	998	7	US-10-027-632-31285	Sequence 31285, A
C 915	229.8	10.1	75007	16	US-10-990-328-93232	Sequence 93232, A	C 988	229.4	10.0	998	8	US-10-027-632-31285	Sequence 31285, A
C 916	229.8	10.1	149133	16	US-10-990-328-94291	Sequence 94291, A	C 989	229.4	10.0	1000	21	US-11-266-748A-205592	Sequence 205592,
C 917	229.8	10.1	152335	20	US-11-121-086-67	Sequence 67, Appl	C 990	229.4	10.0	1412	4	US-09-925-065A-63600	Sequence 63600, A
C 918	229.8	10.1	179666	20	US-11-121-086-67	Sequence 67, Appl	C 991	229.4	10.0	1412	4	US-09-925-065A-63601	Sequence 63601, A
C 919	229.8	10.1	318999	16	US-10-990-328-94160	Sequence 94160, A	C 992	229.4	10.0	1412	4	US-09-925-065A-63602	Sequence 63602, A
C 920	229.8	10.1	368716	23	US-11-033-056A-38696	Sequence 38696, A	C 993	229.4	10.0	1412	4	US-09-925-065A-63603	Sequence 63603, A
C 921	229.8	10.1	483728	10	US-10-699-158-2	Sequence 2, Appl	C 994	229.4	10.0	1412	5	US-09-925-065A-63600	Sequence 63600, A
C 922	229.8	10.1	816609	22	US-11-073-360-1606	Sequence 1606, App	C 995	229.4	10.0	1412	5	US-09-925-065A-63601	Sequence 63601, A
C 923	229.8	10.1	1080000	11	US-10-928-446A-1	Sequence 1, Appl	C 996	229.4	10.0	1412	5	US-09-925-065A-63602	Sequence 63602, A
C 924	229.8	10.1	1080000	11	US-10-928-446A-181	Sequence 181, App	C 997	229.4	10.0	1412	5	US-09-925-065A-63603	Sequence 63603, A
C 925	229.8	10.1	1080000	11	US-10-928-446A-183	Sequence 183, App	C 998	229.4	10.0	1412	13	US-10-301-480-164838	Sequence 164838,
C 926	229.8	10.1	1080000	11	US-10-928-446A-185	Sequence 185, App	C 999	229.4	10.0	1412	13	US-10-301-480-164839	Sequence 164839,
C 927	229.8	10.1	1080000	11	US-10-928-446A-187	Sequence 187, App	C1000	229.4	10.0	1412	13	US-10-301-480-164840	Sequence 164840,
C 928	229.8	10.1	1080000	11	US-10-928-446A-189	Sequence 189, App	C1001	229.4	10.0	1412	13	US-10-301-480-164841	Sequence 164841,
C 929	229.8	10.1	1080000	11	US-10-928-446A-191	Sequence 191, App	C1002	229.4	10.0	1412	13	US-10-301-480-164842	Sequence 164842,
C 930	229.8	10.1	1080000	11	US-10-928-446A-193	Sequence 193, App	C1003	229.4	10.0	1412	13	US-10-301-480-778247	Sequence 778247,
C 931	229.8	10.1	1080000	11	US-10-928-446A-195	Sequence 195, App	C1004	229.4	10.0	1412	13	US-10-301-480-778248	Sequence 778248,
C 932	229.8	10.1	1080000	11	US-10-928-446A-197	Sequence 197, App	C1005	229.4	10.0	1412	13	US-10-301-480-778249	Sequence 778249,
C 933	229.8	10.1	1080000	11	US-10-928-446A-199	Sequence 199, App	C1006	229.4	10.0	2300	27	US-11-636-385-35742	Sequence 35742, A
C 934	229.8	10.1	1080000	11	US-10-928-446A-199	Sequence 199, App	C1007	229.4	10.0	27499	9	US-10-367-094-111	Sequence 111, App
C 935	229.8	10.1	1656406	23	US-11-033-056A-37967	Sequence 37967, A	C1008	229.4	10.0	28693	11	US-10-995-561-13341	Sequence 13341, A
C 936	229.6	10.1	1645	16	US-10-917-503-13851	Sequence 13851, A	C1009	229.4	10.0	37976	16	US-10-940-774-13441	Sequence 13441, A
C 937	229.6	10.1	1645	26	US-11-443-428A-237126	Sequence 237126, A	C1010	229.4	10.0	42790	21	US-11-266-748A-23980	Sequence 23980, A
C 938	229.6	10.1	2300	27	US-11-636-385-18680	Sequence 18680, A	C1011	229.4	10.0	67810	7	US-10-087-192-1738	Sequence 1738, App
C 939	229.6	10.1	12945	16	US-10-990-328-97961	Sequence 97961, A	C1012	229.4	10.0	72602	16	US-10-940-774-14385	Sequence 14385, A
C 940	229.6	10.1	14050	16	US-10-990-328-93390	Sequence 93390, A	C1013	229.4	10.0	79417	16	US-10-990-328-93614	Sequence 93614, A
C 941	229.6	10.1	15696	15	US-10-105-299-7386	Sequence 7386, App	C1014	229.4	10.0	95597	16	US-10-990-328-95297	Sequence 95297, A
C 942	229.6	10.1	15696	16	US-10-868-184-5235	Sequence 5235, App	C1015	229.4	10.0	98302	16	US-10-940-774-16847	Sequence 16847, A
C 943	229.6	10.1	20840	16	US-10-940-774-14115	Sequence 14115, A	C1016	229.4	10.0	112507	16	US-10-940-774-12420	Sequence 12420, A
C 944	229.6	10.1	21850	12	US-10-330-773-474	Sequence 474, App	C1017	229.4	10.0	112507	16	US-10-940-774-12794	Sequence 12794, A
C 945	229.6	10.1	21850	14	US-10-540-898-474	Sequence 474, App	C1018	229.4	10.0	112508	16	US-10-940-774-16589	Sequence 16589, A
C 946	229.6	10.1	32248	7	US-09-764-860-802	Sequence 802, App	C1019	229.4	10.0	112508	16	US-10-940-774-16590	Sequence 16590, A
C 947	229.6	10.1	32248	7	US-10-074-095-802	Sequence 802, App	C1020	229.4	10.0	113042	16	US-10-940-774-12343	Sequence 12343, A
C 948	229.6	10.1	32248	8	US-10-212-872-802	Sequence 802, App	C1021	229.4	10.0	113042	16	US-10-940-774-15246	Sequence 15246, A
C 949	229.6	10.1	36731	16	US-10-940-774-13770	Sequence 13770, A	C1022	229.4	10.0	119472	10	US-10-741-600-17865	Sequence 17865, A
C 950	229.6	10.1	40441	16	US-10-990-328-96946	Sequence 96946, A	C1023	229.4	10.0	121053	16	US-10-990-328-95324	Sequence 95324, A
C 951	229.6	10.1	64291	16	US-10-940-774-16278	Sequence 16278, A	C1024	229.4	10.0	125522	23	US-11-033-056A-37659	Sequence 37659, A
C 952	229.6	10.1	79977	11	US-10-737-082-58	Sequence 58, Appl	C1025	229.4	10.0	128668	7	US-10-087-192-340	Sequence 340, App
C 953	229.6	10.1	79977	11	US-10-765-790-58	Sequence 58, Appl	C1026	229.4	10.0	129042	7	US-10-087-192-1240	Sequence 1240, App
C 954	229.6	10.1	84587	16	US-10-940-774-15733	Sequence 15733, A	C1027	229.4	10.0	162025	3	US-09-834-700-13	Sequence 13, Appl
C 955	229.6	10.1	113033	16	US-10-990-328-95526	Sequence 95526, A	C1028	229.4	10.0	162025	3	US-09-834-700-14	Sequence 14, Appl
C 956	229.6	10.1	117410	16	US-10-940-774-12262	Sequence 12262, A	C1029	229.4	10.0	162025	3	US-09-834-700-17	Sequence 17, Appl
C 957	229.6	10.1	121033	17	US-10-674-575-1159	Sequence 1159, App	C1030	229.4	10.0	162025	3	US-09-834-700-18	Sequence 18, Appl
C 958	229.6	10.1	133632	7	US-10-087-192-1810	Sequence 1810, App	C1031	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 959	229.6	10.1	133632	14	US-10-669-920-805	Sequence 805, App	C1032	229.4	10.0	162025	8	US-10-272-665-36	Sequence 36, Appl
C 960	229.6	10.1	144362	16	US-10-940-774-16066	Sequence 16066, A	C1033	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 961	229.6	10.1	171452	23	US-11-033-056A-36473	Sequence 36473, A	C1034	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 962	229.6	10.1	193689	16	US-10-990-328-93508	Sequence 93508, A	C1035	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 963	229.6	10.1	198522	7	US-10-087-192-244	Sequence 244, App	C1036	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 964	229.6	10.1	304905	9	US-10-271-416-1	Sequence 1, Appl	C1037	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 965	229.6	10.1	332350	23	US-11-033-056A-38154	Sequence 38154, A	C1038	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
C 966	229.6	10.1	567564	10	US-10-699-156-3	Sequence 3, Appl	C1039	229.4	10.0	162025	17	US-10-548-336A-13	Sequence 13, Appl
C 967	229.6	10.1	699032	16	US-10-990-328-96764	Sequence 96764, A	C1040	229.4	10.0	162025	17	US-10-548-336A-14	Sequence 14, Appl
C 968	229.6	10.1	766455	16	US-10-990-328-98054	Sequence 98054, A	C1041	229.4	10.0	162025	17	US-10-548-336A-18	Sequence 18, Appl
C 969	229.4	10.0	571	4	US-09-925-065A-327160	Sequence 327160, A	C1042	229.4	10.0	162025	17	US-10-548-336A-18	Sequence 18, Appl
C 970	229.4	10.0	571	4	US-09-925-065A-327161	Sequence 327161, A	C1043	229.4	10.0	177077	16	US-10-940-774-14125	Sequence 14125, A
C 971	229.4	10.0	571	5	US-09-925-065A-327161	Sequence 327161, A	C1044	229.4	10.0	179012	16	US-10-990-328-94764	Sequence 94764, A
C 972	229.4	10.0	571	5	US-09-925-065A-327161	Sequence 327161, A	C1045	229.4	10.0	183873	16	US-10-990-328-93609	Sequence 93609, A
C 973	229.4	10.0	576	13	US-10-301-480-401206	Sequence 401206, A	C1046	229.4	10.0	186391	7	US-10-087-192-136	Sequence 136, App
C 974	229.4	10.0	576	13	US-10-301-480-401207	Sequence 401207, A	C1047	229.4	10.0	225587	12	US-10-330-773-374	Sequence 374, App

1048	229.4	10.0	225587	14	US-10-540-898-374	Sequence 374, App	1121	229	10.0	2246	26	US-11-443-428A-362345	Sequence 362345,
1049	229.4	10.0	227979	16	US-10-940-774-11842	Sequence 11842, A	1122	229	10.0	2281	26	US-11-443-428A-362359	Sequence 362359,
c1050	229.4	10.0	349863	16	US-10-990-328-94039	Sequence 94039, A	1123	229	10.0	2300	27	US-11-636-385-286	Sequence 286, App
c1051	229.4	10.0	405740	25	US-11-066-316A-9907	Sequence 9907, Ap	1124	229	10.0	2300	27	US-11-636-385-28167	Sequence 28167, A
c1052	229.4	10.0	435039	16	US-10-990-328-97683	Sequence 97683, A	1125	229	10.0	2300	27	US-11-636-385-38310	Sequence 38310, A
1053	229.4	10.0	443039	14	US-10-669-920-1185	Sequence 1185, Ap	1126	229	10.0	2311	26	US-11-443-428A-362339	Sequence 362339,
1054	229.4	10.0	452182	23	US-11-033-056A-36232	Sequence 36232, A	1127	229	10.0	2437	26	US-11-443-428A-362340	Sequence 362340,
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c1056	229.4	10.0	505854	16	US-10-990-328-94315	Sequence 94315, A	1129	229	10.0	2495	11	US-10-872-229-104	Sequence 104, App
c1057	229.2	10.0	454	10	US-10-357-930-50096	Sequence 50096, A	1130	229	10.0	2495	11	US-10-872-229-104	Sequence 104, App
c1058	229.2	10.0	601	16	US-10-940-774-114088	Sequence 114088,	1131	229	10.0	2539	26	US-11-443-428A-362360	Sequence 362360,
c1059	229.2	10.0	601	16	US-10-940-774-154401	Sequence 154401,	1132	229	10.0	3961	3	US-09-764-891-6205	Sequence 6205, Ap
c1060	229.2	10.0	601	16	US-10-940-774-154402	Sequence 154402,	1133	229	10.0	3961	3	US-09-764-891-6205	Sequence 6206, Ap
1061	229.2	10.0	656	4	US-09-925-065A-675446	Sequence 675446,	1134	229	10.0	9900	16	US-10-940-774-13392	Sequence 13392, A
1062	229.2	10.0	656	5	US-09-925-065A-675446	Sequence 675446,	1135	229	10.0	10758	3	US-09-764-869-1647	Sequence 1647, Ap
1063	229.2	10.0	759	7	US-10-027-632-147208	Sequence 147208,	1136	229	10.0	10758	3	US-09-764-869-1650	Sequence 1650, Ap
1064	229.2	10.0	759	7	US-10-027-632-147209	Sequence 147209,	1137	229	10.0	10758	7	US-10-091-504-1647	Sequence 1647, Ap
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1066	229.2	10.0	759	8	US-10-027-632-147209	Sequence 147209,	1139	229	10.0	10758	8	US-10-227-577-1647	Sequence 1647, Ap
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c1068	229.2	10.0	2300	27	US-11-636-385-18004	Sequence 18004, A	1141	229	10.0	10759	3	US-09-764-869-1649	Sequence 1649, Ap
c1069	229.2	10.0	2300	27	US-11-636-385-19010	Sequence 19010, A	1142	229	10.0	10759	3	US-09-764-869-1649	Sequence 1649, Ap
c1070	229.2	10.0	2300	27	US-11-636-385-31359	Sequence 31359, A	1143	229	10.0	10759	7	US-10-091-504-1649	Sequence 1649, Ap
1071	229.2	10.0	19377	16	US-10-940-774-15198	Sequence 15198, A	1144	229	10.0	10759	7	US-10-091-504-1649	Sequence 1649, Ap
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c1073	229.2	10.0	28874	16	US-10-990-328-93465	Sequence 93465, A	1146	229	10.0	10759	7	US-10-091-504-1649	Sequence 1649, Ap
c1074	229.2	10.0	31670	8	US-10-004-113-22	Sequence 22, Appl	1147	229	10.0	10759	8	US-10-227-577-1649	Sequence 1649, Ap
c1075	229.2	10.0	31670	15	US-10-035-833-974	Sequence 974, App	1148	229	10.0	12585	16	US-10-990-328-97219	Sequence 97219, A
c1076	229.2	10.0	31670	22	US-11-330-648-22	Sequence 22, Appl	1149	229	10.0	18328	16	US-10-990-328-9323	Sequence 9323, A
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c1078	229.2	10.0	32111	23	US-11-033-056A-35657	Sequence 35657, A	1151	229	10.0	33870	16	US-10-990-328-97220	Sequence 97220, A
c1079	229.2	10.0	32111	23	US-11-033-056A-35658	Sequence 35658, A	1152	229	10.0	36578	10	US-10-741-600-17600	Sequence 17600, A
c1080	229.2	10.0	32111	23	US-11-033-056A-35659	Sequence 35659, A	1153	229	10.0	36578	16	US-10-990-328-93825	Sequence 93825, A
c1081	229.2	10.0	32111	23	US-11-033-056A-38047	Sequence 38047, A	1154	229	10.0	65745	16	US-10-940-774-12591	Sequence 12591, A
1082	229.2	10.0	42808	23	US-11-033-056A-36928	Sequence 36928, A	1155	229	10.0	65745	16	US-10-940-774-12591	Sequence 12591, A
1083	229.2	10.0	50694	23	US-11-033-056A-36122	Sequence 36122, A	1156	229	10.0	65813	23	US-11-033-056A-36364	Sequence 36364, A
1084	229.2	10.0	52317	16	US-10-990-328-94375	Sequence 94375, A	1157	229	10.0	65813	23	US-11-033-056A-36365	Sequence 36365, A
c1085	229.2	10.0	52715	16	US-10-990-328-97873	Sequence 97873, A	1158	229	10.0	74562	23	US-11-033-056A-38685	Sequence 38685, A
1086	229.2	10.0	54070	16	US-10-990-328-94433	Sequence 94433, A	1159	229	10.0	85920	14	US-10-669-920-938	Sequence 938, App
c1087	229.2	10.0	69821	23	US-11-033-056A-38626	Sequence 38626, A	1160	229	10.0	151754	16	US-10-990-328-95375	Sequence 95375, A
c1088	229.2	10.0	129554	23	US-11-033-543-755	Sequence 755, App	1161	229	10.0	201143	21	US-10-240-425-1099	Sequence 1099, Ap
c1089	229.2	10.0	143418	23	US-11-033-056A-36118	Sequence 36118, A	1162	229	10.0	431987	21	US-11-266-748A-28210	Sequence 28210, A
c1090	229.2	10.0	146656	20	US-11-121-086-68	Sequence 68, Appl	1163	228.8	10.0	452163	23	US-11-033-056A-37365	Sequence 37365, A
c1091	229.2	10.0	193169	16	US-10-940-774-15091	Sequence 15091, A	1164	228.8	10.0	560	4	US-09-925-065A-589226	Sequence 589226,
c1092	229.2	10.0	203249	23	US-11-033-056A-36674	Sequence 36674, A	1165	228.8	10.0	560	5	US-09-925-065A-589226	Sequence 589226,
1093	229.2	10.0	601	4	US-09-925-065A-811520	Sequence 811520,	1166	228.8	10.0	601	16	US-11-443-428A-250605	Sequence 250605,
1094	229.2	10.0	601	4	US-09-925-065A-812401	Sequence 812401,	1167	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
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c1097	229.2	10.0	601	16	US-10-940-774-51144	Sequence 51144, A	1170	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
c1098	229.2	10.0	601	16	US-10-940-774-109427	Sequence 109427,	1171	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
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c1103	229.2	10.0	713	4	US-09-925-065A-93711	Sequence 93711, A	1176	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
c1104	229.2	10.0	713	5	US-09-925-065A-93711	Sequence 93711, A	1177	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
c1105	229.2	10.0	713	5	US-10-301-480-194953	Sequence 194953,	1178	228.8	10.0	839	26	US-10-301-480-1218700	Sequence 1218700,
c1106	229.2	10.0	713	13	US-10-301-480-808362	Sequence 808362,	1179	228.8	10.0	839	26	US-10-301-480-1218700	Sequence 1218700,
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c1112	229.2	10.0	988	13	US-10-301-480-578759	Sequence 578759,	1185	228.8	10.0	839	26	US-10-301-480-1218700	Sequence 1218700,
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c1114	229.2	10.0	988	13	US-10-301-480-1192168	Sequence 1192168,	1187	228.8	10.0	839	26	US-10-301-480-1218700	Sequence 1218700,
c1115	229.2	10.0	988	13	US-10-301-480-1192169	Sequence 1192169,	1188	228.8	10.0	839	26	US-10-301-480-1218700	Sequence 1218700,
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c1197	228.6	10.0	10093	3	US-09-764-869-1390	Sequence 1390, Ap	1270	228.2	10.0	407	3	US-09-803-719-1531	Sequence 1531, Ap
c1198	228.6	10.0	10093	3	US-10-091-504-1390	Sequence 1390, Ap	1271	228.2	10.0	407	11	US-10-779-543-14801	Sequence 14801, A
c1199	228.6	10.0	10093	8	US-10-227-577-1390	Sequence 1390, Ap	1272	228.2	10.0	546	4	US-09-925-065A-799095	Sequence 799095,
c1200	228.6	10.0	10093	8	US-10-100-683-11550	Sequence 11550, A	1273	228.2	10.0	546	5	US-09-925-065A-799095	Sequence 799095,
c1201	228.6	10.0	10093	23	US-11-001-793-11550	Sequence 11550, A	c1274	228.2	10.0	601	16	US-10-940-774-64990	Sequence 64990, A
1202	228.6	10.0	13203	16	US-10-940-774-17544	Sequence 17544, A	c1275	228.2	10.0	601	16	US-10-940-774-178794	Sequence 178794,
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1204	228.6	10.0	28693	16	US-10-990-328-96937	Sequence 96937, A	1277	228.2	10.0	601	23	US-11-033-545-9469	Sequence 9469, Ap
1205	228.6	10.0	28693	10	US-10-741-600-17761	Sequence 17761, A	1278	228.2	10.0	604	4	US-09-925-065A-799096	Sequence 799096,
c1206	228.6	10.0	34110	16	US-10-990-328-93738	Sequence 93738, A	1279	228.2	10.0	604	5	US-09-925-065A-799096	Sequence 799096,
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c1208	228.6	10.0	46725	16	US-10-940-774-15680	Sequence 15680, A	c1281	228.2	10.0	635	5	US-09-925-065A-856307	Sequence 856307,
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1210	228.6	10.0	48453	23	US-11-033-056A-35921	Sequence 35921, A	1283	228.2	10.0	1437	5	US-09-925-065A-694852	Sequence 694852,
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1212	228.6	10.0	98828	16	US-10-940-774-16630	Sequence 16630, A	c1285	228.2	10.0	3208	25	US-11-437-797-367	Sequence 367, App
1213	228.6	10.0	112141	16	US-10-990-328-93217	Sequence 93217, A	1286	228.2	10.0	11850	8	US-10-017-161-669	Sequence 669, App
1214	228.6	10.0	161323	16	US-10-990-328-94088	Sequence 94088, A	1287	228.2	10.0	24486	16	US-10-990-328-95087	Sequence 95087, A
1215	228.6	10.0	164875	8	US-10-085-117-322	Sequence 322, App	1288	228.2	10.0	32726	16	US-10-990-328-95087	Sequence 95087, A
1216	228.6	10.0	166004	23	US-11-417-450-26	Sequence 26, Appl	c1289	228.2	10.0	34547	15	US-10-105-299-7482	Sequence 7482, Ap
c1217	228.6	10.0	166111	20	US-11-112-908-47	Sequence 47, Appl	c1290	228.2	10.0	34547	15	US-10-868-184-5331	Sequence 5331, Ap
c1218	228.6	10.0	168298	17	US-10-674-575-90	Sequence 90, Appl	c1291	228.2	10.0	35574	16	US-10-990-328-94436	Sequence 94436, A
1219	228.6	10.0	188409	23	US-11-417-450-27	Sequence 27, Appl	c1292	228.2	10.0	58191	16	US-10-990-328-97833	Sequence 97833, A
c1220	228.6	10.0	223051	16	US-10-990-328-94106	Sequence 94106, A	1293	228.2	10.0	60593	16	US-10-940-774-13779	Sequence 13779, A
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1222	228.6	10.0	257744	16	US-10-990-328-94040	Sequence 94040, A	1295	228.2	10.0	61985	23	US-11-033-056A-36230	Sequence 36230, A
1223	228.6	10.0	294836	16	US-10-940-774-15974	Sequence 15974, A	1296	228.2	10.0	61985	23	US-11-033-056A-36231	Sequence 36231, A
c1224	228.6	10.0	312470	7	US-10-940-774-14043	Sequence 14043, A	c1297	228.2	10.0	63588	7	US-10-243-735-3	Sequence 3, Appli
1225	228.6	10.0	330973	16	US-10-087-192-1498	Sequence 1498, Ap	c1298	228.2	10.0	63588	9	US-10-730-010-3	Sequence 3, Appli
c1226	228.6	10.0	36024	16	US-10-940-774-12373	Sequence 12373, A	c1299	228.2	10.0	73909	23	US-11-033-056A-38645	Sequence 38645, A
1227	228.6	10.0	505854	16	US-10-990-328-94315	Sequence 94315, A	c1300	228.2	10.0	84171	16	US-10-940-774-16356	Sequence 16356, A
1228	228.4	10.0	599	4	US-09-925-065A-557593	Sequence 557593, A	1301	228.2	10.0	87417	17	US-10-674-575-155	Sequence 155, App
1229	228.4	10.0	599	5	US-09-925-065A-557593	Sequence 557593, A	1302	228.2	10.0	156321	13	US-10-960-414-483	Sequence 483, App
c1230	228.4	10.0	626	4	US-09-925-065A-709437	Sequence 709437, A	1303	228.2	10.0	163487	23	US-11-033-056A-36408	Sequence 36408, A
c1231	228.4	10.0	626	5	US-09-925-065A-709437	Sequence 709437, A	c1304	228.2	10.0	171660	23	US-11-033-056A-38706	Sequence 38706, A
1232	228.4	10.0	874	13	US-10-301-480-571170	Sequence 571170, A	c1305	228.2	10.0	173787	16	US-10-940-774-12542	Sequence 12542, A
1233	228.4	10.0	874	13	US-10-301-480-571170	Sequence 1184579, A	c1306	228.2	10.0	173791	16	US-10-940-774-17302	Sequence 17302, A
c1234	228.4	10.0	1000	21	US-11-266-748A-196274	Sequence 196274, A	c1307	228.2	10.0	193702	16	US-10-796-307-8804	Sequence 8804, Ap
c1235	228.4	10.0	2300	27	US-11-636-385-2368	Sequence 2368, Ap	1308	228.2	10.0	254025	23	US-11-033-056A-36184	Sequence 36184, A
1236	228.4	10.0	2300	27	US-11-636-385-25642	Sequence 25642, A	c1309	228.2	10.0	285020	7	US-10-087-192-1666	Sequence 1666, Ap
c1237	228.4	10.0	12458	10	US-10-100-683-12638	Sequence 12638, A	c1310	228.2	10.0	430700	23	US-11-033-056A-37994	Sequence 37994, A
c1238	228.4	10.0	12458	3	US-11-001-793-12638	Sequence 12638, A	c1311	228.2	10.0	757875	23	US-11-033-056A-38439	Sequence 38439, A
c1239	228.4	10.0	15849	3	US-09-880-107-2362	Sequence 2362, Ap	1312	228	10.0	601	16	US-10-940-774-66391	Sequence 66391, A
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SUMMARIES

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14	217.6	9.5	5232	8	US-11-509-784-3
15	217.6	9.5	5915	8	US-11-699-930-11
16	217.6	9.5	5915	8	US-11-699-930-12
17	217.6	9.5	5915	8	US-11-699-930-13
18	217.6	9.5	5915	8	US-11-699-930-14
19	217.6	9.5	5915	8	US-11-699-930-16
20	217.4	9.5	87723	8	US-11-505-577-13
21	217	9.5	310268	8	US-11-257-477-195
22	216	9.5	5915	8	US-11-699-930-15
23	215.6	9.4	277616	8	US-11-257-477-83
24	214.2	9.4	87723	8	US-11-505-577-13
25	213.4	9.3	1666	8	US-11-713-306-7

C 26	212.8	9.3	290547	8	US-11-257-477-77	Sequence 77, Appl
C 27	212.4	9.3	83517	8	US-11-257-477-50	Sequence 50, Appl
C 28	212	9.3	138363	8	US-11-257-477-117	Sequence 117, Appl
C 29	211.8	9.3	49356	8	US-11-257-477-66	Sequence 66, Appl
C 30	210.8	9.2	102790	8	US-11-257-477-163	Sequence 163, Appl
C 31	210.6	9.2	310268	8	US-11-257-477-195	Sequence 195, Appl
C 32	210.4	9.2	10616	8	US-11-600-739-3	Sequence 3, Appl
C 33	210	9.2	49175	8	US-11-257-477-4	Sequence 4, Appl
C 34	209.8	9.2	69034	8	US-11-699-785-6	Sequence 6, Appl
C 35	208.6	9.1	29328	8	US-11-257-477-189	Sequence 189, Appl
C 36	208.6	9.1	49356	8	US-11-257-477-66	Sequence 66, Appl
C 37	208.2	9.1	26815	8	US-11-257-477-26	Sequence 26, Appl
C 38	208.2	9.1	117750	8	US-11-257-477-169	Sequence 169, Appl
C 39	208	9.1	1601	8	US-10-533-069-642	Sequence 642, Appl
C 40	207.8	9.1	130505	8	US-11-257-477-10	Sequence 10, Appl
C 41	207.6	9.1	142976	8	US-11-257-477-99	Sequence 99, Appl
C 42	207.6	9.1	277616	8	US-11-257-477-83	Sequence 83, Appl
C 43	206.4	9.0	42450	8	US-11-730-664-3	Sequence 3, Appl
C 44	206	9.0	47096	8	US-11-257-477-151	Sequence 151, Appl
C 45	205.8	9.0	7967	1	US-10-568-695-1	Sequence 1, Appl
C 46	205.8	9.0	9821	1	US-10-568-695-2	Sequence 2, Appl
C 47	205.6	9.0	21808	8	US-11-698-245-6	Sequence 6, Appl
C 48	205.4	9.0	28778	8	US-11-657-313-6	Sequence 6, Appl
C 49	205.2	9.0	3495	8	US-11-738-671-19	Sequence 19, Appl
C 50	204.6	9.0	5932	1	US-10-533-069-1145	Sequence 1145, Ap
C 51	204.2	8.9	518360	8	US-11-257-477-125	Sequence 125, Appl
C 52	204	8.9	1024	8	US-11-599-517-87	Sequence 87, Appl
C 53	203.8	8.9	59194	8	US-11-655-858-22	Sequence 22, Appl
C 54	203.8	8.9	65423	8	US-11-257-477-32	Sequence 32, Appl
C 55	203.6	8.9	125958	8	US-11-505-577-26	Sequence 26, Appl
C 56	203.4	8.9	163382	8	US-11-257-477-179	Sequence 179, Appl
C 57	203.4	8.9	102790	8	US-11-257-477-163	Sequence 163, Appl
C 58	203	8.9	59365	8	US-11-257-477-74	Sequence 74, Appl
C 59	202.8	8.9	2468	8	US-11-551-744-100	Sequence 100, Appl
C 60	202.4	8.9	2213	8	US-11-552-437-169	Sequence 169, Appl
C 61	202.2	8.9	47096	8	US-11-257-477-151	Sequence 151, Appl
C 62	202	8.8	2044	1	US-10-533-069-13	Sequence 13, Appl
C 63	201.8	8.8	24810	8	US-11-257-477-145	Sequence 145, Appl
C 64	201.8	8.8	29018	8	US-11-257-477-105	Sequence 105, Appl
C 65	201.8	8.8	37961	8	US-11-257-477-16	Sequence 16, Appl
C 66	201.8	8.8	130505	8	US-11-257-477-10	Sequence 10, Appl
C 67	201.8	8.8	149082	8	US-11-257-477-93	Sequence 93, Appl
C 68	201.6	8.8	28778	8	US-11-657-313-6	Sequence 6, Appl
C 69	201.4	8.8	21808	8	US-11-698-245-6	Sequence 6, Appl
C 70	201.2	8.8	1710	8	US-11-407-888-17	Sequence 17, Appl
C 71	201.2	8.8	85389	8	US-11-498-489-25	Sequence 25, Appl
C 72	200.8	8.8	2112	1	US-10-533-069-1542	Sequence 1542, Ap
C 73	200.8	8.8	2673	1	US-10-562-377-33	Sequence 33, Appl
C 74	200.8	8.8	3915	8	US-11-699-930-8	Sequence 8, Appl
C 75	200.8	8.8	12169	8	US-11-656-316-16	Sequence 16, Appl
C 76	200.8	8.8	23965	8	US-11-257-477-139	Sequence 139, Appl
C 77	200.8	8.8	50927	8	US-11-257-477-56	Sequence 56, Appl
C 78	200	8.8	59365	8	US-11-257-477-74	Sequence 74, Appl
C 79	199.8	8.7	27499	8	US-11-257-477-111	Sequence 111, Appl
C 80	199.6	8.7	2508	1	US-10-562-377-34	Sequence 34, Appl
C 81	199.6	8.7	15418	8	US-11-710-864-1	Sequence 1, Appl
C 82	199.4	8.7	4196	1	US-10-533-069-1684	Sequence 1684, Ap
C 83	199.4	8.7	7012	1	US-11-607-348A-38	Sequence 38, Appl
C 84	199.2	8.7	2425	1	US-10-533-069-616	Sequence 616, Appl
C 85	198.8	8.7	22685	8	US-11-629-808-8	Sequence 8, Appl
C 86	198.8	8.7	40782	1	US-10-592-435-11	Sequence 11, Appl
C 87	198.4	8.7	2487	8	US-11-365-630-18	Sequence 18, Appl
C 88	198.4	8.7	2499	8	US-11-365-630-17	Sequence 17, Appl
C 89	198.4	8.7	2601	8	US-11-365-630-16	Sequence 16, Appl
C 90	198.4	8.7	6669	8	US-11-509-784-5	Sequence 5, Appl
C 91	198.4	8.7	29328	8	US-11-257-477-189	Sequence 189, Appl
C 92	198.4	8.7	59194	8	US-11-655-858-22	Sequence 22, Appl
C 93	197.8	8.7	10001	8	US-11-615-454-13	Sequence 13, Appl
C 94	197.6	8.7	5857	1	US-10-533-069-1003	Sequence 1003, Ap
C 95	197.6	8.7	45944	8	US-11-257-477-38	Sequence 38, Appl
C 96	197.6	8.7	85389	8	US-11-498-489-25	Sequence 25, Appl
C 97	197.2	8.6	4910	1	US-10-533-069-1983	Sequence 1983, Ap
C 98	197.2	8.6	10001	8	US-11-615-454-12	Sequence 12, Appl

C 99	197.2	8.6	10001	8	US-11-615-454-13	Sequence 13, Appl	172	183.4	8.0	4132	1	US-10-533-069-473	Sequence 473, Appl
C 100	196.8	8.6	3580	8	US-11-551-744-59	Sequence 99, Appl	C 173	183.2	8.0	2308	1	US-10-562-377-18	Sequence 18, Appl
C 101	196.4	8.6	17788	8	US-11-498-489-38	Sequence 38, Appl	C 174	183.2	8.0	2308	8	US-11-407-888-11	Sequence 11, Appl
C 102	196.2	8.6	4445	1	US-10-533-069-1223	Sequence 1223, Ap	C 175	183.2	8.0	4286	8	US-11-615-454-5	Sequence 5, Appl
C 103	196	8.6	7080	8	US-11-703-333-12	Sequence 12, Appl	C 176	183	8.0	1784	8	US-11-595-320-1	Sequence 1, Appl
C 104	196	8.6	138363	8	US-11-257-477-117	Sequence 117, Appl	C 177	182.8	8.0	2673	1	US-10-562-377-33	Sequence 33, Appl
C 105	195.8	8.6	42450	8	US-11-730-664-3	Sequence 3, Appl	C 178	182.6	8.0	1255	1	US-10-533-069-1121	Sequence 1121, Ap
C 106	195.2	8.5	49175	8	US-11-257-477-4	Sequence 4, Appl	C 179	182.6	8.0	1632	1	US-10-533-069-119	Sequence 119, Appl
C 107	195	8.5	1015	8	US-11-632-012-49	Sequence 49, Appl	C 180	182.6	8.0	2604	1	US-10-533-069-439	Sequence 439, Appl
C 108	195	8.5	2308	8	US-10-533-069-600	Sequence 600, Appl	C 181	181.8	8.0	2176	1	US-10-533-069-2322	Sequence 2322, Ap
C 109	195	8.5	5338	1	US-10-533-069-1036	Sequence 1036, Ap	C 182	181.8	8.0	4028	1	US-10-533-069-1739	Sequence 1739, Ap
C 110	194.8	8.5	149062	8	US-11-257-477-93	Sequence 93, Appl	C 183	181.6	8.0	9229	1	US-10-594-969-3	Sequence 3, Appl
C 111	194.6	8.5	2439	8	US-11-112-327-32	Sequence 32, Appl	C 184	181.4	7.9	12169	8	US-11-656-116-16	Sequence 16, Appl
C 112	194.6	8.5	2448	8	US-11-112-327-24	Sequence 24, Appl	C 185	181.2	7.9	2547	1	US-10-533-069-1969	Sequence 1969, Ap
C 113	194.6	8.5	4592	8	US-11-498-489-26	Sequence 26, Appl	C 186	180.2	7.9	5232	8	US-11-509-784-3	Sequence 3, Appl
C 114	194.6	8.5	4592	8	US-11-498-489-26	Sequence 28, Appl	C 187	179.4	7.9	735	8	US-11-632-012-42	Sequence 42, Appl
C 115	194.6	8.5	17788	8	US-11-498-489-38	Sequence 38, Appl	C 188	179.4	7.9	735	8	US-11-680-414-17	Sequence 17, Appl
C 116	194.4	8.5	4098	8	US-11-365-630-5	Sequence 5, Appl	C 189	178.8	7.8	1177	8	US-11-552-437-211	Sequence 211, App
C 117	194.2	8.5	24810	8	US-11-257-477-145	Sequence 145, Appl	C 190	178.6	7.8	2688	1	US-10-533-069-1731	Sequence 1731, App
C 118	193.6	8.5	9229	1	US-10-594-969-3	Sequence 3, Appl	C 191	177.8	7.8	1683	1	US-10-533-069-1586	Sequence 1586, Ap
C 119	193	8.5	21478	8	US-11-257-477-201	Sequence 201, Appl	C 192	177.8	7.8	2040	1	US-10-533-069-2389	Sequence 2389, Ap
C 120	192.8	8.4	3105	8	US-11-551-744-156	Sequence 156, Appl	C 193	177.8	7.8	2294	8	US-11-552-437-181	Sequence 181, App
C 121	192.8	8.4	9803	1	US-10-565-626-73	Sequence 73, Appl	C 194	177.4	7.8	2446	1	US-10-533-069-1911	Sequence 1911, Ap
C 122	192.8	8.4	9803	1	US-10-565-626-74	Sequence 74, Appl	C 195	177	7.7	1976	8	US-11-234-694-71	Sequence 71, Appl
C 123	192.6	8.4	5207	1	US-10-533-069-2055	Sequence 2055, Ap	C 196	176.4	7.7	2507	1	US-10-533-069-1126	Sequence 1126, Ap
C 124	192.6	8.4	10380	8	US-11-657-766-3	Sequence 3, Appl	C 197	176.2	7.7	2307	1	US-10-533-069-202	Sequence 202, App
C 125	192.4	8.4	5990	8	US-11-407-888-3	Sequence 3, Appl	C 198	176.2	7.7	32677	8	US-11-257-477-133	Sequence 133, App
C 126	192	8.4	5985	1	US-10-565-626-76	Sequence 76, Appl	C 199	175.8	7.7	2698	1	US-10-533-069-2401	Sequence 2401, Ap
C 127	192	8.4	7136	1	US-10-533-069-2395	Sequence 2395, Ap	C 200	175.4	7.7	2377	1	US-10-562-377-7	Sequence 7, Appl
C 128	192	8.4	26815	8	US-11-257-477-26	Sequence 26, Appl	C 201	175.2	7.7	2619	1	US-10-533-069-2271	Sequence 2271, Ap
C 129	192	8.4	142976	8	US-11-257-477-99	Sequence 99, Appl	C 202	175	7.7	2280	1	US-10-565-626-75	Sequence 75, Appl
C 130	191.8	8.4	10380	8	US-11-657-766-3	Sequence 3, Appl	C 203	175	7.7	5985	1	US-10-565-626-76	Sequence 76, Appl
C 131	191.6	8.4	163382	8	US-11-257-477-179	Sequence 179, Appl	C 204	175	7.7	9803	1	US-10-565-626-73	Sequence 73, Appl
C 132	191.2	8.4	37961	8	US-11-257-477-16	Sequence 16, Appl	C 205	175	7.7	9803	1	US-10-565-626-74	Sequence 74, Appl
C 133	190.8	8.4	10616	8	US-11-600-739-3	Sequence 3, Appl	C 206	175	7.7	18524	8	US-11-650-478-12	Sequence 12, Appl
C 134	190.2	8.3	170061	1	US-10-586-772A-1	Sequence 1, Appl	C 207	175	7.7	18524	8	US-11-650-479-12	Sequence 12, Appl
C 135	190	8.3	23965	8	US-11-257-477-139	Sequence 139, Appl	C 208	174.8	7.7	1410	8	US-11-632-012-63	Sequence 63, Appl
C 136	189.6	8.3	50927	8	US-11-257-477-56	Sequence 56, Appl	C 209	174.8	7.7	2475	1	US-10-562-377-1	Sequence 1, Appl
C 137	189.4	8.3	15418	8	US-11-710-864-1	Sequence 1, Appl	C 210	174.8	7.7	2475	1	US-10-562-377-3	Sequence 3, Appl
C 138	189.2	8.3	3941	1	US-10-533-069-1287	Sequence 1287, Ap	C 211	174.2	7.6	3178	1	US-10-533-069-541	Sequence 541, App
C 139	189.2	8.3	21725	8	US-11-700-462-1	Sequence 1, Appl	C 212	174.2	7.6	9963	1	US-10-369-909-14	Sequence 14, Appl
C 140	189	8.3	22685	8	US-11-629-808-8	Sequence 8, Appl	C 213	174	7.6	3381	1	US-10-533-069-311	Sequence 311, App
C 141	188.8	8.3	3999	8	US-11-712-222-5	Sequence 5, Appl	C 214	173.8	7.6	1169	1	US-10-533-069-676	Sequence 676, App
C 142	188.6	8.3	1660	8	US-11-713-306-5	Sequence 5, Appl	C 215	173.4	7.6	12354	8	US-11-596-506-1	Sequence 1, Appl
C 143	188.4	8.2	2368	1	US-10-562-377-21	Sequence 21, Appl	C 216	173	7.6	2990	1	US-10-533-069-2318	Sequence 2318, Ap
C 144	188.2	8.2	2651	1	US-10-533-069-1947	Sequence 1947, Ap	C 217	172.8	7.6	2345	1	US-10-562-377-4	Sequence 4, Appl
C 145	188.2	8.2	5036	8	US-11-365-630-10	Sequence 10, Appl	C 218	172.8	7.6	4429	8	US-11-407-888-55	Sequence 55, Appl
C 146	188	8.2	2818	1	US-10-562-377-20	Sequence 20, Appl	C 219	172.2	7.5	3916	1	US-10-533-069-2354	Sequence 2354, Ap
C 147	188	8.2	3073	8	US-11-234-694-77	Sequence 77, Appl	C 220	170.8	7.5	1180	8	US-11-738-671-21	Sequence 21, Appl
C 148	187.6	8.2	1405	8	US-11-738-671-40	Sequence 40, Appl	C 221	170.8	7.5	3452	1	US-10-533-069-644	Sequence 644, App
C 149	187.2	8.2	1766	8	US-11-234-694-47	Sequence 47, Appl	C 222	170.8	7.5	3452	1	US-10-533-069-830	Sequence 830, App
C 150	186.8	8.2	5659	8	US-11-585-666-44	Sequence 44, Appl	C 223	170.4	7.5	4261	1	US-10-573-215-3	Sequence 3, Appl
C 151	186.8	8.2	12354	8	US-11-596-506-1	Sequence 1, Appl	C 224	170.4	7.5	16781	1	US-10-586-772A-6	Sequence 6, Appl
C 152	186.8	8.2	13602	8	US-11-650-478-1	Sequence 1, Appl	C 225	170.2	7.5	2259	1	US-10-533-459-1	Sequence 1, Appl
C 153	186.8	8.2	13602	8	US-11-650-479-1	Sequence 1, Appl	C 226	169.6	7.4	1295	8	US-11-725-076-8	Sequence 8, Appl
C 154	186.8	8.2	17534	8	US-11-650-478-7	Sequence 7, Appl	C 227	169	7.4	2239	1	US-10-596-627-7	Sequence 7, Appl
C 155	186.8	8.2	17534	8	US-11-650-479-7	Sequence 7, Appl	C 228	168.6	7.4	2420	8	US-11-600-739-4	Sequence 4, Appl
C 156	186.8	8.2	30756	8	US-11-650-478-16	Sequence 16, Appl	C 229	168.4	7.4	5350	1	US-10-533-069-2297	Sequence 2297, Ap
C 157	186.8	8.2	30756	8	US-11-650-479-16	Sequence 16, Appl	C 230	167.8	7.3	2420	8	US-11-600-739-4	Sequence 4, Appl
C 158	186.2	8.2	2910	1	US-10-533-069-531	Sequence 531, Appl	C 231	167.8	7.3	4685	1	US-10-533-069-2175	Sequence 2175, Ap
C 159	186.2	8.2	3322	1	US-10-533-069-136	Sequence 136, Appl	C 232	167.4	7.3	3430	1	US-10-533-069-764	Sequence 764, App
C 160	186.2	8.2	21725	8	US-11-700-462-1	Sequence 1, Appl	C 233	166.6	7.3	1349	1	US-10-533-069-1235	Sequence 1235, Ap
C 161	186.2	8.2	45944	8	US-11-257-477-38	Sequence 38, Appl	C 234	165.6	7.3	1741	1	US-10-533-069-2097	Sequence 2097, Ap
C 162	186	8.1	2956	1	US-10-533-069-1241	Sequence 1241, Ap	C 235	164.2	7.2	6406	1	US-10-533-069-656	Sequence 656, App
C 163	186	8.1	4513	8	US-11-257-477-11	Sequence 11, Appl	C 236	164.2	7.2	40782	1	US-10-592-435-11	Sequence 11, Appl
C 164	185.2	8.1	1185	1	US-10-533-069-1319	Sequence 1319, Ap	C 237	164	7.2	6834	1	US-10-533-069-389	Sequence 389, App
C 165	184.8	8.1	1914	8	US-11-257-477-21	Sequence 21, Appl	C 238	163.6	7.2	2396	1	US-10-562-377-27	Sequence 27, Appl
C 166	184.6	8.1	65423	8	US-11-257-477-32	Sequence 32, Appl	C 239	162.8	7.1	14248	1	US-10-533-069-1584	Sequence 1584, Ap
C 167	184.4	8.1	2291	1	US-10-562-377-5	Sequence 5, Appl	C 240	162.4	7.1	3118	1	US-10-533-069-1446	Sequence 1446, Ap
C 168	183.8	8.0	2346	1	US-10-562-377-36	Sequence 36, Appl	C 241	161.6	7.1	2088	8	US-11-625-795-18	Sequence 18, Appl
C 169	183.6	8.0	7967	1	US-10-568-695-1	Sequence 1, Appl	C 242	161.4	7.1	2507	1	US-10-533-069-1126	Sequence 1126, Ap
C 170	183.6	8.0	9821	1	US-10-568-695-2	Sequence 2, Appl	C 243	161.4	7.1	2751	1	US-10-533-069-1782	Sequence 1782, Ap
C 171	183.4	8.0	2116	1	US-10-533-069-2107	Sequence 2107, Ap	C 244	160	7.0	2331	8	US-11-632-012-39	Sequence 39, Appl

C 245	159.4	7.0	3915	8	US-11-699-930-8	Sequence 8, Appli	C 318	116.8	5.1	3925	1	US-10-533-069-939	Sequence 939, App
C 246	159.4	7.0	5915	8	US-11-699-930-11	Sequence 11, Appl	C 319	116.8	5.1	7044	8	US-11-551-744-95	Sequence 95, Appl
C 247	159.4	7.0	5915	8	US-11-699-930-12	Sequence 12, Appl	C 320	116.4	5.1	619	8	US-11-744-695-17	Sequence 17, Appl
C 248	159.4	7.0	5915	8	US-11-699-930-13	Sequence 13, Appl	C 321	115.6	5.1	2508	1	US-10-562-377-184	Sequence 184, App
C 249	159.4	7.0	5915	8	US-11-699-930-14	Sequence 14, Appl	C 322	115.6	5.0	2346	1	US-10-562-377-110	Sequence 110, App
C 250	159.4	7.0	5915	8	US-11-699-930-15	Sequence 15, Appl	C 323	113.2	5.0	2673	1	US-10-562-377-104	Sequence 104, App
C 251	159.4	7.0	5915	8	US-11-699-930-16	Sequence 16, Appl	C 324	113.2	5.0	2673	1	US-10-562-377-182	Sequence 182, App
C 252	159.4	7.0	18524	8	US-11-650-478-12	Sequence 12, Appl	C 325	113	4.9	2591	8	US-11-112-327-21	Sequence 21, Appl
C 253	159.4	7.0	18524	8	US-11-650-478-12	Sequence 12, Appl	C 326	113	4.9	2591	8	US-11-112-327-28	Sequence 28, Appl
C 254	159.2	7.0	2894	1	US-10-533-069-2198	Sequence 2198, Ap	C 327	111.6	4.9	2333	1	US-10-533-069-2387	Sequence 2387, Ap
C 255	158.2	6.9	1135	8	US-11-632-012-41	Sequence 41, Appl	C 328	111.6	4.9	2368	8	US-10-562-377-20	Sequence 20, Appl
C 256	158	6.9	4316	8	US-11-510-314-3	Sequence 3, Appli	C 329	111.6	4.9	2652	8	US-11-738-671-23	Sequence 23, Appl
C 257	157.8	6.9	1914	1	US-10-533-069-1508	Sequence 1508, Ap	C 330	111.2	4.9	1774	8	US-11-680-414-20	Sequence 20, Appl
C 258	157	6.9	3200	1	US-10-533-069-301	Sequence 301, App	C 331	110.2	4.8	2346	1	US-10-562-377-188	Sequence 188, App
C 259	156.2	6.8	4152	1	US-10-533-069-2295	Sequence 2295, Ap	C 332	110	4.8	2475	1	US-10-562-377-40	Sequence 40, Appl
C 260	155.4	6.8	3487	1	US-10-533-069-917	Sequence 917, App	C 333	110	4.8	2475	1	US-10-562-377-44	Sequence 44, Appl
C 261	155	6.8	8158	8	US-11-496-050-30	Sequence 30, Appl	C 334	109.8	4.8	2002	1	US-10-533-069-961	Sequence 961, App
C 262	154.4	6.8	1520	8	US-11-632-012-27	Sequence 27, Appl	C 335	109.6	4.8	2818	8	US-10-562-377-78	Sequence 78, Appl
C 263	154.2	6.8	907	8	US-11-552-437-97	Sequence 97, Appl	C 336	108.8	4.8	3882	8	US-11-407-888-5	Sequence 5, Appli
C 264	153.8	6.7	9886	1	US-10-533-069-905	Sequence 905, App	C 337	108.2	4.7	5000	1	US-10-533-069-2049	Sequence 2049, Ap
C 265	153	6.7	2101	8	US-11-632-012-7	Sequence 7, Appli	C 338	106.2	4.6	2291	1	US-10-562-377-127	Sequence 127, App
C 266	151	6.6	939	8	US-11-632-012-24	Sequence 24, Appl	C 339	106	4.6	2291	1	US-10-562-377-49	Sequence 49, Appl
C 267	151	6.6	2122	1	US-10-533-069-240	Sequence 240, App	C 340	106	4.6	2475	1	US-10-562-377-118	Sequence 118, App
C 268	150.4	6.6	5237	8	US-11-407-888-59	Sequence 59, Appl	C 341	106	4.6	2475	1	US-10-562-377-122	Sequence 122, App
C 269	149.8	6.6	1774	8	US-11-680-414-20	Sequence 20, Appl	C 342	105.2	4.6	1976	8	US-11-552-437-33	Sequence 33, Appl
C 270	149.2	6.5	32677	8	US-11-234-477-133	Sequence 133, App	C 343	105	4.6	2368	1	US-10-562-377-152	Sequence 152, App
C 271	148.6	6.5	3846	8	US-11-234-694-55	Sequence 55, Appl	C 344	104.6	4.6	2368	1	US-10-562-377-158	Sequence 158, App
C 272	147.8	6.5	1697	1	US-10-533-069-1201	Sequence 1201, Ap	C 345	103.8	4.5	2818	1	US-10-562-377-156	Sequence 156, App
C 273	147.8	6.5	2243	1	US-10-533-069-852	Sequence 852, App	C 346	103.6	4.5	5932	1	US-10-533-069-1145	Sequence 1145, Ap
C 274	147.8	6.5	2518	1	US-10-533-069-1693	Sequence 1693, Ap	C 347	103.4	4.5	2308	1	US-10-562-377-71	Sequence 71, Appl
C 275	147.4	6.5	2049	1	US-10-533-069-808	Sequence 808, App	C 348	102.8	4.5	2368	1	US-10-562-377-84	Sequence 84, Appl
C 276	147	6.4	1709	1	US-10-596-627-6	Sequence 6, Appli	C 349	102.8	4.5	2764	1	US-10-533-069-2311	Sequence 2311, Ap
C 277	145.4	6.4	4828	8	US-11-365-630-6	Sequence 6, Appli	C 350	102	4.5	2673	1	US-10-562-377-104	Sequence 104, App
C 278	144.4	6.3	2308	1	US-10-533-069-588	Sequence 588, App	C 351	101	4.4	2508	1	US-10-562-377-107	Sequence 107, App
C 279	143	6.3	1840	8	US-11-632-012-19	Sequence 19, Appl	C 352	100.6	4.4	2377	1	US-10-562-377-52	Sequence 52, Appl
C 280	142.2	6.2	2196	8	US-11-534-850-1	Sequence 1, Appli	C 353	100.6	4.4	3328	1	US-10-533-069-2285	Sequence 2285, Ap
C 281	142.2	6.2	3583	1	US-10-533-069-2003	Sequence 2003, Ap	C 354	100	4.4	2345	1	US-10-562-377-124	Sequence 124, App
C 282	141.6	6.2	2974	1	US-10-565-068-103	Sequence 103, Appl	C 355	99.8	4.4	2044	1	US-10-533-069-13	Sequence 13, Appl
C 283	140.8	6.2	1167	8	US-11-632-012-10	Sequence 10, Appl	C 356	99.4	4.4	2345	1	US-10-562-377-46	Sequence 46, Appl
C 284	140.2	6.1	29018	8	US-11-257-477-105	Sequence 105, App	C 357	98	4.3	2673	1	US-10-562-377-105	Sequence 105, App
C 285	140	6.1	2338	1	US-10-533-069-1464	Sequence 1464, Ap	C 358	97.6	4.3	2396	1	US-10-562-377-93	Sequence 93, Appl
C 286	139.6	6.1	4604	1	US-10-533-069-467	Sequence 467, App	C 359	96.6	4.2	5496	1	US-10-533-069-2005	Sequence 2005, Ap
C 287	138.6	6.1	1859	8	US-11-632-012-46	Sequence 46, Appl	C 360	96	4.2	2396	1	US-10-562-377-171	Sequence 171, App
C 288	138	6.0	1556	1	US-10-533-069-2338	Sequence 2338, Ap	C 361	95.8	4.2	2377	1	US-10-562-377-130	Sequence 130, App
C 289	136.4	6.0	2597	8	US-11-544-070-1	Sequence 1, Appli	C 362	95.4	4.2	5065	1	US-10-533-069-479	Sequence 479, App
C 290	134	5.9	1024	8	US-11-599-517-44	Sequence 44, Appl	C 363	94.4	4.1	2430	1	US-10-533-069-867	Sequence 867, App
C 291	134	5.9	1024	8	US-11-599-517-102	Sequence 102, App	C 364	93.2	4.1	2871	1	US-10-533-069-2263	Sequence 2263, Ap
C 292	133.8	5.9	1167	8	US-11-632-012-10	Sequence 10, Appl	C 365	93	4.1	2508	1	US-10-562-377-185	Sequence 185, App
C 293	133.6	5.8	2714	1	US-10-533-069-347	Sequence 347, App	C 366	92.2	4.0	2368	1	US-10-562-377-159	Sequence 159, App
C 294	133.6	5.8	5207	1	US-10-533-069-2055	Sequence 2055, Ap	C 367	89.8	3.9	2291	1	US-10-562-377-148	Sequence 48, Appl
C 295	133.2	5.8	2426	1	US-10-533-069-1315	Sequence 1315, Ap	C 368	89.4	3.9	1836	1	US-10-533-069-2315	Sequence 2315, Ap
C 296	132.6	5.8	2120	1	US-10-567-074-1	Sequence 1, Appli	C 369	88.4	3.9	2673	1	US-10-562-377-182	Sequence 182, App
C 297	132.4	5.8	289	1	US-10-596-627-1	Sequence 1, Appli	C 370	88	3.9	5726	1	US-10-533-069-977	Sequence 977, App
C 298	132	5.8	489	8	US-11-634-620-11	Sequence 11, Appl	C 371	87.8	3.8	2117	1	US-10-533-069-1059	Sequence 1059, Ap
C 299	132	5.8	3869	1	US-10-533-069-1488	Sequence 1488, Ap	C 372	85.4	3.7	2818	1	US-10-562-377-79	Sequence 79, Appl
C 300	131.6	5.8	10001	8	US-11-615-454-12	Sequence 12, Appl	C 373	84.4	3.7	1475	8	US-11-680-414-3	Sequence 3, Appli
C 301	131	5.7	2359	8	US-11-327-695-16	Sequence 16, Appl	C 374	84.4	3.7	2308	1	US-10-562-377-75	Sequence 75, Appl
C 302	128.2	5.6	1937	1	US-10-533-069-688	Sequence 688, App	C 375	84.4	3.7	5659	8	US-11-585-666-44	Sequence 44, Appl
C 303	128.2	5.6	1937	1	US-10-533-069-935	Sequence 935, App	C 376	84.2	3.7	2377	1	US-10-562-377-53	Sequence 53, Appl
C 304	126.6	5.5	2843	8	US-11-257-477-61	Sequence 61, Appl	C 377	82	3.6	2673	1	US-10-562-377-183	Sequence 183, App
C 305	125.8	5.5	961	8	US-11-632-012-28	Sequence 28, Appl	C 378	81.4	3.6	1363	1	US-10-533-069-1257	Sequence 1257, Ap
C 306	125.4	5.5	3322	1	US-10-533-069-136	Sequence 136, App	C 379	81.4	3.6	2346	1	US-10-562-377-111	Sequence 111, App
C 307	124.6	5.5	9882	1	US-10-533-069-1708	Sequence 1708, Ap	C 380	80.8	3.5	2088	8	US-11-625-795-18	Sequence 18, Appl
C 308	124.4	5.4	4321	8	US-11-691-348-6	Sequence 6, Appli	C 381	80.8	3.5	2274	1	US-10-533-069-1149	Sequence 1149, Ap
C 309	123.4	5.4	2673	1	US-10-562-377-105	Sequence 105, App	C 382	80	3.5	2818	1	US-10-562-377-157	Sequence 157, App
C 310	123.4	5.4	3319	1	US-10-533-069-566	Sequence 566, App	C 383	79.8	3.5	4674	1	US-10-533-069-55	Sequence 55, Appl
C 311	122.8	5.4	1310	8	US-11-632-012-65	Sequence 65, Appl	C 384	78.6	3.4	2291	1	US-10-562-377-126	Sequence 126, App
C 312	121.8	5.3	2673	1	US-10-562-377-183	Sequence 183, App	C 385	78.4	3.4	2345	1	US-10-562-377-47	Sequence 47, Appl
C 313	121.8	5.3	2818	1	US-10-562-377-20	Sequence 20, Appl	C 386	78.2	3.4	1457	8	US-11-738-671-38	Sequence 38, Appl
C 314	120.6	5.3	3328	1	US-10-533-069-2285	Sequence 2285, Ap	C 387	78.2	3.4	2346	1	US-10-562-377-189	Sequence 189, App
C 315	120.4	5.3	2535	1	US-10-562-377-35	Sequence 35, Appl	C 388	77.4	3.4	1701	8	US-11-632-012-31	Sequence 31, Appl
C 316	119.4	5.2	4565	1	US-10-533-069-2135	Sequence 2135, Ap	C 389	77	3.4	2475	1	US-10-562-377-41	Sequence 41, Appl
C 317	118.8	5.2	2508	1	US-10-562-377-106	Sequence 106, App	C 390	77	3.4	2475	1	US-10-562-377-45	Sequence 45, Appl

391	77	3.4	3819	8	US-11-552-437-133	Sequence 133, App	464	56.8	2.5	836	8	US-11-585-666-12	Sequence 12, Appl
392	76.8	3.4	5511	8	US-11-365-630-4	Sequence 4, Appl	465	56.8	2.5	848	8	US-11-585-666-13	Sequence 13, Appl
393	76.8	3.4	5511	8	US-11-365-630-11	Sequence 11, Appl	466	56.8	2.5	860	8	US-11-585-666-14	Sequence 14, Appl
394	76	3.3	2377	1	US-10-562-377-1131	Sequence 131, App	467	56.6	2.5	1380	8	US-11-632-012-22	Sequence 22, Appl
395	75.2	3.3	711	8	US-11-112-327-16	Sequence 16, Appl	C 468	56.6	2.5	2535	1	US-10-562-377-187	Sequence 187, App
396	75.2	3.3	1437	8	US-11-699-229-46	Sequence 46, Appl	C 469	56.4	2.5	6803	1	US-11-625-795-10	Sequence 10, Appl
397	74.8	3.3	2475	8	US-11-552-437-163	Sequence 163, App	470	55	2.4	1271	8	US-10-533-069-666	Sequence 666, App
398	73.6	3.2	2396	1	US-10-562-377-92	Sequence 92, Appl	471	55	2.4	1271	8	US-11-585-666-21	Sequence 21, Appl
399	73.6	3.2	3858	8	US-11-655-822-2	Sequence 2, Appl	C 472	55	2.4	1364	8	US-11-585-666-20	Sequence 20, Appl
400	73.6	3.2	3858	8	US-11-655-822-4	Sequence 4, Appl	C 473	55	2.4	5428	1	US-10-533-069-545	Sequence 545, App
401	73.6	3.2	3858	8	US-11-655-822-6	Sequence 6, Appl	474	54.6	2.4	1038	8	US-11-728-892-11	Sequence 11, Appl
402	73.6	3.2	3858	8	US-11-655-822-8	Sequence 8, Appl	475	54.6	2.4	1107	8	US-11-728-892-84	Sequence 84, Appl
403	73.6	3.2	3858	8	US-11-655-822-10	Sequence 10, Appl	476	54.4	2.4	2355	8	US-11-632-012-50	Sequence 50, Appl
404	73.6	3.2	3860	8	US-11-655-822-98	Sequence 98, Appl	C 477	54.2	2.4	338	8	US-11-634-620-44	Sequence 44, Appl
405	73.6	3.2	3860	8	US-11-655-822-99	Sequence 99, Appl	478	53.8	2.4	3334	1	US-10-533-069-1410	Sequence 1410, Ap
406	73.6	3.2	3988	8	US-11-655-822-14	Sequence 14, Appl	C 479	53.6	2.3	2571	1	US-10-533-069-1422	Sequence 1422, Ap
407	73.6	3.2	3988	8	US-11-655-822-97	Sequence 97, Appl	C 480	53.4	2.3	3199	8	US-11-112-327-13	Sequence 13, Appl
408	73.2	3.2	1885	8	US-11-705-689-15	Sequence 15, Appl	481	52.8	2.3	4357	1	US-10-533-069-2302	Sequence 2302, Ap
409	73	3.2	5496	1	US-10-533-069-2005	Sequence 2005, Ap	C 482	52.8	2.3	44728	8	US-11-257-477-23	Sequence 23, Appl
410	72.6	3.2	3516	8	US-11-551-744-161	Sequence 161, App	C 483	52.6	2.3	501	8	US-11-632-012-55	Sequence 55, Appl
411	71.8	3.1	885	1	US-10-533-069-626	Sequence 626, App	C 484	52.2	2.3	1787	1	US-10-533-069-2300	Sequence 2300, Ap
412	71.6	3.1	476	8	US-11-634-620-35	Sequence 35, Appl	C 485	52	2.3	1776	8	US-11-738-671-26	Sequence 26, Appl
413	71.2	3.1	5726	1	US-10-533-069-977	Sequence 977, App	486	51.6	2.3	2688	1	US-10-533-069-1731	Sequence 1731, Ap
414	71	3.1	101	8	US-11-640-897-1733	Sequence 1733, Ap	C 487	51.2	2.2	1479	8	US-11-595-320-3	Sequence 3, Appl
415	71	3.1	2280	1	US-10-565-626-75	Sequence 75, Appl	C 488	51	2.2	494	1	US-10-819-557-15	Sequence 15, Appl
416	70.6	3.1	2475	1	US-10-562-377-119	Sequence 119, App	489	50.8	2.2	2883	1	US-10-533-069-1510	Sequence 1510, Ap
417	70.6	3.1	2475	1	US-10-562-377-123	Sequence 123, App	490	50.2	2.2	940	8	US-11-112-327-14	Sequence 14, Appl
418	70	3.1	462	8	US-11-634-620-59	Sequence 59, Appl	491	50.2	2.2	2188	1	US-10-533-069-122	Sequence 122, App
419	69.4	3.0	1414	8	US-11-632-012-64	Sequence 64, Appl	C 492	49.8	2.2	2337	1	US-10-533-069-570	Sequence 570, App
420	69.4	3.0	13602	8	US-11-650-478-1	Sequence 1, Appl	C 493	49.4	2.2	1457	8	US-11-738-671-38	Sequence 38, Appl
421	69.4	3.0	13602	8	US-11-650-478-1	Sequence 1, Appl	C 494	49.4	2.2	2818	1	US-10-562-377-78	Sequence 78, Appl
422	69.4	3.0	17534	8	US-11-650-478-7	Sequence 7, Appl	C 495	49.2	2.2	607	8	US-11-632-012-21	Sequence 21, Appl
423	69.4	3.0	30756	8	US-11-650-478-16	Sequence 16, Appl	C 496	49	2.1	2818	1	US-10-562-377-156	Sequence 156, App
424	69.4	3.0	30756	8	US-11-650-478-16	Sequence 16, Appl	C 497	48	2.1	2061	1	US-10-533-069-774	Sequence 774, App
425	69.4	3.0	30756	8	US-11-650-478-16	Sequence 16, Appl	C 498	47.2	2.1	2535	1	US-10-562-377-186	Sequence 186, App
426	68.6	3.0	374	8	US-11-634-620-62	Sequence 62, Appl	C 499	47	2.1	1070	1	US-10-533-069-1638	Sequence 1638, Ap
427	67	2.9	1225	8	US-11-552-437-37	Sequence 37, Appl	C 500	47	2.1	2876	8	US-11-699-229-28	Sequence 28, Appl
428	67	2.9	2446	1	US-10-533-069-1911	Sequence 1911, Ap	C 501	47	2.1	68487	8	US-11-257-477-71	Sequence 71, Appl
429	66.8	2.9	2308	1	US-10-562-377-153	Sequence 153, App	C 502	46.8	2.0	3335	1	US-10-533-069-986	Sequence 986, App
430	66.8	2.9	4975	1	US-10-533-069-321	Sequence 321, App	C 503	46.6	2.0	450000	1	US-10-650-449-3	Sequence 3, Appl
431	66.4	2.9	7585	1	US-10-533-069-395	Sequence 395, App	C 504	46.2	2.0	1700	1	US-10-533-069-1788	Sequence 1788, Ap
432	66	2.9	2345	1	US-10-562-377-125	Sequence 125, App	C 505	46.2	2.0	2761	8	US-11-738-671-41	Sequence 41, Appl
433	65	2.8	1415	1	US-10-533-069-543	Sequence 543, App	C 506	45.6	2.0	866	8	US-11-632-012-59	Sequence 59, Appl
434	65	2.8	2319	8	US-11-519-397-48	Sequence 48, Appl	C 507	45.6	2.0	2458	8	US-11-552-437-129	Sequence 129, App
435	65	2.8	2396	1	US-10-562-377-170	Sequence 170, App	C 508	45.4	2.0	2291	1	US-10-562-377-5	Sequence 5, Appl
436	64.2	2.8	2014	1	US-10-533-069-2117	Sequence 2117, Ap	C 509	45.2	2.0	411	8	US-11-634-620-74	Sequence 74, Appl
437	63.8	2.8	2117	1	US-10-533-069-1251	Sequence 1251, Ap	C 510	45	2.0	1313	8	US-11-738-671-31	Sequence 31, Appl
438	63.8	2.8	2337	1	US-10-533-069-570	Sequence 570, App	C 511	45	2.0	44728	8	US-11-257-477-23	Sequence 23, Appl
439	63.8	2.8	2675	1	US-10-533-069-1261	Sequence 1261, Ap	C 512	44.8	2.0	418	8	US-11-738-671-32	Sequence 32, Appl
440	63.8	2.8	2745	1	US-10-565-068-100	Sequence 100, App	C 513	44.6	2.0	115780	8	US-11-257-477-96	Sequence 96, Appl
441	63.8	2.8	2745	1	US-10-581-547-147	Sequence 147, App	C 514	44.6	2.0	68487	8	US-11-257-477-71	Sequence 71, Appl
442	63.4	2.8	2818	8	US-10-562-377-79	Sequence 79, Appl	C 515	44.4	1.9	224112	8	US-11-257-477-80	Sequence 80, Appl
443	63.2	2.8	3988	8	US-11-655-822-14	Sequence 14, Appl	C 516	43.8	1.9	1926	8	US-11-561-363-81	Sequence 81, Appl
444	63.2	2.8	3988	8	US-11-655-822-97	Sequence 97, Appl	C 517	43.8	1.9	46030	8	US-11-257-477-1	Sequence 1, Appl
445	63	2.8	2196	1	US-10-562-377-37	Sequence 37, Appl	C 518	43.8	1.9	450000	1	US-10-650-449-3	Sequence 3, Appl
446	62.8	2.7	1842	8	US-11-725-076-11	Sequence 11, Appl	C 519	43.4	1.9	2946	1	US-10-567-764-6	Sequence 6, Appl
447	62.6	2.7	1493	1	US-10-533-069-1414	Sequence 1414, Ap	C 520	43.4	1.9	3024	1	US-10-567-764-10	Sequence 10, Appl
448	62.4	2.7	2306	1	US-10-533-069-1830	Sequence 1830, Ap	C 521	43.4	1.9	3117	1	US-10-567-764-14	Sequence 14, Appl
449	62.4	2.7	2805	1	US-10-533-069-1249	Sequence 1249, Ap	C 522	43.4	1.9	3210	1	US-10-567-764-18	Sequence 18, Appl
450	61.8	2.7	2818	1	US-10-562-377-157	Sequence 157, App	C 523	43.4	1.9	3303	1	US-10-567-764-22	Sequence 22, Appl
451	61.6	2.7	1510	1	US-10-533-069-1408	Sequence 1408, Ap	C 524	43.4	1.9	8049	1	US-10-567-764-5	Sequence 5, Appl
452	60.8	2.7	454	8	US-11-744-695-32	Sequence 32, Appl	C 525	43.2	1.9	761	1	US-10-533-069-997	Sequence 997, App
453	60.8	2.7	2166	1	US-10-533-069-1923	Sequence 1923, Ap	C 526	43.2	1.9	2883	1	US-10-533-069-1510	Sequence 1510, Ap
454	60	2.6	2136	8	US-11-738-671-15	Sequence 15, Appl	C 527	43.2	1.9	34245	8	US-11-257-477-102	Sequence 102, App
455	59.6	2.6	1855	1	US-10-533-069-2394	Sequence 2394, Ap	C 528	43	1.9	3385	1	US-10-533-069-9	Sequence 9, Appl
456	59.2	2.6	2535	1	US-10-562-377-109	Sequence 109, App	C 529	43	1.9	80423	8	US-11-257-477-41	Sequence 41, Appl
457	58.8	2.6	1705	1	US-10-533-069-1937	Sequence 1937, Ap	C 530	42.8	1.9	1664	1	US-10-533-069-1616	Sequence 1616, Ap
458	58.6	2.6	2033	8	US-11-632-012-29	Sequence 29, Appl	C 531	42.8	1.9	30611	8	US-11-257-477-108	Sequence 108, App
459	58.6	2.6	2992	1	US-10-533-069-160	Sequence 160, App	C 532	42	1.8	4040	8	US-10-533-069-624	Sequence 624, App
460	58.6	2.6	3335	1	US-10-533-069-986	Sequence 986, App	C 533	42	1.8	2495	8	US-11-257-477-142	Sequence 142, App
461	58.4	2.6	1093	1	US-10-533-069-1742	Sequence 1742, Ap	C 534	41.8	1.8	480	8	US-11-634-620-16	Sequence 16, Appl
462	58.4	2.6	2535	1	US-10-562-377-108	Sequence 108, App	C 535	41.8	1.8	1242	8	US-11-632-012-48	Sequence 48, Appl
463	57.4	2.5	2435	1	US-10-533-069-897	Sequence 897, App	C 536	41.8	1.8	6406	1	US-10-533-069-656	Sequence 656, App

C 537	41.8	1.8	24495	8	US-11-257-477-142	Sequence 142, App	C 610	35.2	1.5	954	8	US-11-361-092-162	Sequence 162, App
C 538	41.6	1.8	90351	8	US-11-257-477-166	Sequence 166, App	C 611	35.2	1.5	1897	1	US-10-533-069-1339	Sequence 1339, App
C 539	41.4	1.8	139613	8	US-11-257-477-90	Sequence 90, Appl	C 612	35.2	1.5	2239	1	US-10-596-627-7	Sequence 7, Appl
C 540	40.4	1.8	918	8	US-11-599-517-12	Sequence 12, Appl	C 613	35.2	1.5	2728	1	US-10-562-377-102	Sequence 102, App
C 541	40.2	1.8	797	8	US-11-713-768-5845	Sequence 5845, A	C 614	35.2	1.5	39084	8	US-11-257-477-35	Sequence 35, Appl
C 542	40	1.8	1282	8	US-11-632-012-16	Sequence 16, Appl	C 615	35.2	1.5	152372	8	US-11-361-092-171	Sequence 171, App
C 543	40	1.8	1533	8	US-11-713-768-37320	Sequence 37320, A	C 616	35	1.5	1549	8	US-11-514-704-12516	Sequence 12516, A
C 544	40	1.8	37180	8	US-11-257-477-13	Sequence 13, Appl	C 617	35	1.5	3823	8	US-11-514-704-23493	Sequence 23493, A
C 545	40	1.8	80423	8	US-11-257-477-41	Sequence 41, Appl	C 618	34.8	1.5	751	1	US-10-438-246-27956	Sequence 27956, A
C 546	39.8	1.7	1024	8	US-11-599-517-96	Sequence 96, Appl	C 619	34.8	1.5	2830	1	US-10-438-246-565	Sequence 565, App
C 547	39.8	1.7	2271	1	US-10-533-069-244	Sequence 244, App	C 620	34.8	1.5	3801	8	US-11-514-704-19900	Sequence 19900, A
C 548	39.8	1.7	90351	8	US-11-257-477-166	Sequence 166, App	C 621	34.8	1.5	4377	8	US-11-514-704-23607	Sequence 23607, A
C 549	39.6	1.7	1445	8	US-11-632-012-38	Sequence 38, Appl	C 622	34.8	1.5	4572	1	US-10-438-246-15682	Sequence 15682, A
C 550	39.6	1.7	224112	8	US-11-257-477-80	Sequence 80, Appl	C 623	34.6	1.5	101	8	US-11-640-897-695	Sequence 695, App
C 551	39.6	1.7	421609	8	US-11-257-477-122	Sequence 122, App	C 624	34.6	1.5	549	8	US-11-713-768-75454	Sequence 75454, A
C 552	39.4	1.7	1050	1	US-10-533-069-1756	Sequence 1756, App	C 625	34.6	1.5	855	8	US-11-713-768-38540	Sequence 38540, A
C 553	39.4	1.7	1301	8	US-11-595-320-7	Sequence 7, Appl	C 626	34.6	1.5	855	8	US-11-713-768-50066	Sequence 50066, A
C 554	39	1.7	771	8	US-11-632-012-32	Sequence 32, Appl	C 627	34.6	1.5	1419	1	US-10-438-246-28743	Sequence 28743, A
C 555	39	1.7	938	8	US-11-713-768-1268	Sequence 1268, App	C 628	34.6	1.5	1520	8	US-11-713-768-2243	Sequence 2243, App
C 556	39	1.7	1076	8	US-11-514-704-4118	Sequence 4118, App	C 629	34.6	1.5	1653	8	US-11-514-704-7418	Sequence 7418, App
C 557	39	1.7	2126	1	US-10-438-246-26985	Sequence 26985, A	C 630	34.6	1.5	2196	1	US-10-562-377-112	Sequence 112, App
C 558	39	1.7	4080	8	US-11-657-313-4	Sequence 4, Appl	C 631	34.6	1.5	2196	1	US-10-562-377-190	Sequence 190, App
C 559	39	1.7	5092	8	US-11-657-313-5	Sequence 5, Appl	C 632	34.6	1.5	2406	8	US-11-514-704-21128	Sequence 21128, A
C 560	38.6	1.7	1678	8	US-11-713-768-43299	Sequence 43299, A	C 633	34.6	1.5	3271	8	US-11-514-704-5311	Sequence 5311, App
C 561	38.6	1.7	2085	8	US-11-713-768-72372	Sequence 72372, A	C 634	34.6	1.5	421609	8	US-11-257-477-122	Sequence 122, App
C 562	38.6	1.7	2154	8	US-11-713-768-71163	Sequence 71163, A	C 635	34.4	1.5	869	8	US-11-713-768-62035	Sequence 62035, A
C 563	38.6	1.7	30884	8	US-11-257-477-35	Sequence 35, Appl	C 636	34.4	1.5	1372	8	US-11-713-768-1704	Sequence 1704, App
C 564	38.4	1.7	3289	8	US-11-514-704-21524	Sequence 21524, A	C 637	34.4	1.5	1721	8	US-11-649-663A-3507	Sequence 3507, App
C 565	38.4	1.7	3925	1	US-10-533-069-939	Sequence 939, App	C 638	34.4	1.5	1966	8	US-11-514-704-18806	Sequence 18806, A
C 566	38.2	1.7	30304	8	US-11-257-477-128	Sequence 128, App	C 639	34.4	1.5	42203	8	US-11-257-477-53	Sequence 53, Appl
C 567	38.2	1.7	52637	8	US-11-257-477-186	Sequence 186, App	C 640	34.2	1.5	525	1	US-10-438-246-11579	Sequence 11579, A
C 568	38.2	1.7	108845	8	US-11-257-477-7	Sequence 7, Appl	C 641	34.2	1.5	1353	8	US-11-514-704-12636	Sequence 12636, A
C 569	38	1.7	1556	8	US-11-514-704-6219	Sequence 6219, App	C 642	34.2	1.5	2291	1	US-10-562-377-126	Sequence 126, App
C 570	38	1.7	2866	8	US-11-514-704-23606	Sequence 23606, A	C 643	34.2	1.5	4725	8	US-11-514-704-17007	Sequence 17007, App
C 571	38	1.7	3379	8	US-11-514-704-6220	Sequence 6220, App	C 644	34	1.5	625	8	US-11-684-413-11	Sequence 11, Appl
C 572	37.8	1.7	101	8	US-11-640-897-1466	Sequence 1466, App	C 645	34	1.5	625	8	US-11-723-507-9	Sequence 9, Appl
C 573	37.8	1.7	52637	8	US-11-257-477-186	Sequence 186, App	C 646	34	1.5	1553	8	US-11-713-768-56977	Sequence 56977, A
C 574	37.4	1.6	2411	1	US-10-438-246-22503	Sequence 22503, A	C 647	34	1.5	1722	8	US-11-713-768-75614	Sequence 75614, A
C 575	37.4	1.6	46030	8	US-11-257-477-1	Sequence 1, Appl	C 648	34	1.5	1749	8	US-11-713-768-87368	Sequence 87368, A
C 576	37.2	1.6	1353	1	US-10-596-627-28	Sequence 28, Appl	C 649	34	1.5	2343	8	US-11-514-704-8767	Sequence 8767, App
C 577	37.2	1.6	1607	8	US-11-514-704-7133	Sequence 7133, App	C 650	34	1.5	4010	8	US-11-684-413-15	Sequence 15, Appl
C 578	37.2	1.6	5349	8	US-11-514-704-201	Sequence 201, App	C 651	34	1.5	4010	8	US-11-723-507-23	Sequence 23, Appl
C 579	37.2	1.6	10535	8	US-11-514-704-3259	Sequence 3259, App	C 652	33.8	1.5	945	8	US-11-713-768-56946	Sequence 56946, A
C 580	37.2	1.6	100534	8	US-11-257-477-160	Sequence 160, App	C 653	33.8	1.5	963	8	US-11-514-704-23864	Sequence 23864, A
C 581	37	1.6	795	8	US-11-713-768-111455	Sequence 111455, A	C 654	33.8	1.5	1000	8	US-11-360-039-59	Sequence 59, Appl
C 582	37	1.6	1627	8	US-11-713-768-41129	Sequence 41129, A	C 655	33.8	1.5	4306	8	US-11-514-704-6282	Sequence 6282, App
C 583	37	1.6	1956	1	US-10-438-246-13283	Sequence 13283, A	C 656	33.6	1.5	891	1	US-10-438-246-11605	Sequence 11605, A
C 584	37	1.6	2773	8	US-11-649-663A-1465	Sequence 1465, App	C 657	33.6	1.5	1457	1	US-10-438-246-21554	Sequence 21554, A
C 585	37	1.6	2773	8	US-11-713-768-49006	Sequence 49006, A	C 658	33.6	1.5	2474	8	US-11-514-704-5687	Sequence 5687, App
C 586	37	1.6	2791	8	US-11-649-663A-2825	Sequence 2825, App	C 659	33.6	1.5	2568	8	US-11-514-704-5863	Sequence 5863, App
C 587	37	1.6	2791	8	US-11-713-768-45476	Sequence 45476, A	C 660	33.6	1.5	2718	8	US-11-514-704-12773	Sequence 12773, A
C 588	37	1.6	139613	8	US-11-257-477-90	Sequence 90, Appl	C 661	33.6	1.5	2728	1	US-10-562-377-180	Sequence 180, App
C 589	36.8	1.6	2151	8	US-11-514-704-10912	Sequence 10912, A	C 662	33.6	1.5	2728	8	US-11-514-704-13991	Sequence 13991, A
C 590	36.8	1.6	4443	8	US-11-713-768-71358	Sequence 71358, A	C 663	33.6	1.5	3048	8	US-11-713-768-90578	Sequence 90578, A
C 591	36.6	1.6	21166	8	US-11-257-477-138	Sequence 138, App	C 664	33.6	1.5	3048	8	US-11-713-768-94334	Sequence 94334, A
C 592	36.4	1.6	101	8	US-11-640-897-1203	Sequence 1203, App	C 665	33.6	1.5	3087	8	US-11-796-730-1629	Sequence 1629, App
C 593	36.4	1.6	2943	1	US-10-438-246-561	Sequence 561, App	C 666	33.6	1.5	7264	8	US-11-514-704-24394	Sequence 24394, A
C 594	36.4	1.6	3310	1	US-10-438-246-550	Sequence 550, App	C 667	33.6	1.5	37234	8	US-11-257-477-63	Sequence 63, Appl
C 595	36.4	1.6	52138	8	US-11-739-908-75	Sequence 75, Appl	C 668	33.6	1.5	37234	8	US-11-257-477-63	Sequence 63, Appl
C 596	36.4	1.6	52138	8	US-11-739-877-75	Sequence 75, Appl	C 669	33.4	1.5	480	8	US-11-634-620-16	Sequence 16, Appl
C 597	36.4	1.6	100534	8	US-11-257-477-160	Sequence 160, App	C 670	33.4	1.5	682	8	US-11-705-903-53	Sequence 53, Appl
C 598	36.2	1.6	21166	8	US-11-257-477-198	Sequence 198, App	C 671	33.4	1.5	684	8	US-11-705-903-15	Sequence 15, Appl
C 599	36.2	1.6	127767	8	US-11-257-477-176	Sequence 176, App	C 672	33.4	1.5	1720	1	US-10-438-246-27762	Sequence 27762, A
C 600	36.2	1.6	240102	8	US-11-257-477-192	Sequence 192, App	C 673	33.4	1.5	1824	1	US-10-533-069-2115	Sequence 2115, App
C 601	35.8	1.6	7482	1	US-10-438-246-5333	Sequence 5333, App	C 674	33.4	1.5	2306	1	US-10-533-069-1830	Sequence 1830, App
C 602	35.6	1.6	539	1	US-10-575-823-87	Sequence 87, Appl	C 675	33.4	1.5	3248	8	US-11-514-704-17402	Sequence 17402, A
C 603	35.6	1.6	539	1	US-10-575-805-87	Sequence 87, Appl	C 676	33.4	1.5	4578	8	US-11-514-704-7881	Sequence 7881, App
C 604	35.6	1.6	539	1	US-10-576-093-87	Sequence 87, Appl	C 677	33.4	1.5	5015	8	US-11-514-704-17480	Sequence 17480, A
C 605	35.6	1.6	539	1	US-10-576-094A-87	Sequence 87, Appl	C 678	33.4	1.5	5068	8	US-10-533-069-937	Sequence 937, App
C 606	35.6	1.6	623	8	US-11-489-234-19	Sequence 19, Appl	C 679	33.4	1.5	5718	1	US-11-514-704-20708	Sequence 20708, A
C 607	35.6	1.6	1377	8	US-11-632-012-11	Sequence 11, Appl	C 680	33.2	1.5	354	1	US-10-438-246-28024	Sequence 28024, A
C 608	35.4	1.5	1925	1	US-10-438-246-29150	Sequence 29150, A	C 681	33.2	1.5	771	8	US-11-632-012-32	Sequence 32, Appl
C 609	35.4	1.5	4446	1	US-10-438-246-11631	Sequence 11631, A	C 682	33.2	1.5	42203	8	US-11-257-477-53	Sequence 53, Appl

683	33	1.4	1835	8	US-11-514-704-9008	Sequence 9008, Ap	756	31.8	1.4	3293	8	US-11-514-704-18991	Sequence 18991, A
684	33	1.4	3096	8	US-11-514-704-13097	Sequence 13097, A	757	31.8	1.4	3339	8	US-11-514-704-5457	Sequence 5457, Ap
685	33	1.4	4106	8	US-11-514-704-20707	Sequence 20707, A	c 758	31.8	1.4	3389	1	US-10-438-246-27995	Sequence 27995, A
686	33	1.4	5850	1	US-10-438-246-15256	Sequence 15256, A	759	31.8	1.4	3794	1	US-11-514-704-20566	Sequence 20566, A
687	33	1.4	5850	1	US-10-438-246-22882	Sequence 22882, A	c 760	31.8	1.4	4085	1	US-10-585-503-3	Sequence 3, Appl
688	32.8	1.4	233	8	US-11-673-456-25	Sequence 25, Appl	c 761	31.8	1.4	5499	8	US-11-514-704-3073	Sequence 3073, Ap
689	32.8	1.4	1467	8	US-11-649-663A-3187	Sequence 3187, Ap	c 762	31.8	1.4	5499	8	US-11-514-704-22532	Sequence 22532, A
690	32.8	1.4	1718	8	US-11-514-704-11418	Sequence 11418, A	c 763	31.8	1.4	5634	8	US-11-514-704-18677	Sequence 18677, A
691	32.8	1.4	1888	8	US-11-514-704-27929	Sequence 27929, Ap	764	31.8	1.4	6226	8	US-11-514-704-18677	Sequence 18677, A
692	32.8	1.4	2410	8	US-11-649-663A-3823	Sequence 3823, Ap	765	31.8	1.4	6690	1	US-10-438-246-5336	Sequence 5336, Ap
693	32.8	1.4	2623	1	US-10-438-246-27039	Sequence 27039, A	766	31.8	1.4	52138	8	US-11-739-906-75	Sequence 75, Appl
694	32.8	1.4	2899	1	US-10-533-069-23030	Sequence 23030, Ap	c 767	31.8	1.4	52138	8	US-11-739-906-75	Sequence 75, Appl
695	32.8	1.4	2923	8	US-11-514-704-7054	Sequence 7054, Ap	c 768	31.8	1.4	533	8	US-11-514-704-2457	Sequence 2457, Ap
696	32.8	1.4	3459	1	US-10-438-246-12905	Sequence 12905, A	769	31.6	1.4	681	8	US-11-796-730-2225	Sequence 2225, Ap
697	32.8	1.4	3594	1	US-10-438-246-22284	Sequence 22284, A	770	31.6	1.4	1044	1	US-10-438-246-2081	Sequence 2081, Ap
698	32.8	1.4	4642	1	US-11-533-069-1647	Sequence 1647, Ap	771	31.6	1.4	1190	1	US-10-438-246-2754	Sequence 2754, Ap
699	32.8	1.4	5980	8	US-11-514-704-14172	Sequence 14172, A	772	31.6	1.4	1190	8	US-11-514-704-21068	Sequence 21068, A
700	32.8	1.4	18703	1	US-10-550-449-8	Sequence 8, Appl	773	31.6	1.4	1209	8	US-11-649-663A-1609	Sequence 1609, Ap
701	32.6	1.4	101	8	US-11-640-897-2340	Sequence 2340, Ap	774	31.6	1.4	1209	8	US-11-713-768-81597	Sequence 81597, A
702	32.6	1.4	1377	8	US-11-632-012-11	Sequence 11, Appl	775	31.6	1.4	1215	1	US-10-438-246-13195	Sequence 13195, A
703	32.6	1.4	1684	8	US-11-713-768-25966	Sequence 25966, A	776	31.6	1.4	1312	8	US-11-713-768-57601	Sequence 57601, A
704	32.6	1.4	1685	8	US-11-713-768-100603	Sequence 100603, A	777	31.6	1.4	1344	8	US-11-514-704-14371	Sequence 14371, A
705	32.6	1.4	1774	1	US-10-438-246-1222	Sequence 1222, Ap	c 778	31.6	1.4	1391	8	US-11-713-768-59512	Sequence 59512, A
706	32.6	1.4	1970	8	US-11-514-704-8257	Sequence 8257, Ap	779	31.6	1.4	1536	1	US-10-438-246-13194	Sequence 13194, A
707	32.6	1.4	2044	8	US-11-514-704-8672	Sequence 8672, Ap	780	31.6	1.4	1642	1	US-10-438-246-22468	Sequence 22468, A
708	32.6	1.4	2411	8	US-11-351-522A-33	Sequence 33, Appl	c 781	31.6	1.4	1660	8	US-11-649-663A-2925	Sequence 2925, Ap
709	32.6	1.4	2588	8	US-11-514-704-14568	Sequence 14568, A	c 782	31.6	1.4	2082	8	US-11-514-704-16880	Sequence 16880, A
710	32.6	1.4	2684	8	US-11-514-704-16570	Sequence 16570, A	c 783	31.6	1.4	2119	8	US-11-514-704-553	Sequence 553, App
711	32.6	1.4	4735	8	US-11-514-704-16570	Sequence 16570, A	c 784	31.6	1.4	2290	1	US-10-562-377-87	Sequence 87, Appl
712	32.6	1.4	5635	8	US-11-351-522A-3	Sequence 3, Appl	c 785	31.6	1.4	2355	1	US-10-562-377-87	Sequence 87, Appl
713	32.6	1.4	6382	8	US-11-351-522A-29	Sequence 29, Appl	c 786	31.6	1.4	2429	1	US-10-562-377-83	Sequence 83, Appl
714	32.6	1.4	8570	1	US-10-533-069-1572	Sequence 1572, Ap	c 787	31.6	1.4	2556	8	US-11-713-768-70315	Sequence 70315, A
715	32.6	1.4	133462	1	US-11-257-477-114	Sequence 114, App	c 788	31.6	1.4	3278	8	US-11-514-704-23414	Sequence 23414, A
716	32.4	1.4	761	1	US-10-533-069-997	Sequence 997, App	c 789	31.6	1.4	3569	8	US-11-514-704-15131	Sequence 15131, A
717	32.4	1.4	1140	8	US-11-713-768-69106	Sequence 69106, A	790	31.6	1.4	3683	8	US-11-514-704-24323	Sequence 24323, A
718	32.4	1.4	1434	8	US-11-713-768-106394	Sequence 106394, A	791	31.6	1.4	4230	1	US-10-438-246-15250	Sequence 15250, A
719	32.4	1.4	2332	8	US-11-514-704-3597	Sequence 3597, Ap	792	31.6	1.4	4284	1	US-10-438-246-15242	Sequence 15242, A
720	32.4	1.4	2337	8	US-11-796-730-589	Sequence 589, App	793	31.6	1.4	4381	8	US-11-514-704-21067	Sequence 21067, A
721	32.4	1.4	3024	8	US-11-514-704-10800	Sequence 10800, A	794	31.6	1.4	4668	1	US-10-438-246-15694	Sequence 15694, A
722	32.4	1.4	3044	8	US-11-514-704-18247	Sequence 18247, A	795	31.6	1.4	4761	1	US-10-438-246-15237	Sequence 15237, A
723	32.4	1.4	21808	8	US-11-257-477-136	Sequence 136, App	796	31.6	1.4	4806	1	US-10-438-246-15233	Sequence 15233, A
724	32.4	1.4	240102	8	US-11-257-477-192	Sequence 192, App	797	31.6	1.4	4806	1	US-10-438-246-15241	Sequence 15241, A
725	32.2	1.4	1045	8	US-11-713-768-1136	Sequence 1136, Ap	798	31.6	1.4	4806	1	US-10-438-246-15241	Sequence 15241, A
726	32.2	1.4	1110	8	US-11-514-704-9950	Sequence 9950, Ap	799	31.6	1.4	4806	1	US-10-438-246-15247	Sequence 15247, A
727	32.2	1.4	1410	8	US-11-796-730-1819	Sequence 1819, Ap	800	31.6	1.4	4915	1	US-10-438-246-23313	Sequence 23313, A
728	32.2	1.4	1884	8	US-11-713-768-72191	Sequence 72191, A	801	31.6	1.4	5127	1	US-10-438-246-15686	Sequence 15686, A
729	32.2	1.4	1887	8	US-11-713-768-71857	Sequence 71857, A	802	31.6	1.4	5217	1	US-10-438-246-23457	Sequence 23457, A
730	32.2	1.4	1930	8	US-11-514-704-4182	Sequence 4182, Ap	803	31.6	1.4	5271	1	US-10-438-246-23458	Sequence 23458, A
731	32.2	1.4	2093	8	US-11-514-704-18177	Sequence 18177, A	804	31.6	1.4	5311	8	US-11-514-704-14475	Sequence 14475, A
732	32.2	1.4	2354	8	US-10-562-377-136	Sequence 136, App	805	31.6	1.4	5376	1	US-10-438-246-15245	Sequence 15245, A
733	32.2	1.4	2437	8	US-11-514-704-20330	Sequence 20330, Ap	806	31.6	1.4	5484	1	US-10-438-246-15247	Sequence 15247, A
734	32.2	1.4	3087	8	US-11-514-704-8671	Sequence 8671, Ap	807	31.6	1.4	6053	1	US-10-438-246-23315	Sequence 23315, A
735	32.2	1.4	4188	1	US-10-533-069-2161	Sequence 2161, Ap	808	31.6	1.4	6216	1	US-10-438-246-11667	Sequence 11667, A
736	32.2	1.4	4467	8	US-11-514-704-12724	Sequence 12724, A	809	31.6	1.4	6710	8	US-11-514-704-3425	Sequence 3425, Ap
737	32.2	1.4	108845	8	US-11-257-477-7	Sequence 7, Appl	810	31.4	1.4	814	1	US-10-438-246-29536	Sequence 29536, A
738	32	1.4	1364	8	US-11-514-704-11963	Sequence 11963, A	811	31.4	1.4	1113	8	US-11-713-768-90304	Sequence 90304, A
739	32	1.4	1432	8	US-11-514-704-13370	Sequence 13370, A	812	31.4	1.4	1113	8	US-11-713-768-94060	Sequence 94060, A
740	32	1.4	2058	8	US-11-514-704-20311	Sequence 20311, A	813	31.4	1.4	1328	8	US-11-713-768-36434	Sequence 36434, A
741	32	1.4	2196	1	US-10-562-377-113	Sequence 113, App	c 814	31.4	1.4	1374	8	US-11-713-768-51528	Sequence 51528, A
742	32	1.4	2196	1	US-10-562-377-191	Sequence 191, App	c 815	31.4	1.4	1595	8	US-11-713-768-53650	Sequence 53650, A
743	32	1.4	2870	8	US-11-514-704-21377	Sequence 21377, A	816	31.4	1.4	2251	8	US-11-514-704-18493	Sequence 18493, A
744	32	1.4	3112	8	US-11-514-704-24454	Sequence 24454, A	817	31.4	1.4	2253	8	US-11-514-704-10958	Sequence 10958, A
745	32	1.4	3181	8	US-11-713-768-76092	Sequence 76092, A	818	31.4	1.4	2403	8	US-11-514-704-5138	Sequence 5138, Ap
746	32	1.4	3181	8	US-11-713-768-98308	Sequence 98308, A	819	31.4	1.4	2424	8	US-11-514-704-7902	Sequence 7902, Ap
747	31.8	1.4	827	8	US-11-640-897-1520	Sequence 1520, Ap	820	31.4	1.4	2499	8	US-11-514-704-7748	Sequence 7748, Ap
748	31.8	1.4	920	1	US-11-713-768-49404	Sequence 49404, A	821	31.4	1.4	3109	8	US-11-514-704-7417	Sequence 7417, Ap
749	31.8	1.4	989	8	US-10-438-246-29805	Sequence 29805, A	c 822	31.4	1.4	3212	8	US-11-514-704-21898	Sequence 21898, A
750	31.8	1.4	1620	8	US-11-514-704-20891	Sequence 20891, A	823	31.4	1.4	3318	1	US-10-438-246-11282	Sequence 11282, A
751	31.8	1.4	1620	8	US-11-713-768-48248	Sequence 48248, A	824	31.4	1.4	3372	1	US-10-438-246-21032	Sequence 21032, A
752	31.8	1.4	1620	8	US-11-713-768-50818	Sequence 50818, A	c 825	31.4	1.4	3473	8	US-11-514-704-14808	Sequence 14808, A
753	31.8	1.4	2296	8	US-11-514-704-15618	Sequence 15618, A	c 826	31.4	1.4	4865	8	US-11-514-704-19609	Sequence 19609, A
754	31.8	1.4	2728	1	US-10-562-377-180	Sequence 180, App	c 827	31.4	1.4	6669	8	US-11-509-784-5	Sequence 5, Appl
755	31.8	1.4	3077	8	US-11-514-704-14416	Sequence 14416, A	828	31.2	1.4	291	8	US-11-796-730-928	Sequence 928, App

829	31.2	1.4	513	8	US-11-679-492-51	Sequence 51, Appl	902	30.8	1.3	2435	8	US-11-514-704-9287	Sequence 9287, Ap
830	31.2	1.4	799	1	US-10-438-246-27238	Sequence 27238, A	c 903	30.8	1.3	3443	8	US-11-514-704-13827	Sequence 13827, A
831	31.2	1.4	969	8	US-11-713-768-21119	Sequence 21119, A	c 904	30.8	1.3	3548	1	US-10-533-069-315	Sequence 315, App
832	31.2	1.4	970	8	US-11-713-768-78164	Sequence 78164, A	c 905	30.8	1.3	3614	1	US-10-438-246-637	Sequence 637, App
c 833	31.2	1.4	1002	8	US-11-514-704-20841	Sequence 20841, A	c 906	30.8	1.3	4044	1	US-11-361-092-158	Sequence 158, App
c 834	31.2	1.4	1198	8	US-11-514-704-17788	Sequence 17788, A	c 907	30.8	1.3	4131	1	US-10-438-246-26533	Sequence 26533, A
c 835	31.2	1.4	1257	8	US-11-559-024-17	Sequence 17, Appl	c 908	30.8	1.3	4376	8	US-11-514-704-17236	Sequence 17236, A
c 836	31.2	1.4	1449	1	US-10-438-246-2495	Sequence 2495, Ap	c 909	30.8	1.3	4560	8	US-11-514-704-13871	Sequence 13871, A
c 837	31.2	1.4	1926	8	US-11-514-704-16080	Sequence 16080, A	c 910	30.8	1.3	5616	8	US-11-514-704-4461	Sequence 4461, Ap
c 838	31.2	1.4	1976	8	US-11-514-704-15594	Sequence 15594, A	c 911	30.8	1.3	8399	8	US-11-514-704-6949	Sequence 6949, Ap
c 839	31.2	1.4	2237	1	US-11-496-050-11	Sequence 11, Appl	c 912	30.8	1.3	9963	1	US-10-369-909-14	Sequence 14, Appl
c 840	31.2	1.4	2387	1	US-10-562-377-99	Sequence 99, Appl	c 913	30.8	1.3	152372	8	US-11-361-092-171	Sequence 171, App
c 841	31.2	1.4	2387	1	US-10-562-377-177	Sequence 177, App	c 914	30.6	1.3	1017	1	US-10-438-246-15326	Sequence 15326, A
c 842	31.2	1.4	2390	8	US-11-514-704-8552	Sequence 8552, Ap	c 915	30.6	1.3	1077	8	US-11-713-768-109951	Sequence 109951, A
c 843	31.2	1.4	2425	1	US-10-562-377-68	Sequence 68, Appl	c 916	30.6	1.3	1081	1	US-10-438-246-28121	Sequence 28121, A
c 844	31.2	1.4	2425	1	US-10-562-377-146	Sequence 146, App	c 917	30.6	1.3	1122	1	US-10-438-246-23339	Sequence 23339, A
c 845	31.2	1.4	2628	8	US-11-717-713-127	Sequence 127, App	c 918	30.6	1.3	1169	1	US-10-438-246-12292	Sequence 12292, A
c 846	31.2	1.4	2631	8	US-11-717-713-125	Sequence 125, App	c 919	30.6	1.3	1283	8	US-11-713-768-58949	Sequence 58949, A
c 847	31.2	1.4	2631	8	US-11-717-713-129	Sequence 129, App	c 920	30.6	1.3	1283	8	US-11-713-768-58949	Sequence 4633, Ap
c 848	31.2	1.4	2643	8	US-11-717-713-123	Sequence 123, App	c 921	30.6	1.3	2122	1	US-10-438-246-4633	Sequence 58, Appl
c 849	31.2	1.4	2708	8	US-11-717-713-131	Sequence 131, App	c 922	30.6	1.3	2354	1	US-10-562-377-58	Sequence 136, App
c 850	31.2	1.4	2739	8	US-11-717-713-115	Sequence 115, App	c 923	30.6	1.3	2354	1	US-10-562-377-136	Sequence 1138, A
c 851	31.2	1.4	2831	8	US-11-717-713-133	Sequence 133, App	c 924	30.6	1.3	2413	8	US-11-514-704-11938	Sequence 23230, A
c 852	31.2	1.4	3647	8	US-11-717-713-134	Sequence 134, App	c 925	30.6	1.3	2466	8	US-11-514-704-23230	Sequence 11792, A
c 853	31.2	1.4	4056	1	US-10-438-246-15695	Sequence 15695, A	c 926	30.6	1.3	2539	8	US-11-514-704-11792	Sequence 10543, A
c 854	31.2	1.4	4118	8	US-11-514-704-14178	Sequence 14178, A	c 927	30.6	1.3	2540	8	US-11-514-704-10543	Sequence 22973, A
c 855	31.2	1.4	4886	8	US-11-717-713-136	Sequence 136, App	c 928	30.6	1.3	2847	1	US-10-438-246-22973	Sequence 20087, A
c 856	31.2	1.4	5055	8	US-11-514-704-15502	Sequence 15502, A	c 929	30.6	1.3	2847	1	US-10-438-246-20087	Sequence 11, Appl
c 857	31.2	1.4	5076	8	US-11-717-713-135	Sequence 135, App	c 930	30.6	1.3	2676	8	US-11-700-267-11	Sequence 13621, A
c 858	31.2	1.4	5360	1	US-10-533-069-660	Sequence 660, App	c 931	30.6	1.3	2676	8	US-11-514-704-1408	Sequence 1408, Ap
c 859	31.2	1.4	5939	8	US-11-551-744-96	Sequence 96, Appl	c 932	30.6	1.3	2885	1	US-10-438-246-29311	Sequence 29311, A
c 860	31.2	1.4	7044	8	US-11-551-744-95	Sequence 95, Appl	c 933	30.6	1.3	3221	1	US-10-438-246-2717	Sequence 2717, Ap
c 861	31.2	1.4	21808	8	US-11-257-477-136	Sequence 136, App	c 934	30.6	1.3	3737	8	US-11-514-704-17192	Sequence 17192, A
c 862	31	1.4	475	8	US-11-713-768-15040	Sequence 15040, A	c 935	30.6	1.3	6258	8	US-11-514-704-7695	Sequence 7695, Ap
c 863	31	1.4	1143	8	US-11-649-663A-1917	Sequence 1917, Ap	c 936	30.6	1.3	133462	8	US-11-257-477-114	Sequence 114, App
c 864	31	1.4	1143	8	US-11-713-768-89390	Sequence 89390, A	c 937	30.4	1.3	454	8	US-11-744-695-32	Sequence 32, Appl
c 865	31	1.4	1143	8	US-11-713-768-93146	Sequence 93146, A	c 938	30.4	1.3	590	8	US-11-556-211-3	Sequence 3, Appli
c 866	31	1.4	1382	8	US-11-713-768-99282	Sequence 99282, A	c 939	30.4	1.3	603	8	US-11-713-768-100908	Sequence 100908, A
c 867	31	1.4	1383	8	US-11-713-768-23208	Sequence 23208, A	c 940	30.4	1.3	643	8	US-11-514-704-14151	Sequence 14151, A
c 868	31	1.4	1647	8	US-11-713-768-52739	Sequence 52739, A	c 941	30.4	1.3	864	8	US-11-556-211-2	Sequence 2, Appli
c 869	31	1.4	1742	8	US-11-713-768-67512	Sequence 67512, A	c 942	30.4	1.3	1071	8	US-11-514-704-997	Sequence 997, App
c 870	31	1.4	2087	8	US-11-514-704-22492	Sequence 22492, A	c 943	30.4	1.3	1118	8	US-11-514-704-10502	Sequence 10502, A
c 871	31	1.4	2283	8	US-11-713-768-47906	Sequence 47906, A	c 944	30.4	1.3	1124	8	US-11-713-768-41940	Sequence 41940, A
c 872	31	1.4	2290	1	US-10-562-377-165	Sequence 165, App	c 945	30.4	1.3	1126	8	US-11-556-211-1	Sequence 1, Appli
c 873	31	1.4	2290	1	US-10-562-377-165	Sequence 165, App	c 946	30.4	1.3	1345	8	US-11-649-663A-4661	Sequence 4661, Ap
c 874	31	1.4	2591	1	US-10-562-377-48	Sequence 48, Appl	c 947	30.4	1.3	1689	1	US-10-438-246-22677	Sequence 22677, A
c 875	31	1.4	3507	1	US-10-438-246-15690	Sequence 15690, A	c 948	30.4	1.3	1791	8	US-11-514-704-6944	Sequence 6944, Ap
c 876	31	1.4	3507	1	US-10-438-246-15696	Sequence 15696, A	c 949	30.4	1.3	1945	8	US-11-713-768-66483	Sequence 66483, Ap
c 877	31	1.4	4442	8	US-11-514-704-743	Sequence 743, App	c 950	30.4	1.3	1971	8	US-11-713-768-15947	Sequence 15947, A
c 878	31	1.4	4452	1	US-10-438-246-23453	Sequence 23453, A	c 951	30.4	1.3	1971	8	US-11-713-768-19579	Sequence 19579, A
c 879	31	1.4	4830	8	US-11-514-704-2946	Sequence 2946, Ap	c 952	30.4	1.3	1971	8	US-11-713-768-19579	Sequence 16000, A
c 880	31	1.4	7026	8	US-11-407-888-43	Sequence 43, Appl	c 953	30.4	1.3	2001	8	US-11-514-704-16000	Sequence 15999, A
c 881	31	1.4	7029	1	US-10-533-069-1102	Sequence 1102, Ap	c 954	30.4	1.3	2005	8	US-11-514-704-15999	Sequence 8, Appli
c 882	31	1.4	7767	1	US-10-438-246-15738	Sequence 15738, A	c 955	30.4	1.3	2282	1	US-10-596-627-8	Sequence 1247, Ap
c 883	31	1.4	42360	8	US-11-257-477-148	Sequence 148, App	c 956	30.4	1.3	2282	1	US-11-514-704-1247	Sequence 137, App
c 884	30.8	1.3	744	8	US-11-796-730-1934	Sequence 1934, Ap	c 957	30.4	1.3	2354	1	US-10-562-377-137	Sequence 137, App
c 885	30.8	1.3	1189	8	US-11-514-704-9949	Sequence 9949, Ap	c 958	30.4	1.3	2522	8	US-11-514-704-15691	Sequence 15691, A
c 886	30.8	1.3	1469	8	US-11-514-704-22082	Sequence 22082, A	c 959	30.4	1.3	2681	8	US-11-514-704-996	Sequence 996, App
c 887	30.8	1.3	1500	8	US-11-713-768-59255	Sequence 59255, A	c 960	30.4	1.3	2725	8	US-11-514-704-5659	Sequence 5659, App
c 888	30.8	1.3	1599	1	US-10-438-246-13633	Sequence 13633, A	c 961	30.4	1.3	3312	8	US-11-713-768-91073	Sequence 91073, A
c 889	30.8	1.3	1640	8	US-11-489-234-24	Sequence 24, Appl	c 962	30.4	1.3	3312	8	US-11-713-768-94829	Sequence 94829, A
c 890	30.8	1.3	1689	8	US-11-713-768-57018	Sequence 57018, A	c 963	30.4	1.3	4693	8	US-11-514-704-19043	Sequence 19043, A
c 891	30.8	1.3	1729	8	US-11-514-704-1136	Sequence 1136, Ap	c 964	30.4	1.3	4801	1	US-11-705-903-68	Sequence 68, Appl
c 892	30.8	1.3	1786	1	US-10-438-246-28667	Sequence 28667, A	c 965	30.4	1.3	6991	1	US-10-438-246-12924	Sequence 12924, A
c 893	30.8	1.3	1789	1	US-10-438-246-22714	Sequence 22714, A	c 966	30.4	1.3	7449	1	US-10-438-246-12925	Sequence 12925, A
c 894	30.8	1.3	1791	8	US-11-514-704-6944	Sequence 6944, Ap	c 967	30.2	1.3	7810	1	US-10-438-246-22655	Sequence 22655, A
c 895	30.8	1.3	1799	8	US-11-514-704-5069	Sequence 5069, Ap	c 968	30.2	1.3	456	1	US-10-438-246-11585	Sequence 11585, A
c 896	30.8	1.3	1850	8	US-11-713-768-53395	Sequence 53395, A	c 969	30.2	1.3	456	1	US-10-438-246-11586	Sequence 11586, A
c 897	30.8	1.3	1904	1	US-10-438-246-24764	Sequence 24764, A	c 970	30.2	1.3	590	1	US-10-438-246-21211	Sequence 21211, A
c 898	30.8	1.3	2272	8	US-11-713-768-111597	Sequence 111597, A	c 971	30.2	1.3	609	1	US-10-438-246-27258	Sequence 27258, A
c 899	30.8	1.3	2403	8	US-11-514-704-20947	Sequence 20947, A	c 972	30.2	1.3	878	8	US-11-514-704-6221	Sequence 6221, Ap
c 900	30.8	1.3	2432	8	US-11-514-704-18064	Sequence 18064, A	c 973	30.2	1.3	898	8	US-11-514-704-2153	Sequence 2153, Ap
c 901	30.8	1.3	2432	8	US-11-514-704-18548	Sequence 18548, A	c 974	30.2	1.3	964	8	US-11-514-704-2152	Sequence 2152, Ap
							c 975	30.2	1.3	1147	8	US-11-514-704-2931	Sequence 2931, Ap

975	30.2	1.3	1205	8	US-11-713-768-64299	Sequence 64299, A	1048	29.8	1.3	594	8	US-11-713-768-52880	Sequence 52880, A
c 976	30.2	1.3	1270	8	US-11-514-704-10724	Sequence 10724, A	1049	29.8	1.3	665	8	US-11-713-768-61286	Sequence 61286, A
c 977	30.2	1.3	1413	8	US-11-713-768-63866	Sequence 63866, A	c1050	29.8	1.3	716	1	US-10-438-246-27374	Sequence 27374, A
978	30.2	1.3	1487	8	US-11-514-704-13021	Sequence 13021, A	1051	29.8	1.3	756	1	US-10-533-069-877	Sequence 877, App
979	30.2	1.3	1665	8	US-11-514-704-6262	Sequence 6262, App	c1052	29.8	1.3	780	8	US-11-632-012-20	Sequence 20, Appl
980	30.2	1.3	1741	8	US-11-649-663A-725	Sequence 725, App	1053	29.8	1.3	846	8	US-11-514-704-18264	Sequence 18264, A
981	30.2	1.3	1741	8	US-11-713-768-3093	Sequence 3093, App	1054	29.8	1.3	944	8	US-11-713-768-105518	Sequence 105518, A
c 982	30.2	1.3	1777	8	US-11-713-768-2478	Sequence 2478, App	1055	29.8	1.3	961	8	US-11-713-768-23292	Sequence 23292, A
983	30.2	1.3	1993	1	US-10-438-246-27994	Sequence 27994, A	1056	29.8	1.3	966	8	US-11-713-768-77679	Sequence 77679, A
984	30.2	1.3	2117	8	US-11-514-704-4842	Sequence 4842, App	1057	29.8	1.3	994	1	US-10-438-246-26487	Sequence 26487, A
985	30.2	1.3	2257	8	US-11-514-704-15874	Sequence 15874, A	1058	29.8	1.3	996	8	US-11-713-768-3361	Sequence 3361, App
986	30.2	1.3	2403	8	US-11-514-704-20947	Sequence 20947, A	1059	29.8	1.3	1091	8	US-11-713-768-1457	Sequence 1457, App
c 987	30.2	1.3	2429	1	US-10-562-377-161	Sequence 161, App	1060	29.8	1.3	1171	1	US-10-438-246-29070	Sequence 29070, A
988	30.2	1.3	2466	8	US-11-514-704-18272	Sequence 18272, A	c1061	29.8	1.3	1201	8	US-11-649-663A-2185	Sequence 2185, App
c 989	30.2	1.3	2991	8	US-11-514-704-1139	Sequence 1139, App	c1062	29.8	1.3	1218	8	US-11-514-704-3115	Sequence 3115, App
c 990	30.2	1.3	3540	1	US-11-514-704-15288	Sequence 15288, A	1063	29.8	1.3	1300	8	US-11-713-768-52939	Sequence 52939, A
991	30.2	1.3	3744	1	US-10-438-246-15248	Sequence 15248, A	c1064	29.8	1.3	1331	8	US-11-514-704-1593	Sequence 1593, App
c 992	30.2	1.3	3834	8	US-11-514-704-7373	Sequence 7373, App	1065	29.8	1.3	1369	1	US-10-438-246-29069	Sequence 29069, A
993	30.2	1.3	4561	1	US-10-533-069-738	Sequence 738, App	1066	29.8	1.3	1431	8	US-11-632-012-53	Sequence 53, Appl
c 994	30.2	1.3	4708	8	US-11-514-704-9515	Sequence 9515, App	1067	29.8	1.3	1529	8	US-11-514-704-8568	Sequence 8568, App
c 995	30.2	1.3	5033	8	US-11-646-784-1	Sequence 1, Appl	1068	29.8	1.3	1605	8	US-11-514-704-11664	Sequence 11664, A
c 996	30.2	1.3	5033	8	US-11-646-945-1	Sequence 1, Appl	c1069	29.8	1.3	1642	8	US-11-625-698-3	Sequence 3, Appl
997	30.2	1.3	186854	8	US-11-796-028-34	Sequence 34, Appl	c1070	29.8	1.3	1754	8	US-11-552-437-87	Sequence 87, Appl
c 998	30.2	1.3	186854	8	US-11-796-027-34	Sequence 34, Appl	c1071	29.8	1.3	1856	8	US-11-514-704-3256	Sequence 3256, App
1000	30	1.3	521	1	US-10-438-246-23269	Sequence 23269, A	1072	29.8	1.3	1823	8	US-11-544-679-14	Sequence 14, Appl
1001	30	1.3	1031	1	US-10-438-246-2753	Sequence 2753, App	1073	29.8	1.3	1958	8	US-11-713-768-8207	Sequence 8207, App
1002	30	1.3	1245	1	US-10-438-246-4423	Sequence 4423, App	1074	29.8	1.3	1958	8	US-11-713-768-15424	Sequence 15424, A
1003	30	1.3	1245	8	US-11-514-704-19161	Sequence 19161, A	c1075	29.8	1.3	1991	1	US-10-438-246-29849	Sequence 29849, A
c1004	30	1.3	1295	8	US-11-514-704-21501	Sequence 21501, A	1076	29.8	1.3	2001	8	US-11-713-768-17829	Sequence 17829, A
c1005	30	1.3	1481	8	US-11-713-768-67332	Sequence 67332, A	1077	29.8	1.3	2001	8	US-11-514-704-2759	Sequence 2759, App
c1006	30	1.3	1547	8	US-11-649-663A-281	Sequence 281, App	c1078	29.8	1.3	2122	1	US-10-533-069-240	Sequence 240, App
c1007	30	1.3	1830	1	US-10-438-246-5031	Sequence 5031, App	1079	29.8	1.3	2148	8	US-11-713-768-85258	Sequence 85258, A
c1008	30	1.3	1956	8	US-11-514-704-1183	Sequence 1183, App	1080	29.8	1.3	2157	8	US-11-713-768-81583	Sequence 81583, A
1009	30	1.3	2028	8	US-11-713-768-75152	Sequence 75152, A	1081	29.8	1.3	2175	1	US-10-438-246-29068	Sequence 29068, A
1010	30	1.3	2075	8	US-11-713-768-87853	Sequence 87853, A	c1082	29.8	1.3	2303	8	US-11-713-768-95758	Sequence 95758, A
1011	30	1.3	2086	8	US-11-713-768-40602	Sequence 40602, A	1083	29.8	1.3	2331	8	US-11-514-704-12982	Sequence 12982, A
1012	30	1.3	2115	8	US-11-713-768-66036	Sequence 66036, A	1084	29.8	1.3	2688	8	US-11-514-704-1721	Sequence 1721, App
c1013	30	1.3	2189	8	US-11-713-768-19423	Sequence 19423, A	c1085	29.8	1.3	2820	1	US-10-438-246-2559	Sequence 2559, App
c1014	30	1.3	2337	8	US-11-713-768-100364	Sequence 100364, A	1086	29.8	1.3	2910	1	US-10-438-246-22109	Sequence 22109, A
1015	30	1.3	2307	8	US-11-713-768-78784	Sequence 78784, A	c1087	29.8	1.3	2945	8	US-11-514-704-22190	Sequence 22190, A
c1016	30	1.3	2366	8	US-11-514-704-361	Sequence 361, App	1088	29.8	1.3	2958	1	US-10-533-069-1975	Sequence 1975, App
c1017	30	1.3	2395	8	US-11-713-768-75383	Sequence 75383, A	c1089	29.8	1.3	3084	1	US-10-438-246-12698	Sequence 12698, A
1018	30	1.3	2649	8	US-11-713-768-46527	Sequence 46527, A	c1090	29.8	1.3	3084	1	US-10-438-246-22109	Sequence 22109, A
1019	30	1.3	2765	8	US-11-713-768-47944	Sequence 47944, A	1091	29.8	1.3	3462	1	US-10-438-246-11799	Sequence 11799, A
1020	30	1.3	2765	8	US-11-713-768-48036	Sequence 48036, A	1092	29.8	1.3	3462	1	US-10-438-246-21370	Sequence 21370, A
1021	30	1.3	2864	8	US-11-514-704-22992	Sequence 22992, A	1093	29.8	1.3	3637	8	US-11-544-679-13	Sequence 13, Appl
c1022	30	1.3	3060	8	US-11-552-437-215	Sequence 215, App	c1094	29.8	1.3	4226	8	US-11-514-704-5183	Sequence 5183, App
c1023	30	1.3	3089	8	US-11-514-704-496	Sequence 496, App	c1095	29.8	1.3	4281	1	US-10-438-246-15319	Sequence 15319, A
c1024	30	1.3	3094	8	US-11-514-704-7352	Sequence 7352, App	1096	29.8	1.3	4281	1	US-10-438-246-22896	Sequence 22896, A
1025	30	1.3	3139	8	US-11-514-704-16842	Sequence 16842, A	c1098	29.8	1.3	4634	8	US-11-514-704-7885	Sequence 7885, App
c1026	30	1.3	3190	1	US-10-562-377-72	Sequence 72, Appl	1099	29.8	1.3	4635	1	US-10-438-246-15318	Sequence 15318, A
c1027	30	1.3	3190	1	US-10-562-377-94	Sequence 94, Appl	1100	29.8	1.3	4635	1	US-10-438-246-22895	Sequence 22895, A
c1028	30	1.3	3231	8	US-11-514-704-12648	Sequence 12648, A	c1101	29.8	1.3	5057	8	US-11-514-704-17543	Sequence 17543, A
1029	30	1.3	3237	8	US-11-796-730-1375	Sequence 1375, App	1102	29.6	1.3	6135	8	US-11-514-704-18013	Sequence 18013, A
1030	30	1.3	3566	8	US-11-514-704-18208	Sequence 18208, A	1103	29.6	1.3	711	1	US-10-438-246-12987	Sequence 12987, A
c1031	30	1.3	4131	1	US-10-438-246-26553	Sequence 26553, A	c1105	29.6	1.3	742	8	US-11-514-704-14660	Sequence 14660, A
c1032	30	1.3	4361	8	US-11-514-704-20282	Sequence 20282, A	c1105	29.6	1.3	879	1	US-10-438-246-12514	Sequence 12514, A
1033	30	1.3	4597	8	US-11-723-507-4	Sequence 4, Appl	1106	29.6	1.3	926	8	US-11-713-768-743	Sequence 743, App
c1034	30	1.3	4611	1	US-10-438-246-13849	Sequence 13849, A	1107	29.6	1.3	982	8	US-11-713-768-10318	Sequence 10318, A
1035	30	1.3	4650	1	US-10-438-246-13996	Sequence 13996, A	c1108	29.6	1.3	1003	1	US-10-438-246-27872	Sequence 27872, A
1036	30	1.3	4650	1	US-10-438-246-23054	Sequence 23054, A	1109	29.6	1.3	1037	8	US-11-713-768-9951	Sequence 9951, App
1037	30	1.3	4806	1	US-10-438-246-15249	Sequence 15249, A	1110	29.6	1.3	1085	1	US-10-438-246-20256	Sequence 20256, A
1038	30	1.3	4950	1	US-10-438-246-13840	Sequence 13840, A	1111	29.6	1.3	1101	1	US-10-438-246-13276	Sequence 13276, A
1039	30	1.3	5175	1	US-10-438-246-13800	Sequence 13800, A	1112	29.6	1.3	1107	8	US-11-514-704-18785	Sequence 18785, A
1040	30	1.3	5196	1	US-10-438-246-13832	Sequence 13832, A	1113	29.6	1.3	1233	8	US-11-514-704-12640	Sequence 12640, A
1041	30	1.3	5392	8	US-11-514-704-14144	Sequence 14144, A	c1114	29.6	1.3	1253	8	US-11-713-768-44730	Sequence 44730, A
c1042	30	1.3	6116	8	US-11-514-704-13101	Sequence 13101, A	1115	29.6	1.3	1334	8	US-11-713-768-53246	Sequence 53246, A
1043	30	1.3	6220	8	US-11-723-507-3	Sequence 3, Appl	1116	29.6	1.3	1398	8	US-11-713-768-5511	Sequence 5511, App
c1044	30	1.3	7581	8	US-11-514-704-20599	Sequence 20599, A	c1117	29.6	1.3	1415	1	US-10-438-246-28381	Sequence 28381, App
1045	30	1.3	8285	1	US-10-438-246-22987	Sequence 22987, A	1118	29.6	1.3	1451	8	US-11-713-768-60684	Sequence 60684, A
1046	30	1.3	8922	8	US-11-514-704-19573	Sequence 19573, A	1119	29.6	1.3	1484	8	US-11-514-704-19816	Sequence 19816, A
1047	30	1.3	10053	1	US-10-438-246-13851	Sequence 13851, A	c1120	29.6	1.3	1507	8	US-11-713-768-52831	Sequence 52831, A

c1121	29.6	1.3	1530	1	US-10-438-246-22499	Sequence 22499, A	1194	29.4	1.3	5533	1	US-10-533-069-198	Sequence 198, App
c1122	29.6	1.3	1540	8	US-11-713-768-51642	Sequence 51642, A	c1195	29.4	1.3	5805	8	US-11-514-704-13868	Sequence 13868, A
c1123	29.6	1.3	1574	8	US-11-514-704-5453	Sequence 5453, Ap	c1196	29.4	1.3	6565	8	US-11-514-704-3312	Sequence 3312, Ap
c1124	29.6	1.3	1614	8	US-11-713-768-49209	Sequence 49209, A	c1197	29.4	1.3	7325	8	US-11-514-704-14679	Sequence 1469, Ap
c1125	29.6	1.3	1703	1	US-10-438-246-22340	Sequence 22340, A	c1198	29.4	1.3	7825	8	US-11-514-704-1679	Sequence 1679, Ap
c1126	29.6	1.3	1833	1	US-10-438-246-27366	Sequence 27366, A	c1199	29.4	1.3	14756	1	US-10-586-772A-2	Sequence 2, Appli
c1127	29.6	1.3	1833	8	US-11-514-704-20121	Sequence 20121, A	c1200	29.4	1.3	14792	1	US-10-586-772A-4	Sequence 4, Appli
c1128	29.6	1.3	2045	8	US-11-713-768-44758	Sequence 44758, A	c1201	29.4	1.3	37180	8	US-11-257-477-13	Sequence 13, Appl
c1129	29.6	1.3	2668	8	US-11-514-704-1785	Sequence 1785, Ap	c1202	29.2	1.3	574	8	US-11-713-768-62259	Sequence 62259, A
c1130	29.6	1.3	2521	8	US-11-713-768-79500	Sequence 79500, A	c1203	29.2	1.3	612	8	US-10-438-246-11588	Sequence 11588, A
c1131	29.6	1.3	2675	8	US-11-514-704-6581	Sequence 6581, Ap	c1204	29.2	1.3	622	8	US-11-713-768-68894	Sequence 68894, A
c1132	29.6	1.3	2700	8	US-11-713-768-46823	Sequence 46823, A	c1205	29.2	1.3	642	8	US-11-796-730-1115	Sequence 1115, Ap
c1133	29.6	1.3	2769	8	US-11-649-663A-3393	Sequence 3393, Ap	c1206	29.2	1.3	864	1	US-10-438-246-11321	Sequence 11321, A
c1134	29.6	1.3	3077	8	US-11-519-397-45	Sequence 45, Appl	c1207	29.2	1.3	876	1	US-10-438-246-11923	Sequence 11923, A
c1135	29.6	1.3	3876	8	US-11-514-704-23552	Sequence 23552, A	c1208	29.2	1.3	878	1	US-10-438-246-21214	Sequence 21214, A
c1136	29.6	1.3	6148	8	US-11-514-704-54394	Sequence 5446, Ap	c1209	29.2	1.3	984	1	US-10-438-246-29367	Sequence 29367, A
c1137	29.6	1.3	7264	8	US-11-514-704-24394	Sequence 24394, A	c1210	29.2	1.3	1007	8	US-11-649-663A-5059	Sequence 5099, Ap
c1138	29.6	1.3	30304	8	US-11-257-477-128	Sequence 128, App	c1211	29.2	1.3	1121	8	US-11-713-768-41966	Sequence 41966, A
c1139	29.6	1.3	43816	8	US-11-699-229-58	Sequence 58, Appl	c1212	29.2	1.3	1135	1	US-10-438-246-26744	Sequence 26744, A
c1140	29.4	1.3	750	8	US-11-514-704-24161	Sequence 24161, A	c1213	29.2	1.3	1187	1	US-10-438-246-26539	Sequence 26539, A
c1141	29.4	1.3	768	8	US-11-514-704-5414	Sequence 5414, Ap	c1214	29.2	1.3	1200	8	US-10-547-956-361	Sequence 361, App
c1142	29.4	1.3	819	8	US-11-514-704-9895	Sequence 9895, Ap	c1215	29.2	1.3	1368	8	US-11-407-888-60	Sequence 60, Appl
c1143	29.4	1.3	820	8	US-11-514-704-19278	Sequence 19278, A	c1216	29.2	1.3	1431	1	US-10-533-069-1085	Sequence 1085, Ap
c1144	29.4	1.3	903	8	US-11-514-704-17429	Sequence 17429, A	c1217	29.2	1.3	1490	8	US-11-713-768-53125	Sequence 53125, A
c1145	29.4	1.3	951	1	US-10-438-246-11710	Sequence 11710, A	c1218	29.2	1.3	1504	8	US-11-514-704-11750	Sequence 11750, A
c1146	29.4	1.3	1000	8	US-11-360-039-59	Sequence 59, Appl	c1219	29.2	1.3	1506	1	US-10-438-246-21570	Sequence 21570, A
c1147	29.4	1.3	1023	8	US-11-514-704-19266	Sequence 19266, A	c1220	29.2	1.3	1559	8	US-11-713-768-102276	Sequence 102276, A
c1148	29.4	1.3	1024	8	US-11-360-039-67	Sequence 67, Appl	c1221	29.2	1.3	1608	8	US-11-713-768-23812	Sequence 23812, A
c1149	29.4	1.3	1097	1	US-10-438-246-13807	Sequence 13807, A	c1222	29.2	1.3	1608	8	US-11-713-768-43938	Sequence 43938, A
c1150	29.4	1.3	1099	1	US-10-438-246-29727	Sequence 29727, A	c1223	29.2	1.3	1621	8	US-11-713-768-6229	Sequence 6229, Ap
c1151	29.4	1.3	1315	8	US-11-514-704-6516	Sequence 6516, Ap	c1224	29.2	1.3	1635	8	US-11-713-768-75144	Sequence 75144, A
c1152	29.4	1.3	1335	8	US-11-713-768-56948	Sequence 56948, A	c1225	29.2	1.3	1647	1	US-10-438-246-26477	Sequence 26477, A
c1153	29.4	1.3	1502	8	US-11-728-567-133	Sequence 133, App	c1226	29.2	1.3	1655	8	US-11-713-768-59271	Sequence 59271, A
c1154	29.4	1.3	1519	1	US-10-438-246-21303	Sequence 21303, A	c1227	29.2	1.3	1762	8	US-11-514-704-14659	Sequence 14659, A
c1155	29.4	1.3	1635	1	US-10-438-246-247	Sequence 247, App	c1228	29.2	1.3	1896	8	US-11-713-768-52988	Sequence 52988, A
c1156	29.4	1.3	1636	8	US-11-514-704-20652	Sequence 20652, A	c1229	29.2	1.3	1898	1	US-10-438-246-26498	Sequence 26498, A
c1157	29.4	1.3	1745	8	US-11-514-704-7596	Sequence 7596, Ap	c1230	29.2	1.3	1912	8	US-11-713-768-108947	Sequence 108947, A
c1158	29.4	1.3	1784	8	US-11-514-704-14638	Sequence 14638, A	c1231	29.2	1.3	1980	8	US-11-514-704-15437	Sequence 15437, A
c1159	29.4	1.3	1801	8	US-11-649-663A-2659	Sequence 2659, Ap	c1232	29.2	1.3	1987	8	US-11-713-768-84539	Sequence 84539, A
c1160	29.4	1.3	1806	1	US-10-438-246-12797	Sequence 12797, A	c1233	29.2	1.3	2089	8	US-11-713-768-41897	Sequence 41897, A
c1161	29.4	1.3	1861	8	US-11-514-704-19267	Sequence 19267, A	c1234	29.2	1.3	2220	1	US-10-533-069-431	Sequence 431, App
c1162	29.4	1.3	1955	8	US-11-713-768-110274	Sequence 110274, A	c1235	29.2	1.3	2231	8	US-11-560-738A-19	Sequence 19, Appl
c1163	29.4	1.3	1971	8	US-11-713-768-89083	Sequence 89083, A	c1236	29.2	1.3	2320	8	US-11-514-704-7832	Sequence 7832, Ap
c1164	29.4	1.3	1971	8	US-11-713-768-92839	Sequence 92839, A	c1237	29.2	1.3	2326	8	US-11-514-704-24623	Sequence 24623, A
c1165	29.4	1.3	1988	8	US-11-649-663A-2859	Sequence 2859, Ap	c1238	29.2	1.3	2345	1	US-10-562-377-124	Sequence 124, App
c1166	29.4	1.3	2025	8	US-11-713-768-69474	Sequence 69474, A	c1239	29.2	1.3	2354	1	US-10-562-377-59	Sequence 59, Appl
c1167	29.4	1.3	2053	8	US-11-514-704-10379	Sequence 10379, A	c1240	29.2	1.3	2356	1	US-10-562-377-133	Sequence 133, App
c1168	29.4	1.3	2080	8	US-11-713-768-48947	Sequence 48947, A	c1241	29.2	1.3	2412	8	US-11-514-704-13567	Sequence 13567, A
c1169	29.4	1.3	2090	8	US-11-514-704-15955	Sequence 15955, A	c1242	29.2	1.3	2624	8	US-11-514-704-18528	Sequence 18528, A
c1170	29.4	1.3	2116	8	US-11-514-704-7949	Sequence 7949, Ap	c1243	29.2	1.3	2823	8	US-11-514-704-13564	Sequence 13564, A
c1171	29.4	1.3	2117	1	US-10-438-246-22226	Sequence 22226, A	c1244	29.2	1.3	2882	8	US-11-514-704-6843	Sequence 6843, Ap
c1172	29.4	1.3	2286	8	US-11-514-704-8891	Sequence 8891, Ap	c1245	29.2	1.3	2916	8	US-11-514-704-6874	Sequence 6874, Ap
c1173	29.4	1.3	2290	1	US-10-562-377-87	Sequence 87, Appl	c1246	29.2	1.3	2924	1	US-10-438-246-28088	Sequence 28088, A
c1174	29.4	1.3	2320	8	US-11-713-768-107648	Sequence 107648, A	c1247	29.2	1.3	3077	8	US-11-514-704-18561	Sequence 18561, A
c1175	29.4	1.3	2354	1	US-10-562-377-58	Sequence 58, Appl	c1248	29.2	1.3	3089	8	US-11-514-704-19908	Sequence 19908, A
c1176	29.4	1.3	2415	8	US-11-649-663A-1563	Sequence 1563, Ap	c1249	29.2	1.3	3384	8	US-11-713-768-70196	Sequence 70196, A
c1177	29.4	1.3	2415	8	US-11-713-768-80296	Sequence 80296, A	c1250	29.2	1.3	4038	1	US-10-438-246-14518	Sequence 14518, A
c1178	29.4	1.3	2528	8	US-10-533-069-196	Sequence 196, App	c1251	29.2	1.3	4336	1	US-11-514-704-5780	Sequence 5780, Ap
c1179	29.4	1.3	3100	8	US-11-514-704-5336	Sequence 5336, Ap	c1252	29.2	1.3	5103	1	US-10-438-246-11671	Sequence 11671, A
c1180	29.4	1.3	3108	8	US-11-514-704-5389	Sequence 5389, Ap	c1253	29.2	1.3	6125	8	US-11-514-704-13369	Sequence 13369, A
c1181	29.4	1.3	3316	8	US-11-514-704-7331	Sequence 7331, Ap	c1254	29.2	1.3	6606	8	US-11-514-704-21836	Sequence 21836, A
c1182	29.4	1.3	3879	1	US-10-438-246-15692	Sequence 15692, A	c1255	29.2	1.3	6701	8	US-11-514-704-11834	Sequence 11834, A
c1183	29.4	1.3	3881	8	US-11-738-671-20	Sequence 20, Appl	c1256	29.2	1.3	7536	1	US-10-438-246-5331	Sequence 5331, Ap
c1184	29.4	1.3	3887	8	US-11-514-704-24455	Sequence 24455, A	c1257	29.2	1.3	8937	1	US-10-438-246-14551	Sequence 14551, A
c1185	29.4	1.3	3977	8	US-11-514-704-913	Sequence 913, App	c1258	29.2	1.3	12179	1	US-10-566-593-4	Sequence 4, Appli
c1186	29.4	1.3	4097	8	US-11-514-704-10929	Sequence 10929, A	c1259	29	1.3	537	1	US-10-554-789-3	Sequence 3, Appli
c1187	29.4	1.3	4274	8	US-11-514-704-22738	Sequence 22738, A	c1260	29	1.3	566	8	US-10-438-246-942	Sequence 942, App
c1188	29.4	1.3	4587	1	US-10-438-246-13990	Sequence 13990, A	c1261	29	1.3	594	8	US-11-796-730-1801	Sequence 1801, Ap
c1189	29.4	1.3	4656	8	US-11-514-704-18405	Sequence 18405, A	c1262	29	1.3	683	1	US-10-438-246-28053	Sequence 28053, A
c1190	29.4	1.3	4803	1	US-10-438-246-15681	Sequence 15681, A	c1263	29	1.3	826	1	US-10-533-069-1677	Sequence 1677, Ap
c1191	29.4	1.3	4803	1	US-10-438-246-23455	Sequence 23455, A	c1264	29	1.3	837	8	US-11-728-567-857	Sequence 857, App
c1192	29.4	1.3	5118	1	US-10-438-246-11002	Sequence 11002, A	c1265	29	1.3	878	1	US-10-438-246-4019	Sequence 4019, Ap
c1193	29.4	1.3	5528	8	US-11-524-550-1	Sequence 1, Appli	c1266	29	1.3	981	8	US-11-796-730-1444	Sequence 1444, Ap

1267	29	1.3	1228	8	US-11-713-768-2985	Sequence 2985, Ap	c1340	28.8	1.3	1151	8	US-11-514-704-23748	Sequence 23748, A
1268	29	1.3	1236	8	US-11-514-704-20464	Sequence 20464, A	1341	28.8	1.3	1152	8	US-11-552-437-243	Sequence 243, App
1269	29	1.3	1257	8	US-11-559-024-17	Sequence 17, Appl	1342	28.8	1.3	1152	8	US-11-565-395-1	Sequence 1, Appl
1270	29	1.3	1262	8	US-11-514-704-4391	Sequence 4391, Ap	c1343	28.8	1.3	1156	8	US-11-713-768-62840	Sequence 62840, A
1271	29	1.3	1266	1	US-10-547-956-211	Sequence 211, App	1344	28.8	1.3	1167	1	US-10-533-069-1428	Sequence 1428, Ap
1272	29	1.3	1280	8	US-11-514-704-12788	Sequence 12788, A	c1345	28.8	1.3	1167	8	US-11-649-663A-4519	Sequence 4519, Ap
1273	29	1.3	1295	8	US-11-514-704-4141	Sequence 4141, Ap	1346	28.8	1.3	1175	8	US-11-713-768-10322	Sequence 10322, A
1274	29	1.3	1337	8	US-11-514-704-11624	Sequence 11624, A	1347	28.8	1.3	1191	8	US-11-713-768-58812	Sequence 58812, A
1275	29	1.3	1438	8	US-11-514-704-21006	Sequence 21006, A	1348	28.8	1.3	1229	8	US-11-713-768-52951	Sequence 52951, A
1276	29	1.3	1484	8	US-11-514-704-24884	Sequence 24884, A	c1349	28.8	1.3	1259	1	US-10-533-069-1754	Sequence 1754, Ap
1277	29	1.3	1488	1	US-10-554-789-6	Sequence 6, Appli	1350	28.8	1.3	1271	8	US-11-713-768-28009	Sequence 28009, A
1278	29	1.3	1530	8	US-11-514-704-12269	Sequence 12269, A	1351	28.8	1.3	1271	8	US-11-713-768-31599	Sequence 31599, A
1279	29	1.3	1567	8	US-10-438-246-21446	Sequence 21446, A	1352	28.8	1.3	1272	8	US-11-514-704-1648	Sequence 1648, Ap
1280	29	1.3	1776	8	US-11-713-768-105081	Sequence 105081, A	c1353	28.8	1.3	1362	1	US-10-438-246-3898	Sequence 3898, Ap
1281	29	1.3	1780	8	US-11-713-768-62051	Sequence 62051, A	1354	28.8	1.3	1371	8	US-11-649-663A-4219	Sequence 4219, Ap
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1283	29	1.3	1839	8	US-11-713-768-103368	Sequence 103368, A	1356	28.8	1.3	1377	1	US-10-438-246-22173	Sequence 22173, A
1284	29	1.3	1840	8	US-11-713-768-42079	Sequence 42079, A	1357	28.8	1.3	1395	8	US-11-713-768-69218	Sequence 69218, A
1285	29	1.3	1848	8	US-11-514-704-15820	Sequence 15820, A	1358	28.8	1.3	1498	8	US-11-514-704-18972	Sequence 18972, A
1286	29	1.3	1879	8	US-11-713-768-28153	Sequence 28153, A	1359	28.8	1.3	1564	8	US-11-649-663A-797	Sequence 797, App
1287	29	1.3	1879	8	US-11-713-768-31743	Sequence 31743, A	1360	28.8	1.3	1564	8	US-11-713-768-8191	Sequence 8191, Ap
1288	29	1.3	1879	8	US-11-713-768-38559	Sequence 38559, A	c1361	28.8	1.3	1579	8	US-11-514-704-22822	Sequence 22822, A
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1290	29	1.3	1925	8	US-11-713-768-55443	Sequence 55443, A	1363	28.8	1.3	1740	8	US-11-728-567-1003	Sequence 1003, Ap
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1292	29	1.3	2000	8	US-11-514-704-11794	Sequence 11794, A	1365	28.8	1.3	1811	8	US-11-514-704-8579	Sequence 8579, Ap
1293	29	1.3	2098	8	US-11-713-768-60838	Sequence 60838, A	1366	28.8	1.3	1815	8	US-11-514-704-8458	Sequence 8458, Ap
1294	29	1.3	2284	8	US-10-562-377-133	Sequence 8607, Ap	c1367	28.8	1.3	1948	8	US-11-514-704-23749	Sequence 23749, A
1295	29	1.3	2356	1	US-10-562-377-133	Sequence 133, App	1368	28.8	1.3	1970	8	US-11-514-704-1864	Sequence 1864, Ap
1296	29	1.3	2369	8	US-11-514-704-15701	Sequence 15701, A	1369	28.8	1.3	1993	8	US-11-713-768-83127	Sequence 83127, A
1297	29	1.3	2377	8	US-11-514-704-9965	Sequence 9965, Ap	1370	28.8	1.3	2041	8	US-11-514-704-16217	Sequence 16217, A
1298	29	1.3	2419	8	US-11-514-704-8150	Sequence 8150, Ap	1371	28.8	1.3	2053	1	US-10-438-246-3623	Sequence 3623, Ap
1299	29	1.3	2516	8	US-11-713-768-20812	Sequence 20812, A	c1372	28.8	1.3	2060	1	US-10-438-246-26854	Sequence 26854, A
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1301	29	1.3	2590	8	US-11-514-704-23487	Sequence 23487, A	1374	28.8	1.3	2105	8	US-11-514-704-10607	Sequence 10607, A
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1303	29	1.3	2998	8	US-11-514-704-7985	Sequence 7985, Ap	1376	28.8	1.3	2232	8	US-11-514-704-15330	Sequence 15330, A
1304	29	1.3	3014	8	US-11-514-704-7799	Sequence 7799, Ap	1377	28.8	1.3	2329	8	US-11-713-768-90716	Sequence 90716, A
1305	29	1.3	3044	8	US-10-533-069-311	Sequence 311, App	1378	28.8	1.3	2330	8	US-11-713-768-30481	Sequence 30481, A
1306	29	1.3	3381	1	US-10-533-069-311	Sequence 195, App	1379	28.8	1.3	2330	8	US-11-713-768-34071	Sequence 34071, A
1307	29	1.3	3404	1	US-10-562-377-195	Sequence 195, App	1380	28.8	1.3	2355	8	US-11-713-768-106758	Sequence 106758, A
1308	29	1.3	3649	8	US-11-514-704-15819	Sequence 15819, A	c1381	28.8	1.3	2396	1	US-10-438-246-4519	Sequence 4519, Ap
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1310	29	1.3	3825	1	US-10-438-246-22257	Sequence 22257, A	1383	28.8	1.3	2502	8	US-11-514-704-3392	Sequence 3392, Ap
1311	29	1.3	4019	8	US-11-514-704-530	Sequence 530, App	1384	28.8	1.3	2519	8	US-11-514-704-20661	Sequence 20661, A
1312	29	1.3	4052	8	US-11-514-704-24062	Sequence 24062, A	1385	28.8	1.3	2561	8	US-11-514-704-1085	Sequence 1085, Ap
1313	29	1.3	4077	1	US-10-533-069-2360	Sequence 2360, Ap	c1386	28.8	1.3	2618	8	US-11-514-704-10818	Sequence 10818, A
1314	29	1.3	4243	1	US-10-533-069-1848	Sequence 1848, Ap	1387	28.8	1.3	2693	8	US-11-514-704-13841	Sequence 13841, A
1315	29	1.3	4428	1	US-10-438-246-15680	Sequence 15680, A	c1388	28.8	1.3	2759	8	US-11-514-704-21301	Sequence 21301, A
1316	29	1.3	4501	1	US-10-438-246-23452	Sequence 23452, A	1389	28.8	1.3	2798	8	US-11-514-704-8268	Sequence 8268, Ap
1317	29	1.3	5207	1	US-10-438-246-5098	Sequence 5098, Ap	c1390	28.8	1.3	2866	8	US-11-514-704-8268	Sequence 8268, Ap
1318	29	1.3	5700	8	US-11-514-704-10512	Sequence 10512, A	c1391	28.8	1.3	2895	1	US-10-438-246-27996	Sequence 27996, A
1319	29	1.3	6405	8	US-11-496-050-26	Sequence 26, Appl	c1392	28.8	1.3	2992	8	US-11-514-704-12865	Sequence 12865, A
1320	29	1.3	7024	8	US-11-514-704-22807	Sequence 22807, A	c1393	28.8	1.3	3328	8	US-11-514-704-3378	Sequence 3378, Ap
1321	29	1.3	7209	8	US-11-514-704-17883	Sequence 17883, A	1394	28.8	1.3	3398	8	US-11-514-704-3571	Sequence 3571, Ap
1322	29	1.3	10003	8	US-11-514-704-4952	Sequence 4952, Ap	1395	28.8	1.3	3798	8	US-11-713-768-88621	Sequence 88621, A
1323	28.8	1.3	426	8	US-11-713-768-69109	Sequence 69109, A	1396	28.8	1.3	3798	8	US-11-713-768-92377	Sequence 92377, A
1324	28.8	1.3	540	8	US-11-713-768-57546	Sequence 57546, A	1397	28.8	1.3	3873	8	US-11-514-704-17339	Sequence 17339, A
1325	28.8	1.3	558	8	US-11-796-730-1330	Sequence 1330, Ap	1398	28.8	1.3	3890	8	US-11-514-704-12112	Sequence 12112, A
1326	28.8	1.3	594	8	US-11-796-730-2142	Sequence 2142, Ap	1399	28.8	1.3	4161	8	US-10-438-246-74098	Sequence 74098, Ap
1327	28.8	1.3	641	8	US-11-514-704-16168	Sequence 16168, A	c1400	28.8	1.3	4266	1	US-10-438-246-4996	Sequence 4996, Ap
1328	28.8	1.3	809	8	US-11-514-704-5550	Sequence 5550, Ap	c1401	28.8	1.3	4445	8	US-11-514-704-4680	Sequence 4680, Ap
1329	28.8	1.3	870	8	US-11-713-768-42515	Sequence 42515, A	1402	28.8	1.3	4812	8	US-11-514-704-18708	Sequence 18708, A
1330	28.8	1.3	890	8	US-11-713-768-100538	Sequence 100538, A	c1403	28.8	1.3	5009	8	US-11-514-704-17657	Sequence 17657, A
1331	28.8	1.3	927	1	US-10-438-246-1303	Sequence 1303, Ap	c1404	28.8	1.3	6058	8	US-11-514-704-556	Sequence 556, App
1332	28.8	1.3	971	8	US-11-514-704-23751	Sequence 23751, A	1405	28.8	1.3	6488	8	US-11-713-768-11131	Sequence 11131, A
1333	28.8	1.3	983	8	US-11-552-437-47	Sequence 47, Appl	1406	28.6	1.3	510	1	US-10-438-246-12421	Sequence 12421, A
1334	28.8	1.3	990	8	US-11-713-768-71362	Sequence 71362, A	1407	28.6	1.3	658	8	US-11-514-704-5120	Sequence 5120, Ap
1335	28.8	1.3	1022	8	US-11-514-704-15709	Sequence 15709, A	1408	28.6	1.3	713	8	US-11-713-768-465	Sequence 465, App
1336	28.8	1.3	1050	1	US-10-438-246-27331	Sequence 27331, A	1409	28.6	1.3	795	8	US-11-713-768-105161	Sequence 105161, A
1337	28.8	1.3	1078	8	US-11-713-768-54359	Sequence 54359, A	1410	28.6	1.3	800	8	US-11-713-768-20823	Sequence 20823, A
1338	28.8	1.3	1139	8	US-11-739-906-62	Sequence 62, Appl	1411	28.6	1.3	825	8	US-11-524-564-199	Sequence 199, App
1339	28.8	1.3	1139	8	US-11-739-872-62	Sequence 62, Appl	c1412	28.6	1.3	827	8	US-11-514-704-1933	Sequence 1933, Ap

1413	28.6	1.3	828	8	US-11-713-768-75717	Sequence 75717, A	1486	28.6	1.3	4723	1	US-10-438-246-199	Sequence 139, App
cl1414	28.6	1.3	852	8	US-11-514-704-7305	Sequence 7305, Ap	1487	28.6	1.3	4788	1	US-10-533-069-1582	Sequence 1582, Ap
1415	28.6	1.3	917	8	US-11-713-768-61858	Sequence 61858, A	1488	28.6	1.3	5451	8	US-11-514-704-5218	Sequence 5218, Ap
1416	28.6	1.3	936	1	US-10-438-246-12090	Sequence 12090, A	cl1489	28.6	1.3	5562	8	US-11-649-451-17	Sequence 17, Appl
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1418	28.6	1.3	982	8	US-11-713-768-5942	Sequence 5942, Ap	1491	28.6	1.3	5730	8	US-11-514-704-63	Sequence 63, Appl
1419	28.6	1.3	1017	1	US-10-438-246-13607	Sequence 13607, A	1492	28.6	1.3	5941	8	US-11-514-704-2030	Sequence 2030, Ap
cl1420	28.6	1.3	1029	1	US-10-438-246-28606	Sequence 28606, A	cl1493	28.6	1.3	6129	8	US-11-257-477-81	Sequence 81, Appl
cl1421	28.6	1.3	1061	1	US-10-533-069-465	Sequence 465, App	1494	28.6	1.3	6180	8	US-11-514-704-2652	Sequence 2652, Ap
1422	28.6	1.3	1114	1	US-10-438-246-2694	Sequence 22694, A	1495	28.6	1.3	7287	8	US-11-514-704-23094	Sequence 23094, A
1423	28.6	1.3	1130	8	US-11-514-704-15977	Sequence 15977, A	1496	28.6	1.3	9501	1	US-10-533-069-194	Sequence 194, App
cl1424	28.6	1.3	1134	1	US-10-438-246-3367	Sequence 3367, Ap	cl1497	28.4	1.2	101	8	US-11-640-897-2123	Sequence 2123, Ap
1425	28.6	1.3	1145	8	US-11-649-663A-3303	Sequence 3303, Ap	cl1498	28.4	1.2	440	1	US-10-438-246-28868	Sequence 28868, A
cl1426	28.6	1.3	1198	8	US-11-713-768-78327	Sequence 78327, A	cl1499	28.4	1.2	447	8	US-11-796-730-1155	Sequence 1155, Ap
cl1427	28.6	1.3	1199	8	US-11-713-768-28977	Sequence 28977, A	cl1500	28.4	1.2	731	8	US-11-514-704-17099	Sequence 17099, A
cl1428	28.6	1.3	1199	8	US-11-713-768-32567	Sequence 32567, A							
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1431	28.6	1.3	1248	8	US-11-649-663A-1481	Sequence 1481, Ap							
1432	28.6	1.3	1248	8	US-11-649-663A-2161	Sequence 2161, Ap							
1433	28.6	1.3	1248	8	US-11-713-768-38838	Sequence 38838, A							
1434	28.6	1.3	1248	8	US-11-713-768-78319	Sequence 78319, A							
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cl1436	28.6	1.3	1302	8	US-11-713-768-83857	Sequence 83857, A							
cl1437	28.6	1.3	1309	8	US-11-514-704-20957	Sequence 20957, A							
1438	28.6	1.3	1325	8	US-11-514-704-23475	Sequence 23475, A							
1439	28.6	1.3	1332	1	US-10-438-246-21642	Sequence 21642, A							
1440	28.6	1.3	1332	8	US-11-713-768-42591	Sequence 42591, A							
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1442	28.6	1.3	1403	8	US-11-713-768-6376	Sequence 6376, Ap							
1443	28.6	1.3	1408	8	US-11-713-768-2854	Sequence 2854, Ap							
cl1444	28.6	1.3	1423	1	US-10-438-246-29277	Sequence 29277, A							
1445	28.6	1.3	1446	8	US-11-713-768-57086	Sequence 57086, A							
1446	28.6	1.3	1466	8	US-11-514-704-17104	Sequence 17104, A							
cl1447	28.6	1.3	1482	8	US-11-713-768-41343	Sequence 41343, A							
cl1448	28.6	1.3	1482	8	US-11-713-768-43193	Sequence 43193, A							
cl1449	28.6	1.3	1509	8	US-11-514-704-23502	Sequence 23502, A							
cl1450	28.6	1.3	1543	8	US-11-713-768-56820	Sequence 56820, A							
1451	28.6	1.3	1562	8	US-11-713-768-60275	Sequence 60275, A							
1452	28.6	1.3	1580	8	US-11-649-663A-3607	Sequence 3607, Ap							
1453	28.6	1.3	1582	8	US-11-713-768-17681	Sequence 17681, A							
1454	28.6	1.3	1635	8	US-11-514-704-19013	Sequence 19013, A							
cl1455	28.6	1.3	1685	8	US-11-514-704-23115	Sequence 23115, A							
cl1456	28.6	1.3	1718	8	US-11-713-768-23665	Sequence 23665, A							
1457	28.6	1.3	1746	8	US-11-713-768-8939	Sequence 8939, Ap							
cl1458	28.6	1.3	1754	8	US-11-514-704-20634	Sequence 20634, A							
1459	28.6	1.3	1789	8	US-11-649-663A-4267	Sequence 4267, Ap							
1460	28.6	1.3	1988	8	US-11-514-704-3224	Sequence 3224, Ap							
1461	28.6	1.3	2059	1	US-10-438-246-28248	Sequence 28248, A							
1462	28.6	1.3	2093	8	US-11-514-704-6705	Sequence 6705, Ap							
cl1463	28.6	1.3	2153	8	US-11-713-768-99987	Sequence 99987, A							
cl1464	28.6	1.3	2154	8	US-11-713-768-40477	Sequence 40477, A							
cl1465	28.6	1.3	2173	8	US-11-514-704-5056	Sequence 5056, Ap							
1466	28.6	1.3	2304	8	US-11-514-704-1817	Sequence 1817, Ap							
cl1467	28.6	1.3	2322	8	US-11-713-768-29048	Sequence 29048, A							
cl1468	28.6	1.3	2322	8	US-11-713-768-32638	Sequence 32638, A							
1469	28.6	1.3	2435	1	US-10-438-246-29496	Sequence 29496, A							
1470	28.6	1.3	2601	1	US-10-438-246-28891	Sequence 28891, A							
cl1471	28.6	1.3	2712	1	US-10-533-069-1335	Sequence 1335, Ap							
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cl1473	28.6	1.3	2799	8	US-11-713-768-72400	Sequence 72400, A							
cl1474	28.6	1.3	2828	8	US-11-514-704-22808	Sequence 22808, A							
cl1475	28.6	1.3	2833	8	US-11-713-768-84964	Sequence 84964, A							
cl1476	28.6	1.3	2839	8	US-11-713-768-86823	Sequence 86823, A							
cl1477	28.6	1.3	3019	8	US-11-514-704-17004	Sequence 17004, A							
cl1478	28.6	1.3	3083	8	US-11-512-753-1	Sequence 1, Appl							
cl1479	28.6	1.3	3193	8	US-11-713-768-84960	Sequence 84960, A							
1480	28.6	1.3	3194	8	US-11-514-704-5207	Sequence 5207, Ap							
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Job time : 196 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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53	2284	100.0	2284	37	US-09-997-428-514 Sequence 514, App
67	2284	100.0	2284	47	US-10-429-667-82 Sequence 82, Appl
68	2284	100.0	2284	50	US-10-677-471-82 Sequence 82, Appl
69	2284	100.0	2284	50	US-10-677-669-82 Sequence 82, Appl
70	2284	100.0	2284	56	US-10-735-014-82 Sequence 82, Appl
71	2284	100.0	2284	58	US-10-854-947-82 Sequence 82, Appl
72	2284	100.0	2284	58	US-10-858-981-82 Sequence 82, Appl
73	2284	100.0	2284	58	US-10-858-993-82 Sequence 82, Appl
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139	1071.2	46.9	2487	47	US-10-450-763-14119	Sequence 14119, A	212	422.6	18.5	3114	57	US-10-750-185-32681	Sequence 32681, A
140	1062	46.5	1127	68	US-60-324-185-34241	Sequence 34241, A	213	422.6	18.5	3114	57	US-10-750-622-32681	Sequence 32681, A
141	984.8	43.1	1000	69	US-11-266-748A-289504	Sequence 289504, A	214	422.6	18.5	3114	57	US-10-750-622-32681	Sequence 32681, A
142	984.8	43.1	1000	69	US-11-266-748A-340933	Sequence 340933, A	215	421.4	18.5	423	21	US-09-289-768-515	Sequence 515, App
143	984.8	43.1	1000	69	US-11-266-748A-400544	Sequence 400544, A	216	421.4	18.5	423	35	US-09-939-397-515	Sequence 515, App
144	984.8	43.1	1000	69	US-11-266-748A-471590	Sequence 471590, A	217	421.4	18.5	424	21	US-09-289-768-502	Sequence 502, App
145	969	42.4	1036	21	US-09-203-070-12786	Sequence 12786, A	218	421.4	18.5	424	35	US-09-939-397-502	Sequence 502, App
146	969	42.4	1036	22	US-09-340-623-12786	Sequence 12786, A	219	420.4	18.4	436	22	US-09-353-690-11136	Sequence 11136, A
147	969	42.4	1036	33	US-09-898-888A-12786	Sequence 12786, A	220	420.4	18.4	436	34	US-09-922-340-11136	Sequence 11136, A
148	969	42.4	1036	33	US-09-898-888A-12786	Sequence 12786, A	221	420.4	18.4	436	34	US-09-922-340A-11136	Sequence 11136, A

222	417.2	18.3	422	21	US-09-903-972-28030	Sequence 28030, A	295	304.2	13.3	402	34	US-09-925-564-17772	Sequence 17772, A
223	417.2	18.3	422	34	US-09-904-939-28030	Sequence 28030, A	296	294.8	12.9	339	22	US-09-354-899-4448	Sequence 4448, Ap
224	413.6	18.1	542	22	US-09-306-609-1756	Sequence 1756, Ap	297	294.8	12.9	339	27	US-09-614-387-942	Sequence 942, App
225	413.6	18.1	542	24	US-09-522-251-1756	Sequence 1756, Ap	c 298	292	12.8	377	30	US-09-726-881-1110	Sequence 1110, Ap
226	413.6	18.1	542	38	US-10-025-601-1756	Sequence 1756, Ap		282.4	12.4	285	17	US-08-818-589-1468	Sequence 1468, Ap
227	408.8	17.9	432	23	US-09-489-033-25195	Sequence 25195, A	300	282.4	12.4	285	84	US-09-534-856-24635	Sequence 24635, A
228	408.8	17.9	432	35	US-09-943-143-25195	Sequence 25195, A	301	282.4	12.4	285	85	US-60-015-377-1468	Sequence 1468, Ap
229	408.4	17.9	411	21	US-09-233-972-22541	Sequence 22541, A	302	281.2	12.3	286	19	US-09-036-589-818	Sequence 818, App
230	408.4	17.9	411	34	US-09-904-939-22541	Sequence 22541, A	303	281.2	12.3	286	25	US-09-534-856-24648	Sequence 24648, A
231	407.6	17.8	463	22	US-09-353-690-7966	Sequence 7966, Ap	304	281.2	12.3	286	84	US-60-039-128-818	Sequence 818, App
232	407.6	17.8	463	34	US-09-922-340-7966	Sequence 7966, Ap	305	276	12.1	508	11	US-08-220-691B-7457	Sequence 7457, Ap
233	407.6	17.8	463	34	US-09-922-340A-7966	Sequence 7966, Ap	306	276	12.1	508	11	US-08-220-691B-7457	Sequence 7457, Ap
234	406.6	17.8	425	22	US-09-397-761A-605	Sequence 605, App	307	276	12.1	508	32	US-09-813-153-7457	Sequence 7457, Ap
235	406.6	17.8	425	32	US-09-838-601-605	Sequence 605, App	308	276	12.1	508	34	US-09-912-293-111604	Sequence 111604, A
236	406.2	17.8	546	22	US-09-306-609-12165	Sequence 12165, A	309	272.8	11.9	388	22	US-09-306-350A-11696	Sequence 11696, A
237	406.2	17.8	546	24	US-10-522-251-12165	Sequence 12165, A	310	272.8	11.9	388	34	US-09-909-629-11696	Sequence 11696, A
238	406.2	17.8	546	38	US-10-025-600-12165	Sequence 12165, A	311	270	11.8	280	18	US-08-901-904-6712	Sequence 6712, Ap
c 239	389.8	17.1	400	23	US-09-489-036-1814	Sequence 1814, Ap	312	270	11.8	280	25	US-09-540-208-40338	Sequence 40338, A
c 240	389.8	17.1	400	35	US-09-943-143-1814	Sequence 1814, Ap	313	266.2	11.7	402	23	US-09-465-231-2941	Sequence 2941, Ap
241	388.2	17.0	638	76	US-11-443-428A-108937	Sequence 108937, A	314	266.2	11.7	402	36	US-09-983-965-2941	Sequence 2941, Ap
242	386.8	16.9	422	17	US-08-838-821-46	Sequence 46, Appl	315	257.6	11.3	532	22	US-09-338-425-1598	Sequence 1598, Ap
243	386.8	16.9	422	19	US-09-036-522-46	Sequence 46, Appl	316	257.6	11.3	532	30	US-09-726-790-1598	Sequence 1598, Ap
244	386.8	16.9	422	22	US-09-343-566-46	Sequence 46, Appl	317	256.8	11.2	380	25	US-09-539-331D-33139	Sequence 33139, A
245	386	16.9	386	21	US-09-293-972-28031	Sequence 28031, A	c 318	256.8	11.2	380	25	US-09-540-223-29577	Sequence 29577, A
246	386	16.9	386	34	US-09-904-939-28031	Sequence 28031, A	319	253.2	11.1	388	76	US-11-443-428A-576439	Sequence 576439, A
247	383.2	16.8	390	22	US-09-332-782-11182	Sequence 11182, A	320	252	11.0	252	16	US-08-782-035-1334	Sequence 1334, Ap
248	383.2	16.8	390	24	US-09-515-694-11182	Sequence 11182, A	321	252	11.0	252	16	US-09-534-856-24642	Sequence 24642, A
249	368.4	16.1	383	28	US-09-649-163-2508	Sequence 2508, Ap	322	250.8	11.0	262	16	US-08-748-106-1202	Sequence 1202, Ap
250	368.4	16.1	383	28	US-09-652-916-3749	Sequence 3749, Ap	323	250.8	11.0	262	16	US-09-540-766-3913	Sequence 3913, Ap
251	368	16.1	368	85	US-60-185-215-2729	Sequence 2729, Ap	c 324	248.4	10.9	12351	61	US-10-990-328-96640	Sequence 96640, A
252	363.6	15.9	438	22	US-09-362-510-1230	Sequence 1230, Ap	c 325	248.4	10.9	12351	61	US-10-990-328A-96640	Sequence 96640, A
253	363.6	15.9	438	22	US-09-362-510A-1230	Sequence 1230, Ap	c 326	248.4	10.9	14034	61	US-10-990-328A-96760	Sequence 96760, A
254	363.6	15.9	438	34	US-09-904-013-1230	Sequence 1230, Ap	c 327	248.4	10.9	14034	61	US-10-990-328A-96760	Sequence 96760, A
255	359.4	15.7	445	24	US-09-528-409-42767	Sequence 42767, A	328	246.4	10.8	307	30	US-09-726-806-2237	Sequence 2237, Ap
256	359.4	15.7	445	34	US-09-933-524-42767	Sequence 42767, A	329	245.6	10.8	324	12	US-08-337-601A-5664	Sequence 5664, Ap
257	359.4	15.7	445	35	US-09-933-524A-42767	Sequence 42767, A	330	245.6	10.8	324	14	US-08-530-112A-5664	Sequence 5664, Ap
258	359	15.7	428	23	US-09-489-036-16987	Sequence 16987, A	c 331	244	10.7	29930	59	US-10-940-774-15326	Sequence 15326, A
259	359	15.7	428	23	US-09-943-143-16987	Sequence 16987, A	c 332	244	10.7	29930	59	US-10-940-774A-15326	Sequence 15326, A
260	358.8	15.7	464	38	US-09-644-869-1102	Sequence 1102, Ap	c 333	244	10.7	37929	89	US-60-465-241-52518	Sequence 52518, A
261	353.2	15.5	358	23	US-09-489-036-22888	Sequence 22888, A	c 334	244	10.7	38779	91	US-10-932-349-19348	Sequence 19348, A
262	353.2	15.5	358	23	US-09-489-036-22888	Sequence 22888, A	c 335	244	10.7	38779	91	US-60-500-337-19348	Sequence 19348, A
263	349	15.3	398	28	US-09-943-143-1829	Sequence 1829, Ap	c 336	244	10.7	8886555	35	US-09-947-916-97	Sequence 97, Appl
264	341	14.9	466	24	US-09-528-409-42324	Sequence 42324, A	c 337	243.6	10.7	452163	62	US-11-033-056A-37365	Sequence 37365, A
265	341	14.9	466	34	US-09-933-524-42324	Sequence 42324, A	c 338	243.4	10.7	478	21	US-09-235-076-32190	Sequence 32190, A
266	341	14.9	466	34	US-09-933-524A-42324	Sequence 42324, A	c 339	243.4	10.7	478	21	US-09-289-768-39643	Sequence 39643, A
267	334.8	14.7	562	87	US-60-252-833-27421	Sequence 27421, A	340	243.4	10.7	478	22	US-09-332-782-32190	Sequence 32190, A
c 268	332.2	14.5	367	23	US-09-489-036-17525	Sequence 17525, A	341	243.4	10.7	478	30	US-09-737-223-32190	Sequence 32190, A
c 269	332.2	14.5	367	35	US-09-943-143-17525	Sequence 17525, A	342	243.4	10.7	478	34	US-09-918-993-32190	Sequence 32190, A
c 270	324	14.2	360	69	US-11-266-748A-460080	Sequence 460080, A	343	243.4	10.7	478	35	US-09-939-397-39643	Sequence 39643, A
c 271	324	14.2	360	69	US-11-266-748A-460080	Sequence 460080, A	344	243.2	10.6	146776	87	US-60-248-505-474	Sequence 474, App
272	323.2	14.2	352	25	US-09-540-764-52754	Sequence 52754, A	345	243	10.6	1000	43	US-10-301-480A-155646	Sequence 155646, A
273	323.2	14.2	352	46	US-10-349-781-52754	Sequence 52754, A	346	243	10.6	1000	44	US-10-301-480B-155646	Sequence 155646, A
274	314.2	13.8	399	22	US-09-332-782-3365	Sequence 3365, Ap	347	243	10.6	1000	45	US-10-301-480C-155646	Sequence 155646, A
275	314.2	13.8	399	24	US-09-515-694-5365	Sequence 5365, Ap	348	242.2	10.6	176521	87	US-60-242-679-554	Sequence 554, App
276	314	13.7	519	85	US-60-172-360-7291	Sequence 7291, Ap	349	242	10.6	2300	3	PCT-US06-46920-41807	Sequence 41807, A
277	311	13.6	348	30	US-09-710-282-2282	Sequence 2282, Ap	350	242	10.6	2300	80	US-11-636-385-41807	Sequence 41807, A
278	309.4	13.5	313	17	US-08-822-285-1881	Sequence 1881, Ap	351	242	10.6	2300	80	US-11-636-385A-41807	Sequence 41807, A
279	309.4	13.5	313	25	US-09-539-806-19811	Sequence 19811, A	352	242	10.6	2300	93	US-60-762-056-41807	Sequence 41807, A
280	309.4	13.5	313	25	US-09-539-806B-19811	Sequence 19811, A	353	241.6	10.6	68123	61	US-10-995-561-13348	Sequence 13348, A
281	309.4	13.5	313	84	US-60-013-696-1881	Sequence 1881, Ap	c 354	241.6	10.6	160820	1	PCT-US02-11086-5	Sequence 5, Appl
282	307.8	13.5	311	25	US-09-540-764-46627	Sequence 46627, A	c 355	241.6	10.6	160820	47	US-10-473-939-5	Sequence 5, Appl
283	307.8	13.5	311	46	US-10-349-781-46627	Sequence 46627, A	c 356	241.6	10.6	160820	69	US-11-266-748A-22501	Sequence 22501, A
284	306.4	13.4	370	10	US-08-196-362A-3982	Sequence 3982, Ap	357	241.4	10.6	116750	92	US-60-660-711-33	Sequence 33, Appl
285	306.4	13.4	370	10	US-08-196-362D-3982	Sequence 3982, Ap	c 358	241.4	10.6	197241	66	US-11-114-798-47	Sequence 47, Appl
286	306.4	13.4	370	10	US-08-196-362E-3982	Sequence 3982, Ap	359	241.2	10.6	30520	87	US-60-243-468-218	Sequence 218, App
287	306.4	13.4	370	10	US-08-196-362F-3982	Sequence 3982, Ap	c 360	241.2	10.6	32923	89	US-60-465-241-52298	Sequence 52298, A
288	306.4	13.4	370	10	US-08-196-362G-3982	Sequence 3982, Ap	361	241.2	10.6	52299	50	US-10-674-575-859	Sequence 859, App
289	306	13.4	359	22	US-09-362-510-2132	Sequence 2132, Ap	c 362	241	10.6	50317	61	US-10-990-328-96285	Sequence 96285, A
290	306	13.4	359	22	US-09-362-510A-2132	Sequence 2132, Ap	c 363	241	10.6	50317	61	US-10-990-328A-96285	Sequence 96285, A
291	306	13.4	359	34	US-09-904-013-2132	Sequence 2132, Ap	c 364	240.8	10.5	59828	59	US-10-940-774-16238	Sequence 16238, A
292	304.2	13.3	402	21	US-09-248-797-17772	Sequence 17772, A	365	240.8	10.5	59828	60	US-10-940-774A-16238	Sequence 16238, A
293	304.2	13.3	402	22	US-09-346-956-6701	Sequence 6701, Ap	366	240.8	10.5	67828	90	US-60-466-412-86961	Sequence 86961, A
294	304.2	13.3	402	34	US-09-904-703-6701	Sequence 6701, Ap	367	240.8	10.5	68123	2	PCT-US03-40977-5697	Sequence 5697, Ap

368	240.8	10.5	68123	2	PCT-US03-40978-17774	Sequence 17774, A	C 441	238.8	10.5	63507	61	US-10-990-328-98160	Sequence 98160, A
369	240.8	10.5	68123	56	US-10-741-600-17774	Sequence 17774, A	C 442	238.8	10.5	63507	61	US-10-990-328-98160	Sequence 98160, A
370	240.8	10.5	68123	56	US-10-741-601-5697	Sequence 5697, Ap	C 443	238.8	10.5	77313	60	US-60-466-412-87604	Sequence 87604, A
371	240.8	10.5	68123	59	US-60-568-219-6212	Sequence 6212, Ap	C 444	238.8	10.5	77504	59	US-10-918-711-3720	Sequence 3720, Ap
372	240.8	10.5	85963	91	US-10-940-774-13804	Sequence 13804, A	C 445	238.8	10.5	77504	59	US-10-918-754-16803	Sequence 16803, A
373	240.8	10.5	85963	60	US-10-940-774A-13804	Sequence 13804, A	C 446	238.8	10.5	77504	90	US-60-495-114-16803	Sequence 16803, A
374	240.6	10.5	444922	62	US-11-073-360-1618	Sequence 1618, Ap	C 447	238.8	10.5	77504	90	US-60-495-135-3720	Sequence 3720, Ap
375	240.6	10.5	444922	61	US-60-519-270-2364	Sequence 2364, Ap	C 448	238.8	10.5	176433	50	US-10-660-434-1516	Sequence 1516, Ap
376	240.6	10.5	444922	61	US-60-550-051-3005	Sequence 3005, Ap	C 449	238.8	10.5	176433	58	US-10-861-003-1516	Sequence 1516, Ap
377	240.6	10.5	444922	92	US-60-617-163-138	Sequence 138, App	C 450	238.8	10.5	895651	62	US-11-033-056A-36080	Sequence 36080, A
378	240.4	10.5	601	59	US-10-940-774-69955	Sequence 69955, A	C 451	238.8	10.5	895651	62	US-11-033-056A-36632	Sequence 36632, A
379	240.4	10.5	601	60	US-10-940-774A-69955	Sequence 69955, A	C 452	238.8	10.5	895651	62	US-11-033-056A-36881	Sequence 36881, A
380	240.4	10.5	93962	89	US-60-465-241-52335	Sequence 52335, A	C 453	238.8	10.5	895651	62	US-11-033-056A-37333	Sequence 37333, A
381	240.2	10.5	595	42	US-10-301-480-572904	Sequence 572904, A	C 454	238.8	10.5	895651	62	US-11-033-056A-37715	Sequence 37715, A
382	240.2	10.5	595	42	US-10-301-480-1186313	Sequence 1186313, A	C 455	238.8	10.5	895651	62	US-11-033-056A-37987	Sequence 37987, A
383	240.2	10.5	595	44	US-10-301-480A-948973	Sequence 948973, A	C 456	238.8	10.5	895651	62	US-11-033-056A-38705	Sequence 38705, A
384	240.2	10.5	595	44	US-10-301-480B-948973	Sequence 948973, A	C 457	238.8	10.5	895651	62	US-11-033-056A-38769	Sequence 38769, A
385	240.2	10.5	595	45	US-10-301-480C-948973	Sequence 948973, A	C 458	238.8	10.5	1599662	35	US-09-947-911-108	Sequence 108, App
386	240	10.5	240	17	US-08-846-104-2460	Sequence 2460, Ap	C 459	238.6	10.4	601	35	US-09-948-941-4591	Sequence 4591, Ap
387	240	10.5	240	25	US-09-539-806-11908	Sequence 11908, A	C 460	238.6	10.4	601	58	US-10-896-891-4591	Sequence 4591, Ap
388	240	10.5	240	25	US-09-539-806B-11908	Sequence 11908, A	C 461	238.6	10.4	50807	2	PCT-US03-41389-781	Sequence 781, App
389	240	10.5	767152	62	US-11-033-056A-35780	Sequence 35780, A	C 462	238.6	10.4	50807	46	US-10-330-773-781	Sequence 781, App
390	240	10.5	1059516	35	US-09-947-911-86	Sequence 86, Appl	C 463	238.6	10.4	50807	46	US-10-330-773A-781	Sequence 781, App
391	239.8	10.5	656	27	US-09-634-306B-27832	Sequence 27832, A	C 464	238.6	10.4	50807	48	US-10-540-898-781	Sequence 781, App
392	239.8	10.5	656	38	US-10-027-632-27832	Sequence 27832, A	C 465	238.6	10.4	50807	75	US-11-403-116-781	Sequence 781, App
393	239.8	10.5	7601	1	PCT-US01-01354-36064	Sequence 36064, A	C 466	238.6	10.4	50807	46	US-10-540-898-781	Sequence 781, App
394	239.8	10.5	7601	30	US-09-760-469-1876	Sequence 1876, Ap	C 467	238.6	10.4	246604	62	US-11-033-056A-38635	Sequence 38635, A
395	239.8	10.5	7601	31	US-09-764-905-36064	Sequence 36064, A	C 468	238.6	10.4	469691	90	US-60-466-412-85217	Sequence 85217, A
396	239.8	10.5	7601	38	US-10-092-399-36064	Sequence 36064, A	C 469	238.4	10.4	6000	94	US-60-873-739-3442	Sequence 3442, Ap
397	239.8	10.5	7601	40	US-10-216-583-1876	Sequence 1876, Ap	C 470	238.4	10.4	51529	62	US-11-033-056A-37631	Sequence 37631, A
398	239.8	10.5	31203	1	PCT-US01-01354-36066	Sequence 36066, A	C 471	238.4	10.4	100033	3	PCT-US04-37982-2588	Sequence 2588, Ap
399	239.8	10.5	31203	31	US-09-760-475-4119	Sequence 4119, Ap	C 472	238.4	10.4	199321	66	US-11-121-086-10	Sequence 10, Appl
400	239.8	10.5	31203	31	US-09-764-905-36066	Sequence 36066, A	C 473	238.4	10.4	4148350	35	US-09-947-916-16	Sequence 16, Appl
401	239.8	10.5	31203	38	US-10-092-399-36066	Sequence 36066, A	C 474	238.2	10.4	7928029	35	US-09-947-916-16	Sequence 16, Appl
402	239.8	10.5	31203	40	US-10-227-425-4119	Sequence 4119, Ap	C 475	238.2	10.4	19174	1	PCT-US01-01354-36065	Sequence 36065, A
403	239.8	10.5	96016	92	US-60-679-430-4	Sequence 4, Appl	C 476	238.2	10.4	19174	31	US-09-764-905-36065	Sequence 36065, A
404	239.8	10.5	431350	62	US-11-033-056A-35705	Sequence 35705, A	C 477	238.2	10.4	19174	38	US-10-092-399-36065	Sequence 36065, A
405	239.8	10.5	431350	62	US-11-033-056A-35710	Sequence 35710, A	C 478	238.2	10.4	109906	40	US-60-466-412-86900	Sequence 86900, A
406	239.8	10.5	431350	62	US-11-033-056A-35711	Sequence 35711, A	C 479	238.2	10.4	115617	50	US-10-235-192A-31	Sequence 31, Appl
407	239.8	10.5	4604723	35	US-09-947-916-240	Sequence 240, App	C 480	238.2	10.4	155470	59	US-10-674-575-419	Sequence 419, App
408	239.4	10.5	43208	61	US-10-990-328-95675	Sequence 95675, A	C 481	238.2	10.4	155470	60	US-10-910-811A-373	Sequence 373, App
409	239.4	10.5	43208	61	US-10-990-328A-95675	Sequence 95675, A	C 482	238.2	10.4	15105345	35	US-09-948-128-55	Sequence 55, Appl
410	239.2	10.5	4026	1	PCT-US01-01354-42230	Sequence 42230, A	C 483	238	10.4	7928029	35	US-09-947-916-16	Sequence 16, Appl
411	239.2	10.5	4026	31	US-09-764-905-42230	Sequence 42230, A	C 484	238	10.4	8616041	35	US-09-947-916-16	Sequence 16, Appl
412	239.2	10.5	4026	38	US-10-092-399-42230	Sequence 42230, A	C 485	237.6	10.4	601	35	US-09-949-003C-12304	Sequence 12304, A
413	239.2	10.5	6000	94	US-60-873-737-1791	Sequence 1791, Ap	C 486	237.6	10.4	601	35	US-09-949-003C-73728	Sequence 73728, A
414	239.2	10.5	6000	94	US-60-873-882-7396	Sequence 7396, Ap	C 487	237.6	10.4	7566	1	PCT-US01-01339-10010	Sequence 10010, A
415	239.2	10.5	19784	89	US-60-465-241-53606	Sequence 53606, A	C 488	237.6	10.4	7566	30	US-09-764-891-10010	Sequence 10010, A
416	239.2	10.5	19784	90	US-60-466-412-87887	Sequence 87887, A	C 489	237.6	10.4	32768	87	US-60-234-446-57	Sequence 57, Appl
417	239.2	10.5	28719	86	US-60-226-176-217	Sequence 217, App	C 490	237.6	10.4	39243	61	US-10-990-328A-95548	Sequence 95548, A
418	239.2	10.5	28719	86	US-60-233-468-217	Sequence 217, App	C 491	237.6	10.4	39243	61	US-10-990-328A-95548	Sequence 95548, A
419	239.2	10.5	28719	88	US-60-313-371-217	Sequence 217, App	C 492	237.6	10.4	61835	87	US-60-245-201-106	Sequence 106, App
420	239.2	10.5	32131	89	US-60-465-241-52461	Sequence 52461, A	C 493	237.6	10.4	62873	59	US-10-940-774-15676	Sequence 15676, A
421	239.2	10.5	32131	90	US-60-466-412-86140	Sequence 86140, A	C 494	237.6	10.4	62873	60	US-10-940-774A-15676	Sequence 15676, A
422	239.2	10.5	34497	62	US-11-033-056A-36659	Sequence 36659, A	C 495	237.6	10.4	70659	61	US-10-990-328-95495	Sequence 95495, A
423	239.2	10.5	34497	62	US-11-033-056A-37124	Sequence 37124, A	C 496	237.6	10.4	70659	61	US-10-990-328A-95495	Sequence 95495, A
424	239.2	10.5	34497	62	US-11-033-056A-37680	Sequence 37680, A	C 497	237.4	10.4	13421	90	US-60-466-412-84286	Sequence 84286, A
425	239.2	10.5	4647455	50	US-10-641-321-205	Sequence 205, App	C 498	237.4	10.4	13421	90	US-60-466-412-84286	Sequence 84286, A
426	239	10.5	31331	61	US-10-990-328-94226	Sequence 94226, App	C 499	237.4	10.4	14083	91	US-10-932-349-19584	Sequence 19584, A
427	239	10.5	31331	61	US-10-990-328A-94226	Sequence 94226, A	C 500	237.4	10.4	14083	91	US-60-500-337-19584	Sequence 19584, A
428	239	10.5	98982	50	US-10-674-575-564	Sequence 564, App	C 501	237.4	10.4	15007	60	US-10-940-774-15279	Sequence 15279, A
429	239	10.5	321568	61	US-10-990-328A-96687	Sequence 96687, A	C 502	237.4	10.4	22964	35	US-09-949-003C-3933	Sequence 3933, Ap
430	239	10.5	321568	61	US-10-990-328A-96687	Sequence 96687, A	C 503	237.4	10.4	22964	35	US-09-949-003C-3933	Sequence 3933, Ap
431	239	10.5	321578	89	US-60-461-762-3395	Sequence 3395, Ap	C 504	237.4	10.4	74545	35	US-09-948-933-457	Sequence 457, App
432	239	10.5	321578	90	US-60-470-166-8784	Sequence 8784, Ap	C 505	237.4	10.4	74545	35	US-09-949-003C-3588	Sequence 3588, Ap
433	239	10.5	2300	3	PCT-US06-46920-43683	Sequence 43683, A	C 506	237.4	10.4	74545	35	US-10-902-387-457	Sequence 457, App
434	238.8	10.5	2300	80	US-11-636-385A-43683	Sequence 43683, A	C 507	237.4	10.4	74545	62	US-11-033-545-606	Sequence 606, App
435	238.8	10.5	2300	80	US-11-636-385A-43683	Sequence 43683, A	C 508	237.4	10.4	131860	35	US-09-948-933-531	Sequence 531, App
436	238.8	10.5	7203	35	US-60-762-056-43683	Sequence 43683, A	C 509	237.4	10.4	131860	35	US-09-949-003C-4735	Sequence 4735, Ap
437	238.8	10.5	7203	35	US-09-949-003C-4376	Sequence 4376, Ap	C 510	237.4	10.4	131860	35	US-10-902-387-531	Sequence 531, App
438	238.8	10.5	31958	86	US-60-207-583-332	Sequence 332, App	C 511	237.4	10.4	131860	62	US-11-033-545-730	Sequence 730, App
439	238.8	10.5	31958	86	US-60-230-445-67	Sequence 67, Appl	C 512	237.4	10.4	224675	62	US-11-033-056A-38589	Sequence 38589, A
440	238.8	10.5	56872	90	US-60-466-412-87248	Sequence 87248, A	C 513	237.4	10.4	394468	2	PCT-US03-40978-17952	Sequence 17952, A

514	237.4	10.4	394468	56	US-10-741-600-17952	Sequence 17952, A	587	236.8	10.4	75750	87	US-60-242-679-121	Sequence 121, App
515	237.4	10.4	394468	91	US-60-524-882-9365	Sequence 9365, Ap	588	236.8	10.4	96377	90	US-60-466-412-87093	Sequence 87093, A
516	237.4	10.4	394468	91	US-60-548-091-5725	Sequence 5725, Ap	589	236.8	10.4	152037	90	US-10-756-149-1398	Sequence 198, App
517	237.4	10.4	461086	35	US-09-948-941-623	Sequence 623, App	590	236.8	10.4	152037	91	US-60-592-408-219	Sequence 219, App
518	237.4	10.4	461086	58	US-10-896-891-623	Sequence 623, App	591	236.8	10.4	251664	61	US-10-990-328-94156	Sequence 94156, A
519	237.4	10.4	482119	3	PCT-US04-37982-1034	Sequence 1034, Ap	592	236.8	10.4	251664	61	US-10-990-328A-94156	Sequence 94156, A
520	237.4	10.4	512515	62	US-11-033-056A-36942	Sequence 36942, A	593	236.6	10.4	51517	59	US-10-918-75A-16692	Sequence 16692, A
521	237.2	10.4	584	85	US-60-170-374-276	Sequence 276, App	594	236.6	10.4	51517	61	US-10-990-328-95721	Sequence 95721, A
522	237.2	10.4	6162	86	US-60-213-847-211	Sequence 211, App	595	236.6	10.4	51517	61	US-10-990-328A-95721	Sequence 95721, A
523	237.2	10.4	84336	62	US-11-033-056A-35828	Sequence 35828, A	596	236.6	10.4	51517	61	US-60-495-114-16692	Sequence 16692, A
524	237.2	10.4	126552	66	US-11-121-086-1	Sequence 1, Appli	597	236.6	10.4	100463	59	US-10-940-774A-12511	Sequence 12511, A
525	237.2	10.4	214475	69	US-60-465-241-51534	Sequence 51534, A	598	236.6	10.4	100463	60	US-10-940-774A-12511	Sequence 12511, A
526	237.2	10.4	223587	61	US-10-990-328-93801	Sequence 93801, A	599	236.6	10.4	100468	59	US-10-940-774-13725	Sequence 13725, A
527	237.2	10.4	223587	61	US-10-990-328A-93801	Sequence 93801, A	600	236.6	10.4	100468	60	US-10-940-774A-13725	Sequence 13725, A
528	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	601	236.6	10.4	100468	61	US-10-990-328-98050	Sequence 98050, A
529	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	602	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
530	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	603	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
531	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	604	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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533	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	606	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
534	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	607	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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536	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	609	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
537	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	610	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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539	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	612	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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541	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	614	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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543	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	616	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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547	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	620	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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551	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	624	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
552	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	625	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
553	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	626	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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556	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	629	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
557	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	630	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
558	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	631	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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560	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	633	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
561	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	634	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
562	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	635	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
563	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	636	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
564	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	637	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
565	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	638	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
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567	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	640	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
568	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	641	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
569	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	642	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
570	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	643	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
571	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	644	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
572	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	645	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
573	237.2	10.4	601	35	US-09-948-933-1403	Sequence 93801, A	646	236.6	10.4	100468	61	US-10-990-328A-98050	Sequence 98050, A
574	236.8	10.4	1000	42	US-10-301-480-58461	Sequence 58461, App	647	236	10.3	841	43	US-10-301-480A-214542	Sequence 214542, A
575	236.8	10.4	1000	42	US-10-301-480-1197870	Sequence 1197870, A	648	236	10.3	841	43	US-10-301-480B-214542	Sequence 214542, A
576	236.8	10.4	1000	42	US-10-301-480A-960530	Sequence 960530, A	649	236	10.3	841	43	US-10-301-480C-214542	Sequence 214542, A
577	236.8	10.4	1000	42	US-10-301-480B-960530	Sequence 960530, A	650	236	10.3	841	43	PCT-US06-46920-35983	Sequence 35983, A
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579	236.8	10.4	1000	42	US-10-940-774-15785	Sequence 15785, A	652	236	10.3	841	43	US-11-636-385A-35983	Sequence 35983, A
580	236.8	10.4	10427	59	US-10-940-774-15785	Sequence 15785, A	653	236	10.3	841	43	US-11-636-385-35983	Sequence 35983, A
581	236.8	10.4	20901	60	US-10-940-774A-11866	Sequence 11866, A	654	236	10.3	841	43	PCT-US02-09370-664	Sequence 664, App
582	236.8	10.4	20901	60	US-10-940-774A-11866	Sequence 11866, A	655	236	10.3	841	43	PCT-US02-09370-1145	Sequence 1145, App
583	236.8	10.4	28666	87	US-60-243-468-574	Sequence 574, App	656	236	10.3	841	43	US-09-950-083-7497	Sequence 7497, Ap
584	236.8	10.4	28666	87	US-60-466-412-84368	Sequence 84368, A	657	236	10.3	841	43	US-09-950-083B-7497	Sequence 7497, Ap
585	236.8	10.4	28919	61	US-10-990-328-93981	Sequence 93981, A	658	236	10.3	841	43	US-09-950-083B-8476	Sequence 8476, Ap
586	236.8	10.4	28919	61	US-10-990-328A-93981	Sequence 93981, A	659	236	10.3	841	43	US-10-105-299-9648	Sequence 9648, Ap

C 660	236	10.3	13186	39	US-10-105-299-10627	Sequence 10627, A	C 733	235.8	10.3	2300	3	PCT-US06-46920-4745	Sequence 4745, Ap
C 661	236	10.3	13186	47	US-10-472-963-1145	Sequence 1145, Ap	C 734	235.8	10.3	2300	80	US-11-636-385-4745	Sequence 4745, Ap
C 662	236	10.3	13186	47	US-10-472-965-664	Sequence 664, Ap	C 735	235.8	10.3	2300	80	US-11-636-385A-4745	Sequence 4745, Ap
C 663	236	10.3	13186	58	US-10-868-184-7497	Sequence 7497, Ap	C 736	235.8	10.3	2300	87	US-60-762-056-4745	Sequence 4745, Ap
C 664	236	10.3	13186	58	US-10-868-184-7497	Sequence 7497, Ap	C 737	235.8	10.3	11667	87	US-60-248-505-242	Sequence 242, App
C 665	236	10.3	13186	58	US-10-868-184A-7497	Sequence 7497, Ap	C 738	235.8	10.3	13820	91	US-10-932-349-19521	Sequence 19521, A
C 666	236	10.3	13186	58	US-10-868-184A-7497	Sequence 7497, Ap	C 739	235.8	10.3	13820	91	US-60-500-337-19521	Sequence 19521, A
C 667	236	10.3	13186	58	US-10-868-184B-7497	Sequence 7497, Ap	C 740	235.8	10.3	18888	59	US-10-940-774-16386	Sequence 16386, A
C 668	236	10.3	13186	58	US-10-868-184B-7497	Sequence 7497, Ap	C 741	235.8	10.3	18888	60	US-10-940-774A-16386	Sequence 16386, A
C 669	236	10.3	13186	58	US-10-868-184C-7497	Sequence 7497, Ap	C 742	235.8	10.3	18888	87	US-60-245-241-83	Sequence 83, Appl
C 670	236	10.3	13186	58	US-10-868-184D-7497	Sequence 7497, Ap	C 743	235.8	10.3	18889	87	US-60-266-847-8	Sequence 8, Appl
C 671	236	10.3	13186	58	US-10-868-184D-7497	Sequence 7497, Ap	C 744	235.8	10.3	32198	40	US-10-217-651-652	Sequence 652, App
C 672	236	10.3	13186	58	US-10-868-184D-7497	Sequence 7497, Ap	C 745	235.8	10.3	32198	40	US-10-217-651-723	Sequence 723, App
C 673	236	10.3	13186	58	US-10-868-184B-7497	Sequence 7497, Ap	C 746	235.8	10.3	33656	61	US-10-990-328-95865	Sequence 95865, A
C 674	236	10.3	13186	58	US-10-868-184B-7497	Sequence 7497, Ap	C 747	235.8	10.3	33656	61	US-10-990-328A-95865	Sequence 95865, A
C 675	236	10.3	13186	58	US-10-896-164-7497	Sequence 7497, Ap	C 748	235.8	10.3	51469	1	PCT-US01-01354-25082	Sequence 25082, A
C 676	236	10.3	13186	58	US-10-896-164-7497	Sequence 7497, Ap	C 749	235.8	10.3	51469	1	PCT-US01-01354-25082	Sequence 25082, A
C 677	236	10.3	13186	58	US-10-896-164-7497	Sequence 7497, Ap	C 750	235.8	10.3	51469	1	PCT-US01-01354-25082	Sequence 25082, A
C 678	236	10.3	13186	1	PCT-US02-09257-663	Sequence 663, App	C 751	235.8	10.3	51469	31	US-09-764-905-24134	Sequence 24134, A
C 679	236	10.3	13186	1	PCT-US02-09370-1144	Sequence 1144, Ap	C 752	235.8	10.3	51469	31	US-09-764-905-25082	Sequence 25082, A
C 680	236	10.3	13186	35	US-09-950-083-7496	Sequence 7496, Ap	C 753	235.8	10.3	51469	31	US-09-764-905-33625	Sequence 33625, A
C 681	236	10.3	13186	35	US-09-950-083-7496	Sequence 7496, Ap	C 754	235.8	10.3	51469	38	US-10-092-399-24134	Sequence 24134, A
C 682	236	10.3	13186	35	US-09-950-083B-7496	Sequence 7496, Ap	C 755	235.8	10.3	51469	38	US-10-092-399-25082	Sequence 25082, A
C 683	236	10.3	13186	35	US-09-950-083B-7496	Sequence 7496, Ap	C 756	235.8	10.3	51469	38	US-10-092-399-33625	Sequence 33625, A
C 684	236	10.3	13186	35	US-09-950-083B-7496	Sequence 7496, Ap	C 757	235.8	10.3	58881	59	US-10-932-349-19853	Sequence 19853, A
C 685	236	10.3	13186	39	US-10-105-299-10626	Sequence 10626, A	C 758	235.8	10.3	58881	59	US-60-500-337-19853	Sequence 19853, A
C 686	236	10.3	13186	39	US-10-105-299-10626	Sequence 10626, A	C 759	235.8	10.3	62546	90	US-60-465-241-51910	Sequence 51910, A
C 687	236	10.3	13186	39	US-10-105-299-13374	Sequence 13374, A	C 760	235.8	10.3	62546	90	US-60-466-412-85101	Sequence 85101, A
C 688	236	10.3	13186	47	US-10-472-963-1144	Sequence 1144, Ap	C 761	235.8	10.3	62546	90	US-60-487-610-19475	Sequence 19475, A
C 689	236	10.3	13186	47	US-10-472-965-663	Sequence 663, App	C 762	235.8	10.3	62546	91	US-60-582-609-19475	Sequence 19475, A
C 690	236	10.3	13186	58	US-10-868-184-7496	Sequence 7496, Ap	C 763	235.8	10.3	62555	2	PCT-US03-40978-17630	Sequence 17630, A
C 691	236	10.3	13186	58	US-10-868-184-7496	Sequence 7496, Ap	C 764	235.8	10.3	62555	56	US-10-741-600-17630	Sequence 17630, A
C 692	236	10.3	13186	58	US-10-868-184A-7496	Sequence 7496, Ap	C 765	235.8	10.3	62555	56	US-60-548-091-5623	Sequence 5623, App
C 693	236	10.3	13186	58	US-10-868-184A-7496	Sequence 7496, Ap	C 766	235.8	10.3	62555	91	US-60-548-091-5623	Sequence 5623, App
C 694	236	10.3	13186	58	US-10-868-184A-7496	Sequence 7496, Ap	C 767	235.8	10.3	97600	87	US-60-236-804-129	Sequence 129, App
C 695	236	10.3	13186	58	US-10-868-184A-7496	Sequence 7496, Ap	C 768	235.8	10.3	97600	87	US-60-236-804-129	Sequence 129, App
C 696	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 769	235.8	10.3	105168	59	US-10-940-774A-13296	Sequence 13296, A
C 697	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 770	235.8	10.3	105168	59	US-10-940-774A-13296	Sequence 13296, A
C 698	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 771	235.8	10.3	121167	46	US-10-330-773A-710	Sequence 710, App
C 699	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 772	235.8	10.3	121167	46	US-10-330-773A-710	Sequence 710, App
C 700	236	10.3	13186	58	US-10-868-184C-7496	Sequence 7496, Ap	C 773	235.8	10.3	121167	48	US-10-540-898-710	Sequence 710, App
C 701	236	10.3	13186	58	US-10-868-184C-7496	Sequence 7496, Ap	C 774	235.8	10.3	121167	48	US-10-540-898-710	Sequence 710, App
C 702	236	10.3	13186	58	US-10-868-184D-7496	Sequence 7496, Ap	C 775	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 703	236	10.3	13186	58	US-10-868-184D-7496	Sequence 7496, Ap	C 776	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 704	236	10.3	13186	58	US-10-868-184D-7496	Sequence 7496, Ap	C 777	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 705	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 778	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 706	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 779	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 707	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 780	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 708	236	10.3	13186	58	US-10-868-184B-7496	Sequence 7496, Ap	C 781	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 709	236	10.3	13186	58	US-10-896-164-7496	Sequence 7496, Ap	C 782	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 710	236	10.3	13186	58	US-10-896-164-7496	Sequence 7496, Ap	C 783	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 711	236	10.3	32215	86	US-60-212-655-149	Sequence 149, App	C 784	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 712	236	10.3	32215	86	US-60-212-655-149	Sequence 149, App	C 785	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 713	236	10.3	62267	62	US-11-066-316A-10009	Sequence 10009, A	C 786	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 714	236	10.3	62267	62	US-10-990-328-94216	Sequence 94216, A	C 787	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 715	236	10.3	62267	62	US-10-990-328A-94216	Sequence 94216, A	C 788	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 716	236	10.3	79278	89	US-60-465-241-51894	Sequence 51894, A	C 789	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 717	236	10.3	79278	90	US-60-466-412-85087	Sequence 85087, A	C 790	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 718	236	10.3	79278	90	US-60-470-166-8933	Sequence 8933, Ap	C 791	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 719	236	10.3	108364	62	US-11-033-056A-35821	Sequence 35821, A	C 792	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 720	236	10.3	168174	1	PCT-US02-03546-63	Sequence 63, Appl	C 793	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 721	236	10.3	168174	59	US-10-914-799-63	Sequence 63, Appl	C 794	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 722	236	10.3	168273	1	PCT-US02-03546-2	Sequence 2, Appl	C 795	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 723	236	10.3	168273	59	US-10-914-799-2	Sequence 2, Appl	C 796	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 724	236	10.3	184475	87	US-60-243-468-477	Sequence 477, App	C 797	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
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C 727	236	10.3	334918	50	US-10-674-575-64	Sequence 64, Appl	C 800	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 728	236	10.3	334918	50	US-60-248-499-12	Sequence 12, Appl	C 801	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 729	236	10.3	2307596	35	US-09-948-128-334	Sequence 334, App	C 802	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 730	235.8	10.3	773	1	PCT-US01-01354-36204	Sequence 36204, A	C 803	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 731	235.8	10.3	773	31	US-09-764-905-36204	Sequence 36204, A	C 804	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 732	235.8	10.3	773	38	US-10-092-399-36204	Sequence 36204, A	C 805	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 733	235.8	10.3	1000	69	US-11-266-748A-211062	Sequence 211062, A							

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807	235.4	10.3	63962	61	US-10-990-328A-95230	Sequence 95230, A	880	235	10.3	202100	40	US-10-282-174-484	Sequence 484, App
808	235.4	10.3	67293	90	US-60-466-412-84196	Sequence 84196, A	881	235	10.3	202100	49	US-10-600-009-484	Sequence 484, App
809	235.4	10.3	80505	87	US-60-242-679-379	Sequence 379, App	882	235	10.3	5401257	35	US-09-947-980-209	Sequence 209, App
810	235.4	10.3	87859	87	US-60-242-679-688	Sequence 688, App	883	234.8	10.3	994	42	US-10-301-480-594433	Sequence 594433
811	235.4	10.3	93435	90	US-60-466-412-87963	Sequence 87963, A	884	234.8	10.3	994	42	US-10-301-480A-1207842	Sequence 1207842
812	235.4	10.3	100608	47	US-10-417-375-108	Sequence 108, App	885	234.8	10.3	994	44	US-10-301-480A-970502	Sequence 970502
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816	235.2	10.3	993	43	US-10-301-480A-3063	Sequence 3063, Ap	889	234.8	10.3	5952	76	US-11-443-428A-313691	Sequence 313691
817	235.2	10.3	993	43	US-10-301-480A-304111	Sequence 304111, A	890	234.8	10.3	6491	76	US-11-443-428A-313691	Sequence 313691
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826	235.2	10.3	2300	80	US-11-636-385-7190	Sequence 7190, Ap	899	234.8	10.3	7306	76	US-11-443-428A-313685	Sequence 313685
827	235.2	10.3	2300	80	US-11-636-385A-7190	Sequence 7190, Ap	900	234.8	10.3	15278	35	US-09-948-941-638	Sequence 638, App
828	235.2	10.3	2300	93	US-60-762-056-7190	Sequence 7190, Ap	901	234.8	10.3	15278	58	US-10-896-891-638	Sequence 638, App
829	235.2	10.3	4178	76	US-11-443-428A-313693	Sequence 313693, A	902	234.8	10.3	23277	89	US-60-465-241-52125	Sequence 52125, A
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833	235.2	10.3	62386	60	US-10-940-774A-12823	Sequence 12823, A	906	234.8	10.3	32351	61	US-10-990-328-93698	Sequence 93698, A
834	235.2	10.3	113464	59	US-10-932-349-19435	Sequence 19435, A	907	234.8	10.3	187664	76	US-11-443-428A-735317	Sequence 735317
835	235.2	10.3	113464	91	US-60-500-337-19435	Sequence 19435, A	908	234.8	10.3	187664	76	US-11-443-428A-735341	Sequence 735341
836	235.2	10.3	176956	86	US-60-212-664-142	Sequence 142, App	909	234.8	10.3	187766	76	US-11-443-428A-735330	Sequence 735330
837	235.2	10.3	188788	59	US-10-932-349-19179	Sequence 19179, A	910	234.8	10.3	187766	76	US-11-443-428A-735316	Sequence 735316
838	235.2	10.3	188788	91	US-60-500-337-19179	Sequence 19179, A	911	234.8	10.3	187766	76	US-11-443-428A-735343	Sequence 735343
839	235.2	10.3	238417	87	US-60-242-679-528	Sequence 528, App	912	234.8	10.3	188005	76	US-11-443-428A-735328	Sequence 735328
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841	235.2	10.3	492559	35	US-09-948-128-259	Sequence 128, App	914	234.8	10.3	188005	76	US-11-443-428A-735339	Sequence 735339
842	235	10.3	601	59	US-10-940-774-94321	Sequence 94321, A	915	234.8	10.3	188056	76	US-11-443-428A-735302	Sequence 735302
843	235	10.3	601	59	US-10-940-774-94322	Sequence 94322, A	916	234.8	10.3	188056	76	US-11-443-428A-735312	Sequence 735312
844	235	10.3	601	60	US-10-940-774A-94321	Sequence 94321, A	917	234.8	10.3	188056	76	US-11-443-428A-735337	Sequence 735337
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846	235	10.3	936	43	US-10-301-480A-159147	Sequence 159147, A	919	234.8	10.3	188134	76	US-11-443-428A-735333	Sequence 735333
847	235	10.3	936	44	US-10-301-480B-159147	Sequence 159147, A	920	234.8	10.3	188134	76	US-11-443-428A-735303	Sequence 735303
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849	235	10.3	6000	94	US-60-873-883-1823	Sequence 1823, Ap	922	234.8	10.3	188134	76	US-11-443-428A-735328	Sequence 735328
850	235	10.3	11173	33	PCT-US02-21090-10	Sequence 10, Appl	923	234.8	10.3	188134	76	US-11-443-428A-735339	Sequence 735339
851	235	10.3	11173	33	US-09-898-556A-10	Sequence 10, Appl	924	234.8	10.3	188134	76	US-11-443-428A-735339	Sequence 735339
852	235	10.3	11173	57	US-10-772-542-10	Sequence 10, Appl	925	234.8	10.3	188134	76	US-11-443-428A-735302	Sequence 735302
853	235	10.3	13619	61	US-10-990-328-96037	Sequence 96037, A	926	234.8	10.3	188134	76	US-11-443-428A-735312	Sequence 735312
854	235	10.3	13619	61	US-10-990-328A-96037	Sequence 96037, A	927	234.8	10.3	188134	76	US-11-443-428A-735337	Sequence 735337
855	235	10.3	24177	61	US-10-990-328-96993	Sequence 96993, A	928	234.8	10.3	188134	76	US-11-443-428A-735313	Sequence 735313
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857	235	10.3	58773	87	US-60-243-468-692	Sequence 692, App	930	234.8	10.3	188134	76	US-11-443-428A-735340	Sequence 735340
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860	235	10.3	128034	1	PCT-US02-34679-187	Sequence 187, App	933	234.8	10.3	188134	76	US-11-443-428A-735334	Sequence 735334
861	235	10.3	128034	40	US-10-282-174-186	Sequence 186, App	934	234.8	10.3	188134	76	US-11-443-428A-735311	Sequence 735311
862	235	10.3	128034	40	US-10-282-174-187	Sequence 187, App	935	234.8	10.3	188134	76	US-11-443-428A-735326	Sequence 735326
863	235	10.3	128034	49	US-10-600-009-186	Sequence 186, App	936	234.8	10.3	188134	76	US-11-443-428A-735307	Sequence 735307
864	235	10.3	128034	49	US-10-600-009-187	Sequence 187, App	937	234.8	10.3	188134	76	US-11-443-428A-735314	Sequence 735314
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866	235	10.3	134469	59	US-60-495-114-16364	Sequence 16364, A	939	234.8	10.3	188257	76	US-11-443-428A-735310	Sequence 735310
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868	235	10.3	179790	35	US-09-948-941-716	Sequence 716, App	941	234.8	10.3	188257	76	US-11-443-428A-735335	Sequence 735335
869	235	10.3	179790	58	US-10-896-891-716	Sequence 716, App	942	234.8	10.3	188257	76	US-11-443-428A-735335	Sequence 735335
870	235	10.3	187790	89	US-60-465-241-52660	Sequence 52660, A	943	234.8	10.3	188257	76	US-11-443-428A-735344	Sequence 735344
871	235	10.3	187790	90	US-60-466-412-87780	Sequence 87780, A	944	234.8	10.3	188257	76	US-11-443-428A-735320	Sequence 735320
872	235	10.3	187790	91	US-60-485-450-12163	Sequence 12163, A	945	234.8	10.3	188257	76	US-11-443-428A-735320	Sequence 735320
873	235	10.3	187790	90	US-60-563-440-12163	Sequence 12163, A	946	234.8	10.3	188257	76	US-11-443-428A-735331	Sequence 735331
874	235	10.3	187790	92	US-60-659-397-12163	Sequence 12163, A	947	234.8	10.3	188257	76	US-11-443-428A-735327	Sequence 735327
875	235	10.3	190138	59	US-10-932-333-11946	Sequence 11946, A	948	234.8	10.3	188340	76	US-11-443-428A-735323	Sequence 735323
876	235	10.3	190138	91	US-60-500-315-11946	Sequence 11946, A	949	234.8	10.3	188340	76	US-11-443-428A-735306	Sequence 735306
877	235	10.3	190138	91	US-60-505-218-7472	Sequence 7472, Ap	950	234.8	10.3	188340	76	US-11-443-428A-735321	Sequence 735321
878	235	10.3	198138	3	PCT-US04-37982-1087	Sequence 1087, Ap	951	234.8	10.3	188340	76	US-11-443-428A-735309	Sequence 735309

952	234.8	10.3	188378	76	US-11-443-428A-735298	Sequence 735298,	1025	234.2	10.3	32768	86	US-60-207-954-3	Sequence 3, Appli
953	234.8	10.3	188384	76	US-11-443-428A-735294	Sequence 735294,	1026	234.2	10.3	32768	86	US-60-208-586-3	Sequence 3, Appli
954	234.8	10.3	188385	76	US-11-443-428A-735305	Sequence 735305,	1027	234.2	10.3	32768	86	US-60-212-354-7	Sequence 7, Appli
955	234.8	10.3	188402	76	US-11-443-428A-735301	Sequence 735301,	1028	234.2	10.3	32768	86	US-60-213-164-6	Sequence 6, Appli
956	234.8	10.3	188421	76	US-11-443-428A-735297	Sequence 735297,	1029	234.2	10.3	36799	3	PCT-US04-37982-1416	Sequence 1416, Ap
957	234.8	10.3	188424	76	US-11-443-428A-735319	Sequence 735319,	c1030	234.2	10.3	50836	59	US-10-940-774A-16722	Sequence 16722, A
958	234.8	10.3	188427	76	US-11-443-428A-735295	Sequence 735295,	c1031	234.2	10.3	50836	60	US-10-940-774A-16722	Sequence 16722, A
959	234.8	10.3	188448	76	US-11-443-428A-735322	Sequence 735322,	1032	234.2	10.3	67228	61	US-10-990-328-94343	Sequence 94343, A
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961	234.8	10.3	188505	76	US-11-443-428A-735293	Sequence 735293,	1034	234.2	10.3	125001	92	US-60-660-589-35	Sequence 238, App
962	234.8	10.3	188529	76	US-11-443-428A-735296	Sequence 735296,	1035	234.2	10.3	125001	92	US-10-087-192-238	Sequence 6, Appli
963	234.8	10.3	188548	76	US-11-443-428A-735292	Sequence 735292,	1036	234.2	10.3	128978	38	PCT-US01-17423-6	Sequence 6, Appli
964	234.8	10.3	188438	76	PCT-US04-07141-8717	Sequence 8717, Ap	1037	234.2	10.3	128978	1	PCT-US02-17423-6	Sequence 6, Appli
965	234.8	10.3	400438	57	US-10-796-280-12229	Sequence 12229, A	1038	234.2	10.3	128978	1	PCT-US02-25766-4301	Sequence 4301, Ap
966	234.8	10.3	400438	57	US-10-796-307-8717	Sequence 8717, Ap	1039	234.2	10.3	128978	3	PCT-US04-24424-1791	Sequence 1791, Ap
967	234.8	10.3	2556324	35	US-09-947-911-103	Sequence 95, Appl	1040	234.2	10.3	128978	39	US-10-161-453-6	Sequence 6, Appli
968	234.8	10.3	2813043	35	US-09-947-911-105	Sequence 101, Appl	1041	234.2	10.3	128978	48	US-10-567-867-1791	Sequence 1791, Ap
969	234.8	10.3	4604723	35	US-09-947-916-240	Sequence 240, App	1042	234.2	10.3	128978	57	US-10-775-169-345	Sequence 345, App
970	234.6	10.3	6000	94	US-60-873-739-1321	Sequence 1321, Ap	1043	234.2	10.3	128978	57	US-10-775-169A-345	Sequence 345, App
971	234.6	10.3	13624	61	US-10-990-328-94132	Sequence 94132, A	1044	234.2	10.3	128978	69	US-11-266-748A-61436	Sequence 61436, A
972	234.6	10.3	13624	61	US-10-990-328A-94132	Sequence 94132, A	1045	234.2	10.3	128978	74	US-11-378-923-6	Sequence 6, Appli
973	234.6	10.3	33830	61	US-10-990-328-95071	Sequence 95071, A	1046	234.2	10.3	128978	89	US-60-446-133-345	Sequence 1791, Ap
974	234.6	10.3	33830	61	US-10-990-328A-95071	Sequence 95071, A	1047	234.2	10.3	128978	90	US-60-490-890-1791	Sequence 40, Appl
975	234.6	10.3	58791	90	US-60-466-412-87409	Sequence 87409, A	1048	234.2	10.3	154001	86	US-60-212-664-40	Sequence 12239, A
976	234.6	10.3	60550	61	US-10-990-328-96238	Sequence 96238, A	1049	234.2	10.3	214066	90	US-60-485-450-12239	Sequence 12239, A
977	234.6	10.3	134199	90	US-60-461-762-3394	Sequence 3394, Ap	1050	234.2	10.3	214066	91	US-60-563-440-12239	Sequence 12239, A
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979	234.6	10.3	134199	90	US-60-461-762-3394	Sequence 84515, A	1052	234.2	10.3	232641	61	US-10-990-328-93650	Sequence 93650, A
980	234.6	10.3	134199	90	US-60-470-166-87815	Sequence 87813, Ap	1053	234.2	10.3	232641	61	US-10-990-328A-93650	Sequence 93650, A
981	234.6	10.3	146361	61	US-10-990-328-93202	Sequence 93202, A	1054	234.2	10.3	5506356	35	US-09-948-128-429	Sequence 429, App
982	234.6	10.3	146361	61	US-10-990-328A-93202	Sequence 93202, A	c1055	234	10.2	966	43	US-10-301-480A-122405	Sequence 122405,
983	234.6	10.3	179024	86	US-60-212-664-182	Sequence 182, App	c1056	234	10.2	966	44	US-10-301-480B-122405	Sequence 122405,
984	234.4	10.3	595	44	US-10-301-480A-301161	Sequence 301161,	c1057	234	10.2	966	45	US-10-301-480C-122405	Sequence 122405,
985	234.4	10.3	595	44	US-10-301-480B-301161	Sequence 301161,	1058	234	10.2	24239	59	US-10-940-774A-15452	Sequence 15452, A
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987	234.4	10.3	6000	94	US-60-873-738-760	Sequence 760, App	1060	234	10.2	31871	30	PCT-US01-01322-1403	Sequence 1403, Ap
988	234.4	10.3	70509	50	US-10-676-684-336	Sequence 336, App	1061	234	10.2	31871	30	US-09-764-847-1403	Sequence 1403, Ap
989	234.4	10.3	169495	66	US-11-121-086-61	Sequence 61, Appl	1062	234	10.2	31871	38	US-10-092-154-1403	Sequence 1403, Ap
990	234.4	10.3	462586	47	US-10-476-264-420	Sequence 420, App	1063	234	10.2	40742	1	PCT-US01-01354-22901	Sequence 22901, A
991	234.4	10.3	3037227	35	US-09-947-911-286	Sequence 286, App	1064	234	10.2	40742	1	PCT-US01-01354-22901	Sequence 22901, A
992	234.2	10.3	991	43	US-10-301-480A-256275	Sequence 256275,	1065	234	10.2	40742	31	US-09-764-905-22901	Sequence 22901, A
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994	234.2	10.3	991	45	US-10-301-480C-256275	Sequence 256275,	1067	234	10.2	40742	31	US-09-764-905-22901	Sequence 22901, A
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996	234.2	10.3	992	44	US-10-301-480B-256276	Sequence 256276,	c1069	234	10.2	40742	38	US-10-092-399-22901	Sequence 22901, A
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998	234.2	10.3	992	45	US-10-301-480C-256276	Sequence 60145,	1071	234	10.2	77195	35	US-09-949-003C-4193	Sequence 409, App
999	234.2	10.3	993	42	US-10-301-480-600145	Sequence 1213554,	1072	234	10.2	77695	35	US-09-949-003C-5324	Sequence 5324, Ap
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1002	234.2	10.3	993	45	US-10-301-480C-976214	Sequence 976214,	1075	234	10.2	86361	2	PCT-US03-40978-17803	Sequence 17803, A
1003	234.2	10.3	5819	59	US-10-940-774A-14050	Sequence 14050, A	1076	234	10.2	86361	56	US-10-741-600-17803	Sequence 17803, A
1004	234.2	10.3	5819	60	US-10-940-774A-14050	Sequence 14050, A	1077	234	10.2	86361	56	US-10-741-600-17803	Sequence 17803, A
1005	234.2	10.3	6200	80	US-11-664-374-45	Sequence 45, Appl	1078	234	10.2	86361	61	US-10-995-561-13364	Sequence 13364, A
1006	234.2	10.3	9822	59	US-10-940-774A-15697	Sequence 15697, A	1079	234	10.2	135173	1	PCT-US02-27620-76	Sequence 76, Appl
1007	234.2	10.3	9822	59	US-10-940-774A-15697	Sequence 15697, A	1080	234	10.2	135173	1	PCT-US02-27620-76	Sequence 76, Appl
1008	234.2	10.3	13818	90	US-60-466-412-83234	Sequence 83234, A	1081	234	10.2	143389	66	US-11-112-908-30	Sequence 30, Appl
1009	234.2	10.3	13970	35	US-09-950-083-7492	Sequence 7492, Ap	1082	234	10.2	143389	93	US-60-724-067-30	Sequence 30, Appl
1010	234.2	10.3	13970	35	US-09-950-083B-7492	Sequence 7492, Ap	1083	234	10.2	143389	93	US-60-725-089-30	Sequence 30, Appl
1011	234.2	10.3	13970	38	US-10-105-299-9643	Sequence 9643, Ap	1084	234	10.2	143389	93	US-60-726-029-30	Sequence 30, Appl
1012	234.2	10.3	13970	58	US-10-868-184-7492	Sequence 7492, Ap	1085	234	10.2	143389	93	US-60-726-030-30	Sequence 30, Appl
1013	234.2	10.3	13970	58	US-10-868-184A-7492	Sequence 7492, Ap	1086	234	10.2	143389	93	US-60-726-063-30	Sequence 30, Appl
1014	234.2	10.3	13970	58	US-10-868-184B-7492	Sequence 7492, Ap	1087	234	10.2	143389	93	US-60-726-063-30	Sequence 30, Appl
1015	234.2	10.3	13970	58	US-10-868-184C-7492	Sequence 7492, Ap	1088	234	10.2	150314	66	US-11-112-908-24	Sequence 24, Appl
1016	234.2	10.3	13970	58	US-10-868-184D-7492	Sequence 7492, Ap	1089	234	10.2	150314	66	US-11-112-908-24	Sequence 24, Appl
1017	234.2	10.3	13970	58	US-10-868-184E-7492	Sequence 7492, Ap	1090	234	10.2	150314	93	US-60-725-989-24	Sequence 24, Appl
1018	234.2	10.3	13970	58	US-10-868-184F-7492	Sequence 7492, Ap	1091	234	10.2	150314	93	US-60-725-989-24	Sequence 24, Appl
1019	234.2	10.3	17436	90	US-60-466-412-82879	Sequence 82879, A	1092	234	10.2	150314	93	US-60-726-029-24	Sequence 24, Appl
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1021	234.2	10.3	17880	59	US-10-932-349-19378	Sequence 19378, A	1094	234	10.2	150314	93	US-60-726-063-24	Sequence 24, Appl
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1023	234.2	10.3	29331	62	US-11-033-056A-36084	Sequence 36084, A	1096	234	10.2	220895	57	US-10-775-169-88	Sequence 88, Appl
1024	234.2	10.3	32768	86	US-60-207-421-8	Sequence 8, Appli	1097	234	10.2	220895	57	US-10-775-169A-88	Sequence 88, Appl

c1244	233	10.2	5633	58	US-10-868-184A-11222	Sequence 11222, A	c1317	232.6	10.2	816	43	US-10-301-480A-935104	Sequence 935104,
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c1246	233	10.2	5633	58	US-10-868-184C-11222	Sequence 11222, A	c1319	232.6	10.2	816	45	US-10-301-480C-935104	Sequence 935104,
c1247	233	10.2	5633	58	US-10-868-184D-11222	Sequence 11222, A	c1320	232.6	10.2	16573	59	US-10-940-774A-11764	Sequence 11764, A
c1248	233	10.2	5633	58	US-10-868-194B-11222	Sequence 11222, A	c1321	232.6	10.2	16573	60	US-10-940-774A-11764	Sequence 11764, A
c1249	233	10.2	5633	58	US-10-868-164-11222	Sequence 11222, A	c1322	232.6	10.2	17370	59	US-10-940-774A-17331	Sequence 17331, A
c1250	233	10.2	32768	86	US-60-213-172-35	Sequence 35, Appl	c1323	232.6	10.2	17370	60	US-10-940-774A-17331	Sequence 17331, A
c1251	233	10.2	32768	86	US-60-213-173-35	Sequence 35, Appl	c1324	232.6	10.2	22212	90	US-60-466-412-85895	Sequence 85895, A
c1252	233	10.2	32768	86	US-60-230-445-106	Sequence 106, Appl	c1325	232.6	10.2	24862	90	US-60-466-412-85895	Sequence 85895, A
c1253	233	10.2	32768	86	US-60-230-445-106	Sequence 106, Appl	c1326	232.6	10.2	32768	86	US-60-466-412-85895	Sequence 85895, A
c1254	233	10.2	43104	90	US-60-466-412-83731	Sequence 83731, A	c1327	232.6	10.2	32768	86	US-60-213-181-83	Sequence 83, Appl
c1255	233	10.2	68610	3	PCT-US04-07141-8843	Sequence 8843, Ap	c1328	232.6	10.2	32768	86	US-60-213-181-84	Sequence 84, Appl
c1256	233	10.2	68610	57	US-10-796-280-12467	Sequence 12467, A	c1329	232.6	10.2	32768	86	US-60-229-511-126	Sequence 126, App
c1257	233	10.2	68610	57	US-10-796-307-8843	Sequence 8843, Ap	c1330	232.6	10.2	33924	59	US-10-932-349-19608	Sequence 19608, A
c1258	233	10.2	256493	38	US-10-087-192-1000	Sequence 1000, Ap	c1331	232.6	10.2	33924	59	US-10-932-349-19608	Sequence 19608, A
c1259	233	10.2	1184710	57	US-10-796-280-12394	Sequence 12394, A	c1332	232.6	10.2	33924	59	US-10-932-349-19608	Sequence 19608, A
c1260	232.8	10.2	601	59	US-60-568-845-2921	Sequence 2921, Ap	c1333	232.6	10.2	35336	61	US-10-990-328A-98148	Sequence 98148, A
c1261	232.8	10.2	601	59	US-10-940-774-45773	Sequence 45773, A	c1334	232.6	10.2	35336	61	US-10-990-328A-98148	Sequence 98148, A
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c1263	232.8	10.2	601	60	US-10-940-774A-45774	Sequence 45774, A	c1336	232.6	10.2	35336	61	US-10-990-328A-98148	Sequence 98148, A
c1264	232.8	10.2	797	27	US-09-634-306B-127789	Sequence 127789, A	c1337	232.6	10.2	35336	61	US-10-990-328A-98148	Sequence 98148, A
c1265	232.8	10.2	797	38	US-10-027-633-127789	Sequence 127789, A	c1338	232.6	10.2	35336	61	US-10-990-328A-98148	Sequence 98148, A
c1266	232.8	10.2	32768	86	US-60-233-644-15	Sequence 15, Appl	c1339	232.6	10.2	40210	35	US-09-949-0030-3960	Sequence 3960, Ap
c1267	232.8	10.2	55493	87	US-60-243-734-2	Sequence 2, Appl	c1340	232.6	10.2	40210	35	US-09-949-0030-3960	Sequence 3960, Ap
c1268	232.8	10.2	71418	59	US-10-932-348-5010	Sequence 5010, Ap	c1341	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1269	232.8	10.2	71418	59	US-60-499-964-5010	Sequence 96022, A	c1342	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1270	232.8	10.2	78568	61	US-10-990-328A-96022	Sequence 96022, A	c1343	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1271	232.8	10.2	78568	61	US-10-990-328A-96022	Sequence 96022, A	c1344	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1272	232.8	10.2	109472	61	US-10-990-328A-98005	Sequence 98005, A	c1345	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1273	232.8	10.2	109472	61	US-10-990-328A-98005	Sequence 98005, A	c1346	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1274	232.8	10.2	121160	46	PCT-US03-41389-847	Sequence 847, App	c1347	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1275	232.8	10.2	121160	46	US-10-330-773A-847	Sequence 847, App	c1348	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1276	232.8	10.2	121160	46	US-10-330-773A-847	Sequence 847, App	c1349	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1277	232.8	10.2	121160	46	US-10-540-898-847	Sequence 847, App	c1350	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1278	232.8	10.2	121160	75	US-11-403-116-847	Sequence 847, App	c1351	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1279	232.8	10.2	128900	87	US-60-243-468-623	Sequence 623, App	c1352	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1280	232.8	10.2	136017	61	US-10-990-328A-93377	Sequence 93377, A	c1353	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1281	232.8	10.2	136017	61	US-10-990-328A-93377	Sequence 93377, A	c1354	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1282	232.8	10.2	136017	61	PCT-US03-41389-159	Sequence 159, App	c1355	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1283	232.8	10.2	136017	61	US-10-330-773A-159	Sequence 159, App	c1356	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1284	232.8	10.2	136017	46	US-10-330-773A-159	Sequence 159, App	c1357	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1285	232.8	10.2	136017	46	US-10-540-898-159	Sequence 159, App	c1358	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
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c1287	232.8	10.2	151001	89	US-60-465-241-51897	Sequence 51897, A	c1360	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
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c1294	232.6	10.2	2593930	35	US-09-947-911-54	Sequence 54, Appl	c1367	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1295	232.6	10.2	461	31	US-09-785-276A-49228	Sequence 49228, A	c1368	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1296	232.6	10.2	461	46	US-10-357-930-49228	Sequence 49228, A	c1369	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1297	232.6	10.2	509	34	US-09-528-408-17237	Sequence 17237, A	c1370	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1298	232.6	10.2	509	34	US-09-933-524-17237	Sequence 17237, A	c1371	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1299	232.6	10.2	509	35	US-09-933-524A-17237	Sequence 17237, A	c1372	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1300	232.6	10.2	601	59	US-10-940-774A-87766	Sequence 87766, A	c1373	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1301	232.6	10.2	601	60	US-10-940-774A-87766	Sequence 87766, A	c1374	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1302	232.6	10.2	624	27	US-09-634-306B-78403	Sequence 78403, A	c1375	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1303	232.6	10.2	624	27	US-09-634-306B-78404	Sequence 78404, A	c1376	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1304	232.6	10.2	624	27	US-09-634-306B-78405	Sequence 78405, A	c1377	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1305	232.6	10.2	624	27	US-09-634-306B-78406	Sequence 78406, A	c1378	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1306	232.6	10.2	624	27	US-09-634-306B-78407	Sequence 78407, A	c1379	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1307	232.6	10.2	624	27	US-09-634-306B-78408	Sequence 78408, A	c1380	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1308	232.6	10.2	624	38	US-10-027-632-78403	Sequence 78403, A	c1381	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1309	232.6	10.2	624	38	US-10-027-632-78404	Sequence 78404, A	c1382	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1310	232.6	10.2	624	38	US-10-027-632-78405	Sequence 78405, A	c1383	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1311	232.6	10.2	624	38	US-10-027-632-78406	Sequence 78406, A	c1384	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
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c1313	232.6	10.2	624	38	US-10-027-632-78408	Sequence 78408, A	c1386	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1314	232.6	10.2	765	27	US-09-634-306B-173966	Sequence 173966, A	c1387	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1315	232.6	10.2	765	38	US-10-027-632-173966	Sequence 173966, A	c1388	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
c1316	232.6	10.2	816	42	US-10-301-480-559035	Sequence 559035, A	c1389	232.6	10.2	43537	90	US-60-466-412-87084	Sequence 87084, A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	225.2	9.9	6000	1	PCT-US07-13803-146
5	221.6	9.7	408	7	US-11-881-406-1278
6	221.6	9.7	3102	7	US-11-574-839-13
7	221	9.7	74424	7	US-11-829-279-153
8	220	9.6	6000	1	PCT-US07-13803-189
9	219.2	9.6	1254	7	US-11-781-665-1823
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12	217.8	9.5	6000	1	PCT-US07-13803-226
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18	217	9.5	6000	1	PCT-US07-13803-253
19	216.4	9.5	2996	7	US-11-884-496-556
20	216	9.5	6000	1	PCT-US07-13803-29
21	216	9.5	6000	1	PCT-US07-13803-256
22	216	9.5	6928	7	US-11-490-374A-2139
23	214.8	9.4	267966	7	US-11-852-912-1
24	214.6	9.4	1586	7	US-11-781-665-2560
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26	214.6	9.4	14001	7	US-11-851-267-7

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c 28	214	9.4	1292	7	US-11-781-665-2507	Sequence 2507, Ap
c 29	214	9.4	1292	7	US-11-781-665-2508	Sequence 2508, Ap
c 30	214	9.4	155470	6	US-10-910-811B-373	Sequence 373, App
c 31	214	9.4	155470	6	US-10-945-565B-373	Sequence 373, App
c 32	213.8	9.4	92384	7	US-11-328-881A-80	Sequence 80, Appl
c 33	213.6	9.4	130001	1	PCT-US06-25800-39	Sequence 39, Appl
c 34	213.4	9.3	6907	7	US-11-490-374A-2138	Sequence 2138, Ap
c 35	213	9.3	28001	7	US-11-889-507-3	Sequence 3, Appl
c 36	212.8	9.3	6000	1	PCT-US07-13803-262	Sequence 262, App
c 37	212.4	9.3	6000	1	PCT-US07-13803-71	Sequence 71, Appl
c 38	212.4	9.3	11190	7	US-11-757-860-1	Sequence 1, Appl
c 39	212.2	9.3	6000	1	PCT-US07-13803-217	Sequence 217, App
c 40	211.8	9.3	173637	7	US-11-060-659A-37	Sequence 37, Appl
c 41	211.4	9.3	1001	7	US-11-881-406-1948	Sequence 1948, Ap
c 42	211.2	9.2	6000	1	PCT-US07-13803-53	Sequence 53, Appl
c 43	210.8	9.2	2314	7	US-11-781-665-3059	Sequence 3059, Ap
c 44	210.2	9.2	6000	1	PCT-US07-13803-127	Sequence 127, App
c 45	210.2	9.2	165589	7	US-11-328-881A-81	Sequence 81, Appl
c 46	210	9.2	6000	1	PCT-US07-13803-50	Sequence 50, Appl
c 47	210	9.2	24255	8	US-60-970-396-9	Sequence 9, Appl
c 48	210	9.2	74424	7	US-11-829-279-153	Sequence 153, App
c 49	209.6	9.2	1134	7	US-11-781-665-1744	Sequence 1744, Ap
c 50	209.6	9.2	6000	1	PCT-US07-13803-165	Sequence 165, App
c 51	209.6	9.2	8456	1	PCT-US07-13803-415	Sequence 415, App
c 52	209.2	9.2	6000	1	PCT-US07-13803-51	Sequence 51, Appl
c 53	209	9.2	6000	1	PCT-US07-13803-169	Sequence 169, App
c 54	209	9.2	79666	7	US-11-881-406-1	Sequence 1, Appl
c 55	209	9.2	89728	7	US-11-328-881A-83	Sequence 83, Appl
c 56	208.6	9.1	6000	1	PCT-US07-13803-106	Sequence 106, App
c 57	208.4	9.1	6000	1	PCT-US07-13803-236	Sequence 236, App
c 58	208.4	9.1	6000	1	PCT-US07-13803-249	Sequence 249, App
c 59	208	9.1	2001	7	US-11-881-406-3829	Sequence 3829, Ap
c 60	208	9.1	2001	7	US-11-881-406-3833	Sequence 3833, Ap
c 61	208	9.1	6000	1	PCT-US07-13803-55	Sequence 55, Appl
c 62	208	9.1	165589	7	US-11-328-881A-81	Sequence 81, Appl
c 63	207.8	9.1	382	7	US-11-881-406-2415	Sequence 2415, Ap
c 64	207.6	9.1	1504	7	US-11-235-701A-350	Sequence 350, App
c 65	207.6	9.1	6670	7	US-11-782-310-34	Sequence 34, Appl
c 66	207.6	9.1	60401	1	PCT-US06-25800-36	Sequence 36, Appl
c 67	207.4	9.1	2001	7	US-11-881-406-3889	Sequence 3889, Ap
c 68	207.4	9.1	2001	7	US-11-881-406-3890	Sequence 3890, Ap
c 69	207.2	9.1	1839	7	US-11-781-665-560	Sequence 560, App
c 70	207.2	9.1	173637	7	US-11-060-659A-37	Sequence 37, Appl
c 71	207	9.1	2148	7	US-11-781-665-1183	Sequence 1183, Ap
c 72	207	9.1	5466	7	US-11-490-374A-1510	Sequence 1510, Ap
c 73	207	9.1	6000	1	PCT-US07-13803-6	Sequence 6, Appl
c 74	207	9.1	6000	1	PCT-US07-13803-16	Sequence 16, Appl
c 75	207	9.1	6000	1	PCT-US07-13803-163	Sequence 163, App
c 76	207	9.1	6000	1	PCT-US07-13803-265	Sequence 265, App
c 77	207	9.1	21001	1	PCT-US07-75297-3	Sequence 3, Appl
c 78	206.8	9.1	1001	7	US-11-781-665-193	Sequence 193, App
c 79	206.8	9.1	6000	1	PCT-US07-13803-58	Sequence 58, Appl
c 80	206.8	9.1	6000	1	PCT-US07-13803-149	Sequence 149, App
c 81	206.8	9.1	6000	1	PCT-US07-13803-158	Sequence 158, App
c 82	206.6	9.0	6000	1	PCT-US07-13803-86	Sequence 86, Appl
c 83	206.6	9.0	6000	1	PCT-US07-13803-204	Sequence 204, App
c 84	206.2	9.0	735	7	US-11-781-665-1535	Sequence 1535, Ap
c 85	206	9.0	6000	1	PCT-US07-13803-137	Sequence 137, App
c 86	205.8	9.0	322	6	US-10-594-597-99	Sequence 99, Appl
c 87	205.8	9.0	929	7	US-11-781-665-918	Sequence 918, App
c 88	205.8	9.0	6000	1	PCT-US07-13803-233	Sequence 233, App
c 89	205.8	9.0	14001	7	US-11-851-267-7	Sequence 7, Appl
c 90	205.6	9.0	2446	1	PCT-US07-13803-494	Sequence 494, App
c 91	205.6	9.0	6000	1	PCT-US07-13803-126	Sequence 126, App
c 92	205.6	9.0	167253	7	US-11-328-881A-84	Sequence 84, Appl
c 93	205.6	9.0	168323	7	US-11-328-881A-84	Sequence 84, Appl
c 94	205.2	9.0	1270	7	US-11-781-665-605	Sequence 605, App
c 95	205.2	9.0	6000	1	PCT-US07-13803-62	Sequence 62, Appl
c 96	205.2	9.0	6000	1	PCT-US07-13803-220	Sequence 220, App
c 97	205.2	9.0	79666	7	US-11-881-406-1	Sequence 1, Appl
c 98	205	9.0	6000	1	PCT-US07-13803-124	Sequence 124, App
c 99	205	9.0	6000	1	PCT-US07-13803-170	Sequence 170, App

c 100	204.8	9.0	1538	7	US-11-781-665-568	Sequence 568, App	c 173	200.6	8.8	2129	7	US-11-781-665-1677	Sequence 1677, Ap
c 101	204.8	9.0	1572	7	US-11-831-404-48	Sequence 48, Appl	174	200.4	8.8	2129	1	PCT-US07-13803-248	Sequence 248, App
c 102	204.8	9.0	1932	7	US-11-781-665-1962	Sequence 1962, Ap	175	200	8.8	4121	7	US-11-885-002-1	Sequence 1, Appl
c 103	204.8	9.0	3682	7	US-11-831-404-38	Sequence 38, Appl	176	200	8.8	5225	7	US-11-734-562-3	Sequence 3, Appl
c 104	204.6	9.0	748	7	US-11-781-665-2057	Sequence 2057, Ap	c 177	199.8	8.7	825	7	US-11-781-665-2185	Sequence 2185, Ap
c 105	204.4	8.9	787	7	US-11-781-665-2273	Sequence 2273, Ap	c 178	199.8	8.7	1139	7	US-11-781-665-774	Sequence 774, App
c 106	204.4	8.9	1277	7	US-11-781-665-214	Sequence 214, App	c 179	199.8	8.7	1600	7	US-11-781-665-2966	Sequence 2966, Ap
c 107	204.4	8.9	3347	1	PCT-US07-13803-296	Sequence 296, App	180	199.8	8.7	6000	1	PCT-US07-13803-15	Sequence 15, Appl
c 108	204.4	8.9	3347	1	PCT-US07-13803-441	Sequence 441, App	181	199.8	8.7	6000	1	PCT-US07-13803-253	Sequence 253, App
c 109	204.4	8.9	6000	1	PCT-US07-13803-189	Sequence 189, App	182	199.8	8.7	6594	1	PCT-US07-13803-509	Sequence 509, App
c 110	204.4	8.9	6000	1	PCT-US07-13803-257	Sequence 257, App	c 183	199.6	8.7	798	7	US-11-781-665-2933	Sequence 2933, Ap
c 111	204.4	8.9	33780	6	US-10-148-848D-4	Sequence 4, Appl	c 184	199.4	8.7	6000	1	PCT-US07-13803-235	Sequence 235, App
c 112	204.2	8.9	415	7	US-11-881-406-1457	Sequence 1457, Ap	c 185	199.2	8.7	6000	1	PCT-US07-13803-10	Sequence 10, Appl
c 113	204.2	8.9	812	7	US-11-781-665-2367	Sequence 2367, Ap	c 186	199.2	8.7	28001	7	US-11-889-507-3	Sequence 3, Appl
c 114	204.2	8.9	1487	7	US-11-235-701A-351	Sequence 351, App	c 187	199	8.7	1036	7	US-11-781-665-1682	Sequence 1682, Ap
c 115	204.2	8.9	6000	1	PCT-US07-13803-232	Sequence 232, App	c 188	199	8.7	3627	6	US-11-781-665-1912	Sequence 1912, Ap
c 116	204	8.9	776	7	US-11-781-665-2968	Sequence 2968, Ap	189	199	8.7	3627	6	US-10-858-887A-6	Sequence 6, Appl
c 117	204	8.9	6000	1	PCT-US07-13803-172	Sequence 172, App	c 190	199	8.7	6000	1	PCT-US07-13803-6	Sequence 6, Appl
c 118	204	8.9	7239	7	US-11-794-690-28	Sequence 28, Appl	c 191	199	8.7	6000	1	PCT-US07-13803-239	Sequence 239, App
c 119	204	8.9	13001	1	PCT-US06-25800-38	Sequence 38, Appl	c 192	199	8.7	6000	1	PCT-US07-13803-257	Sequence 257, App
c 120	204	8.9	89728	7	US-11-328-881A-83	Sequence 83, Appl	c 193	199	8.7	6000	1	PCT-US07-13803-264	Sequence 264, App
c 121	203.8	8.9	901	7	US-11-781-665-322	Sequence 322, App	c 194	198.6	8.7	6000	1	PCT-US07-13803-230	Sequence 230, App
c 122	203.8	8.9	6000	1	PCT-US07-13803-12	Sequence 12, Appl	c 195	198.4	8.7	6000	1	PCT-US07-13803-200	Sequence 200, App
c 123	203.8	8.9	6000	1	PCT-US07-13803-82	Sequence 82, Appl	c 196	198.2	8.7	390	7	US-11-881-406-3398	Sequence 3398, Ap
c 124	203.8	8.9	6000	1	PCT-US07-13803-139	Sequence 139, App	c 197	198.2	8.7	392	7	US-11-881-406-3174	Sequence 3174, Ap
c 125	203.6	8.9	389	7	US-11-881-406-1668	Sequence 1668, Ap	c 198	198.2	8.7	2001	7	PCT-US07-13803-109	Sequence 109, App
c 126	203.6	8.9	1733	7	US-11-781-665-557	Sequence 557, App	c 199	198.2	8.7	6000	1	PCT-US07-13803-224	Sequence 224, App
c 127	203.4	8.9	824	7	US-11-781-665-2707	Sequence 2707, Ap	c 200	198.2	8.7	6000	1	US-11-781-665-2603	Sequence 2603, Ap
c 128	203.4	8.9	16015	7	US-11-885-002-74	Sequence 74, Appl	c 201	198	8.7	1753	7	US-11-781-665-2603	Sequence 12, Appl
c 129	203	8.9	2887	7	US-11-825-627-350	Sequence 350, App	c 202	198	8.7	6000	1	PCT-US07-13803-12	Sequence 82, Appl
c 130	203	8.9	6000	1	PCT-US07-13803-40	Sequence 40, Appl	c 203	198	8.7	6000	1	PCT-US07-13803-82	Sequence 2543, Ap
c 131	203	8.9	6000	1	PCT-US07-13803-178	Sequence 178, App	c 204	197.8	8.7	695	7	US-11-781-665-2543	Sequence 2970, Ap
c 132	203	8.9	6000	1	PCT-US07-13803-241	Sequence 241, App	c 205	197.8	8.7	1440	7	US-11-781-665-2970	Sequence 1624, Ap
c 133	202.8	8.9	1862	7	US-11-781-665-2597	Sequence 2597, Ap	c 206	197.8	8.7	1796	7	US-11-781-665-1920	Sequence 22, Appl
c 134	202.8	8.9	6000	1	PCT-US07-13803-260	Sequence 260, App	c 207	197.8	8.7	6000	1	PCT-US07-13803-22	Sequence 23, Appl
c 135	202.6	8.9	6000	1	PCT-US07-13803-269	Sequence 269, App	c 208	197.8	8.7	6000	1	PCT-US07-13803-77	Sequence 77, Appl
c 136	202.4	8.9	6000	1	PCT-US07-13803-258	Sequence 258, App	c 209	197.8	8.7	6000	1	PCT-US07-13803-117	Sequence 117, App
c 137	202.2	8.9	721	7	US-11-781-665-403	Sequence 403, App	c 210	197.8	8.7	868	7	US-11-781-665-1862	Sequence 93, Appl
c 138	202.2	8.9	1298	7	US-11-781-665-2962	Sequence 2962, Ap	c 211	197.6	8.7	6000	1	PCT-US07-13803-1794	Sequence 1794, Ap
c 139	202.2	8.9	6000	1	PCT-US07-13803-69	Sequence 69, Appl	c 212	197.6	8.7	779	7	US-11-781-665-1794	Sequence 3440, Ap
c 140	202.2	8.9	6000	1	PCT-US07-13803-73	Sequence 73, Appl	c 213	197.4	8.6	1325	7	US-11-881-406-3440	Sequence 628, App
c 141	202	8.8	6000	1	PCT-US07-13803-39	Sequence 39, Appl	c 214	197.4	8.6	1585	7	US-11-881-406-3437	Sequence 3437, App
c 142	201.8	8.8	924	7	US-11-781-665-1110	Sequence 1110, Ap	c 215	197.4	8.6	2001	7	US-11-881-406-3441	Sequence 1370, Ap
c 143	201.8	8.8	1032	7	US-11-781-665-2633	Sequence 2633, Ap	c 216	197.4	8.6	2001	7	US-11-881-406-3441	Sequence 217, App
c 144	201.8	8.8	3497	7	US-11-816-601-791	Sequence 791, App	c 217	197.4	8.6	421	7	US-11-881-406-1370	Sequence 217, App
c 145	201.8	8.8	5077	7	US-11-781-665-2326	Sequence 2326, Ap	c 218	197.2	8.6	6000	1	PCT-US07-13803-217	Sequence 252, App
c 146	201.8	8.8	6000	1	PCT-US07-13803-39	Sequence 39, Appl	c 219	197	8.6	6000	1	PCT-US07-13803-252	Sequence 15, Appl
c 147	201.8	8.8	6000	1	PCT-US07-13803-121	Sequence 121, App	c 220	196.8	8.6	6000	1	PCT-US07-13803-117	Sequence 15, Appl
c 148	201.8	8.8	6000	1	PCT-US07-13803-140	Sequence 140, App	c 221	196.8	8.6	7468	7	US-11-797-156-15	Sequence 38, Appl
c 149	201.8	8.8	6000	1	PCT-US07-13803-207	Sequence 207, App	c 222	196.8	8.6	8194	7	US-11-745-857-15	Sequence 890, App
c 150	201.6	8.8	1388	7	US-11-781-665-1127	Sequence 1127, Ap	c 223	196.8	8.6	13001	1	PCT-US06-25800-38	Sequence 28, Appl
c 151	201.6	8.8	5687	6	US-10-590-043-1	Sequence 1, Appl	c 224	196.8	8.6	1786	7	US-11-781-665-890	Sequence 28, Appl
c 152	201.4	8.8	840	7	US-11-781-665-2356	Sequence 2356, Ap	c 225	196.6	8.6	4145	7	US-11-816-601-28	Sequence 28, Appl
c 153	201.4	8.8	1475	7	US-11-781-665-2174	Sequence 2174, App	c 226	196.6	8.6	6000	1	PCT-US07-13803-28	Sequence 268, App
c 154	201.4	8.8	6000	1	PCT-US07-13803-181	Sequence 181, App	c 227	196.6	8.6	6000	1	PCT-US07-13803-268	Sequence 55, Appl
c 155	201.2	8.8	1133	7	US-11-781-665-2829	Sequence 2829, Ap	c 228	196.6	8.6	7392	7	US-11-060-659A-55	Sequence 82, Appl
c 156	201.2	8.8	1467	7	US-11-235-701A-352	Sequence 352, App	c 229	196.6	8.6	167253	7	US-11-328-881A-82	Sequence 812, App
c 157	201.2	8.8	3177	7	US-11-884-496-709	Sequence 709, App	c 230	196.6	8.6	1551	7	US-11-781-665-812	Sequence 254, App
c 158	201.2	8.8	3177	7	US-11-908-114-4	Sequence 4, Appl	c 231	196.4	8.6	6000	1	PCT-US07-13803-41	Sequence 254, App
c 159	201	8.8	1345	7	US-11-781-665-772	Sequence 772, App	c 232	196.4	8.6	6000	1	PCT-US07-13803-132	Sequence 1694, Ap
c 160	201	8.8	5170	7	US-11-733-861-62	Sequence 62, Appl	c 233	196.2	8.6	420	7	US-11-781-665-1694	Sequence 3652, Ap
c 161	201	8.8	6000	1	PCT-US07-13803-42	Sequence 42, Appl	c 234	196.2	8.6	1309	7	US-11-881-406-3652	Sequence 3653, Ap
c 162	201	8.8	6000	1	PCT-US07-13803-54	Sequence 54, Appl	c 235	196.2	8.6	2020	7	US-11-816-601-92	Sequence 409, App
c 163	201	8.8	6000	1	PCT-US07-13803-88	Sequence 88, Appl	c 236	196	8.6	2242	1	PCT-US07-13803-409	Sequence 27, Appl
c 164	201	8.8	6000	1	PCT-US07-13803-89	Sequence 89, Appl	c 237	196	8.6	6000	1	PCT-US07-13803-27	Sequence 41, Appl
c 165	201	8.8	6000	1	PCT-US07-13803-90	Sequence 90, Appl	c 238	196	8.6	6000	1	PCT-US07-13803-41	Sequence 132, App
c 166	201	8.8	6000	1	PCT-US07-13803-153	Sequence 153, App	c 239	196	8.6	6000	1	PCT-US07-13803-132	Sequence 1694, Ap
c 167	201	8.8	6000	1	PCT-US07-13803-159	Sequence 159, App	c 240	195.8	8.6	1671	7	US-11-781-665-1694	Sequence 3652, Ap
c 168	201	8.8	6000	1	PCT-US07-13803-165	Sequence 165, App	c 241	195.8	8.6	2001	7	US-11-881-406-3652	Sequence 3653, Ap
c 169	201	8.8	6000	1	PCT-US07-13803-208	Sequence 208, App	c 242	195.8	8.6	2001	7	US-11-881-406-3653	Sequence 3654, Ap
c 170	201	8.8	33780	6	US-10-148-848D-4	Sequence 4, Appl	c 243	195.8	8.6	2001	7	US-11-881-406-3655	Sequence 3655, Ap
c 171	200.8	8.8	6000	1	PCT-US07-13803-176	Sequence 176, App	c 244	195.8	8.6	2001	7	US-11-881-406-3655	Sequence 2433, Ap
c 172	200.8	8.8	6000	1	PCT-US07-13803-201	Sequence 201, App	c 245	195.8	8.6	2310	7	US-11-781-665-2433	

c 246	195.8	8.6	6000	1	PCT-US07-13803-194	Sequence 194, App	319	192.4	8.4	6000	1	PCT-US07-13803-129	Sequence 129, App
c 247	195.6	8.6	653	7	US-11-781-665-2228	Sequence 2228, App	320	192.2	8.4	2971	7	US-11-781-665-2422	Sequence 2422, App
c 248	195.6	8.6	6000	1	PCT-US07-13803-17	Sequence 17, Appl	321	192.2	8.4	6000	1	PCT-US07-13803-7	Sequence 7, Appl
c 249	195.6	8.6	6000	1	PCT-US07-13803-150	Sequence 150, App	c 322	192.2	8.4	6000	1	PCT-US07-13803-205	Sequence 205, App
c 250	195.6	8.6	6000	1	PCT-US07-13803-251	Sequence 251, App	323	192	8.4	2001	7	US-11-881-406-1098	Sequence 1098, App
c 251	195.4	8.6	421	7	US-11-881-406-2046	Sequence 2046, App	c 324	192	8.4	6000	1	PCT-US07-13803-208	Sequence 208, App
c 252	195.2	8.5	1090	7	US-11-781-665-2840	Sequence 2840, App	c 325	192	8.4	6000	1	PCT-US07-13803-261	Sequence 261, App
c 253	195.2	8.5	2259	7	US-11-781-665-2852	Sequence 2852, App	c 326	191.8	8.4	1703	7	US-11-781-665-2418	Sequence 2418, App
c 254	195	8.5	1157	7	US-11-781-665-1741	Sequence 1741, App	327	191.8	8.4	2135	7	US-11-825-627-79	Sequence 83, Appl
c 255	194.8	8.5	1038	7	US-11-781-665-2202	Sequence 2202, App	328	191.8	8.4	2468	7	US-11-825-627-81	Sequence 81, Appl
c 256	194.8	8.5	1528	7	US-11-781-665-1993	Sequence 1993, App	329	191.8	8.4	2554	7	US-11-825-627-81	Sequence 368, App
c 257	194.8	8.5	2632	7	US-11-781-665-206	Sequence 206, App	330	191.8	8.4	3207	1	PCT-US07-13803-368	Sequence 368, App
c 258	194.8	8.5	3599	7	US-11-908-113-5	Sequence 5, Appl	c 331	191.8	8.4	6000	1	PCT-US07-13803-170	Sequence 170, App
c 259	194.8	8.5	3599	7	US-11-908-114-17	Sequence 17, Appl	332	191.6	8.4	1001	7	US-11-881-406-3894	Sequence 3894, App
c 260	194.8	8.5	6000	1	PCT-US07-13803-68	Sequence 68, Appl	333	191.6	8.4	1435	7	US-11-781-665-2916	Sequence 2916, App
c 261	194.8	8.5	6000	1	PCT-US07-13803-205	Sequence 205, App	c 334	191.6	8.4	1510	7	US-11-781-665-701	Sequence 701, App
c 262	194.6	8.5	1075	7	US-11-781-665-2903	Sequence 2903, App	335	191.6	8.4	1888	7	US-11-781-665-1657	Sequence 1657, App
c 263	194.6	8.5	2253	7	US-11-781-665-2079	Sequence 2079, App	336	191.6	8.4	2122	7	US-11-781-665-1951	Sequence 1951, App
c 264	194.6	8.5	6000	1	PCT-US07-13803-186	Sequence 186, App	337	191.6	8.4	5769	7	US-11-851-267-218	Sequence 218, App
c 265	194.4	8.5	1149	7	US-11-781-665-2265	Sequence 2265, App	338	191.4	8.4	411	7	US-11-881-406-1788	Sequence 1788, App
c 266	194.4	8.5	1425	7	US-11-781-665-874	Sequence 874, App	c 339	191.4	8.4	954	7	US-11-781-665-2047	Sequence 2047, App
c 267	194.4	8.5	1634	7	US-11-781-665-2327	Sequence 2327, App	340	191.4	8.4	2723	6	US-10-549-662-6	Sequence 6, Appl
c 268	194.4	8.5	1780	7	US-11-781-665-916	Sequence 916, App	341	191.4	8.4	2723	6	US-10-549-662-16	Sequence 16, Appl
c 269	194.2	8.5	759	7	US-11-781-665-2206	Sequence 2206, App	c 342	191.4	8.4	2820	7	US-11-781-665-1725	Sequence 1725, App
c 270	194.2	8.5	1325	7	US-11-781-665-2832	Sequence 2832, App	343	191.4	8.4	6000	1	PCT-US07-13803-22	Sequence 22, Appl
c 271	194.2	8.5	2859	7	US-11-848-462-5	Sequence 5, Appl	344	191.4	8.4	6000	1	PCT-US07-13803-23	Sequence 23, Appl
c 272	194.2	8.5	4517	6	US-10-514-040B-3	Sequence 3, Appl	345	191.2	8.4	1365	7	US-11-781-665-636	Sequence 636, App
c 273	194	8.5	908	7	US-11-781-665-364	Sequence 364, App	c 346	191.2	8.4	1447	7	US-11-781-665-2918	Sequence 2918, App
c 274	194	8.5	1377	7	US-11-781-665-1441	Sequence 1441, App	c 347	191.2	8.4	2001	7	US-11-881-406-914	Sequence 914, App
c 275	194	8.5	2001	7	US-11-881-406-3800	Sequence 3800, App	348	191.2	8.4	6000	1	PCT-US07-13803-58	Sequence 58, Appl
c 276	194	8.5	6000	1	PCT-US07-13803-31	Sequence 31, Appl	349	191.2	8.4	6000	1	PCT-US07-13803-358	Sequence 358, App
c 277	194	8.5	6000	1	PCT-US07-13803-255	Sequence 255, App	c 350	191	8.4	401	7	US-11-881-406-3953	Sequence 3953, App
c 278	193.8	8.5	822	7	US-11-881-406-3828	Sequence 3828, App	c 351	191	8.4	405	7	US-11-881-406-2215	Sequence 2215, App
c 279	193.8	8.5	1399	7	US-11-781-665-2892	Sequence 2892, App	c 352	191	8.4	1441	7	US-11-781-665-2556	Sequence 2556, App
c 280	193.8	8.5	1572	7	US-11-781-665-2059	Sequence 2059, App	c 353	191	8.4	6000	1	PCT-US07-13803-179	Sequence 179, App
c 281	193.8	8.5	1593	7	US-11-781-665-2607	Sequence 2607, App	c 354	190.8	8.4	397	7	US-11-881-406-3776	Sequence 3776, App
c 282	193.8	8.5	1891	7	US-11-781-665-64	Sequence 64, Appl	c 355	190.8	8.4	6000	1	PCT-US07-13803-184	Sequence 184, App
c 283	193.8	8.5	6000	1	PCT-US07-13803-121	Sequence 121, App	c 356	190.6	8.3	1184	7	US-11-781-665-2222	Sequence 2222, App
c 284	193.6	8.5	2001	7	US-11-881-406-3619	Sequence 3619, App	c 357	190.6	8.3	2036	7	US-11-235-701A-511	Sequence 511, App
c 285	193.6	8.5	2001	7	US-11-881-406-3620	Sequence 3620, App	c 358	190.6	8.3	6000	1	PCT-US07-13803-106	Sequence 106, App
c 286	193.6	8.5	2001	7	US-11-881-406-3656	Sequence 3656, App	c 359	190.4	8.3	858	7	US-11-781-665-994	Sequence 994, App
c 287	193.6	8.5	2339	4	US-08-444-791C-3	Sequence 3, Appl	c 360	190.4	8.3	2341	7	US-11-816-601-116	Sequence 116, App
c 288	193.6	8.5	8194	7	US-11-797-156-15	Sequence 15, Appl	c 361	190.4	8.3	2341	7	US-11-816-601-303	Sequence 303, App
c 289	193.6	8.5	8194	7	US-11-745-857-15	Sequence 15, Appl	c 362	190.4	8.3	3870	1	PCT-US07-66287-1	Sequence 1, Appl
c 290	193.4	8.5	909	7	US-11-781-665-1936	Sequence 1936, App	c 363	190.4	8.3	6000	1	PCT-US07-13803-147	Sequence 147, App
c 291	193.4	8.5	1446	7	US-11-781-665-1781	Sequence 1781, App	c 364	190.2	8.3	3548	7	US-11-884-496-721	Sequence 721, App
c 292	193.4	8.5	6000	1	PCT-US07-13803-96	Sequence 96, Appl	c 365	190	8.3	1419	7	US-11-781-665-80	Sequence 80, Appl
c 293	193.2	8.5	788	7	US-11-781-665-1327	Sequence 1327, App	c 366	190	8.3	1503	7	US-11-781-665-1829	Sequence 1829, App
c 294	193.2	8.5	3610	7	US-11-908-113-4	Sequence 4, Appl	c 367	190	8.3	1521	7	US-11-781-665-1145	Sequence 1145, App
c 295	193.2	8.5	6000	1	PCT-US07-13803-11	Sequence 11, Appl	368	190	8.3	2135	7	US-11-490-374A-2108	Sequence 2108, App
c 296	193.2	8.5	6000	1	PCT-US07-13803-54	Sequence 54, Appl	369	190	8.3	2135	7	US-11-490-374A-2110	Sequence 2110, App
c 297	193.2	8.5	6000	1	PCT-US07-13803-60	Sequence 60, Appl	370	189.8	8.3	619	7	US-11-881-406-3872	Sequence 3872, App
c 298	193.2	8.5	6042	7	US-11-302-202A-34	Sequence 34, Appl	371	189.8	8.3	6000	1	PCT-US07-13803-76	Sequence 76, Appl
c 299	193	8.5	6000	1	PCT-US07-13803-32	Sequence 32, Appl	372	189.8	8.3	6000	1	PCT-US07-13803-195	Sequence 195, App
c 300	193	8.5	6000	1	PCT-US07-13803-266	Sequence 266, App	c 373	189.8	8.3	6000	1	PCT-US07-13803-202	Sequence 202, App
c 301	193	8.5	6000	1	PCT-US07-13803-267	Sequence 267, App	c 374	189.6	8.3	981	7	US-11-781-665-946	Sequence 946, App
c 302	192.8	8.4	1319	7	US-11-781-665-1971	Sequence 1971, App	c 375	189.6	8.3	1099	7	US-11-781-665-2150	Sequence 2150, App
c 303	192.8	8.4	2001	7	US-11-881-406-3282	Sequence 3282, App	c 376	189.6	8.3	1426	7	US-11-781-665-1057	Sequence 1057, App
c 304	192.8	8.4	6000	1	PCT-US07-13803-24	Sequence 24, App	c 377	189.4	8.3	1320	7	US-11-781-665-2516	Sequence 2516, App
c 305	192.8	8.4	6000	1	PCT-US07-13803-71	Sequence 71, Appl	c 378	189.4	8.3	1768	7	US-11-781-665-2907	Sequence 2907, App
c 306	192.8	8.4	6000	1	PCT-US07-13803-86	Sequence 86, Appl	379	189.4	8.3	1937	6	US-10-433-238B-10	Sequence 10, Appl
c 307	192.8	8.4	6000	1	PCT-US07-13803-174	Sequence 174, App	380	189.4	8.3	1937	7	US-11-841-536-10	Sequence 10, Appl
c 308	192.8	8.4	6000	1	PCT-US07-13803-182	Sequence 182, App	c 381	189.4	8.3	6000	1	PCT-US07-13803-3	Sequence 3, Appl
c 309	192.6	8.4	405	7	US-11-881-406-1876	Sequence 1876, App	c 382	189.2	8.3	2301	7	US-11-781-665-2833	Sequence 2833, App
c 310	192.6	8.4	1472	7	US-11-781-665-2955	Sequence 2955, App	c 383	189.2	8.3	2604	7	US-11-781-665-2407	Sequence 2407, App
c 311	192.6	8.4	5225	7	US-11-734-562-3	Sequence 3, Appl	c 384	189.2	8.3	3342	7	US-11-781-665-539	Sequence 539, App
c 312	192.6	8.4	6000	1	PCT-US07-13803-227	Sequence 227, App	c 385	189.2	8.3	6000	1	PCT-US07-13803-107	Sequence 107, App
c 313	192.6	8.4	6000	1	PCT-US07-13803-250	Sequence 250, App	c 386	189.2	8.3	6000	1	PCT-US07-13803-259	Sequence 259, App
c 314	192.4	8.4	1148	7	US-11-781-665-939	Sequence 939, App	c 387	189	8.3	2001	7	US-11-881-406-3786	Sequence 3786, App
c 315	192.4	8.4	1879	7	US-11-881-406-2011	Sequence 2011, App	c 388	189	8.3	6000	1	PCT-US07-13803-134	Sequence 134, App
c 316	192.4	8.4	2001	7	US-11-881-406-2012	Sequence 2012, App	389	189	8.3	6000	1	PCT-US07-13803-243	Sequence 243, App
c 317	192.4	8.4	6000	1	PCT-US07-13803-50	Sequence 50, Appl	c 390	188.8	8.3	1623	7	US-11-781-665-2555	Sequence 2555, App
c 318	192.4	8.4	6000	1	PCT-US07-13803-105	Sequence 105, App	391	188.8	8.3	6000	1	PCT-US07-13803-108	Sequence 108, App

C 392	188.8	8.3	6000	1	PCT-US07-13803-262	Sequence 262, App	465	185.4	8.1	6000	1	PCT-US07-13803-231	Sequence 231, App
C 393	188.6	8.3	1320	7	US-11-781-665-2734	Sequence 2734, App	466	185.2	8.1	2001	7	US-11-881-406-3582	Sequence 3582, App
C 394	188.6	8.3	1380	7	US-11-781-665-643	Sequence 643, App	467	185.2	8.1	6000	1	PCT-US07-13803-38	Sequence 38, Appl
C 395	188.6	8.3	1847	6	US-10-910-811B-374	Sequence 374, App	C 468	185.2	8.1	6000	1	PCT-US07-13803-140	Sequence 140, App
C 396	188.6	8.3	1847	6	US-10-945-565B-374	Sequence 374, App	C 469	185	8.1	1190	7	US-11-781-665-270	Sequence 270, App
C 397	188.6	8.3	2520	7	US-11-832-009-50	Sequence 50, Appl	C 470	185	8.1	1408	7	US-11-781-665-2652	Sequence 2652, App
C 398	188.6	8.3	6000	1	PCT-US07-13803-179	Sequence 179, App	C 471	185	8.1	2194	1	PCT-US07-13803-453	Sequence 453, App
C 399	188.4	8.2	403	7	US-11-881-406-1885	Sequence 185, App	C 472	185	8.1	6000	1	PCT-US07-13803-31	Sequence 31, Appl
C 400	188.4	8.2	1010	7	US-11-781-665-72	Sequence 72, Appl	C 473	185	8.1	6000	1	PCT-US07-13803-255	Sequence 255, App
C 401	188.4	8.2	1583	7	US-11-781-665-2608	Sequence 2608, App	C 474	184.8	8.1	1776	1	PCT-US07-75115-3	Sequence 3, Appl
C 402	188.4	8.2	1614	7	US-11-781-665-1650	Sequence 1650, App	C 475	184.8	8.1	6000	1	PCT-US07-13803-45	Sequence 45, Appl
C 403	188.4	8.2	2286	7	US-11-781-665-950	Sequence 950, App	C 476	184.8	8.1	6000	1	PCT-US07-13803-92	Sequence 92, Appl
C 404	188.4	8.2	5518	7	US-11-884-496-547	Sequence 547, App	C 477	184.6	8.1	878	7	US-11-781-665-1428	Sequence 1428, App
C 405	188.4	8.2	6444	7	US-11-831-404-85	Sequence 85, Appl	C 478	184.6	8.1	1308	7	US-11-781-665-63	Sequence 63, Appl
C 406	188.2	8.2	1647	7	US-11-781-665-809	Sequence 809, App	C 479	184.6	8.1	1401	7	US-11-798-002-1	Sequence 1, Appl
C 407	188.2	8.2	2154	7	US-11-781-665-1747	Sequence 1747, App	C 480	184.6	8.1	6000	1	PCT-US07-13803-122	Sequence 122, App
C 408	188.2	8.2	5879	7	US-11-816-601-166	Sequence 166, App	C 481	184.6	8.1	6683	1	PCT-US07-13803-493	Sequence 493, App
C 409	188.2	8.2	6000	1	PCT-US07-13803-46	Sequence 46, Appl	C 482	184.4	8.1	657	7	US-11-781-665-2845	Sequence 2845, App
C 410	188.2	8.2	6000	1	PCT-US07-13803-107	Sequence 107, App	C 483	184.4	8.1	4567	7	US-11-847-733-82	Sequence 82, Appl
C 411	188.2	8.2	168323	7	US-11-328-881A-84	Sequence 84, Appl	C 484	184.2	8.1	5144	7	US-11-490-374A-1684	Sequence 1684, App
C 412	188	8.2	414	7	US-11-881-406-1272	Sequence 1272, App	C 485	184.2	8.1	6000	1	PCT-US07-13803-19	Sequence 19, Appl
C 413	188	8.2	1697	7	US-11-781-665-607	Sequence 607, App	C 486	184.2	8.1	6000	1	PCT-US07-13803-57	Sequence 57, Appl
C 414	188	8.2	1779	7	US-11-781-665-1673	Sequence 1673, App	C 487	184.2	8.1	2001	7	PCT-US07-13803-229	Sequence 229, App
C 415	187.8	8.2	5508	7	US-11-490-374A-2137	Sequence 2137, App	C 488	184	8.1	2001	7	US-11-881-406-3537	Sequence 3537, App
C 416	187.8	8.2	6000	1	PCT-US07-13803-1	Sequence 1, Appl	C 489	183.8	8.0	851	7	US-11-781-665-2553	Sequence 2553, App
C 417	187.8	8.2	6000	1	PCT-US07-13803-18	Sequence 18, Appl	C 490	183.8	8.0	1104	7	US-11-781-665-2587	Sequence 2587, App
C 418	187.8	8.2	6000	1	PCT-US07-13803-53	Sequence 53, Appl	C 491	183.6	8.0	859	7	US-11-781-665-1551	Sequence 1551, App
C 419	187.8	8.2	6000	1	PCT-US07-13803-111	Sequence 111, App	C 492	183.6	8.0	6000	1	PCT-US07-13803-88	Sequence 88, Appl
C 420	187.8	8.2	6000	1	PCT-US07-13803-130	Sequence 130, App	C 493	183.6	8.0	6000	1	PCT-US07-13803-89	Sequence 89, Appl
C 421	187.6	8.2	1245	7	US-11-781-665-650	Sequence 650, App	C 494	183.6	8.0	6000	1	PCT-US07-13803-90	Sequence 90, Appl
C 422	187.6	8.2	2612	7	US-11-781-665-2090	Sequence 2090, App	C 495	183.6	8.0	6000	1	PCT-US07-13803-228	Sequence 228, App
C 423	187.6	8.2	6000	1	PCT-US07-13803-167	Sequence 167, App	C 496	183.4	8.0	418	7	US-11-881-406-2206	Sequence 2206, App
C 424	187.6	8.2	6000	1	PCT-US07-13803-203	Sequence 203, App	C 497	183.4	8.0	1182	7	US-11-832-009-54	Sequence 54, Appl
C 425	187.4	8.2	824	7	US-11-781-665-707	Sequence 707, App	C 498	183.4	8.0	1733	7	US-11-781-665-2721	Sequence 2721, App
C 426	187.4	8.2	1268	7	US-11-781-665-2081	Sequence 2081, App	C 499	183.2	8.0	1501	7	US-11-781-665-2615	Sequence 2615, App
C 427	187.4	8.2	1948	7	US-11-781-665-807	Sequence 807, App	C 500	183.2	8.0	1688	7	US-11-781-665-891	Sequence 891, App
C 428	187.4	8.2	6000	1	PCT-US07-13803-139	Sequence 139, App	C 501	183.2	8.0	7028	7	US-11-881-406-39	Sequence 39, Appl
C 429	187.2	8.2	865	7	US-11-781-665-2588	Sequence 2588, App	C 502	183	8.0	419	7	US-11-881-406-927	Sequence 927, App
C 430	187.2	8.2	2075	7	US-11-831-404-99	Sequence 99, Appl	C 503	183	8.0	430	7	US-11-881-406-2918	Sequence 2918, App
C 431	187.2	8.2	6433	7	US-11-490-374A-1949	Sequence 1949, App	C 504	183	8.0	4642	1	PCT-US07-13803-336	Sequence 336, App
C 432	187.2	8.2	6433	7	US-11-490-374A-1950	Sequence 1950, App	C 505	183	8.0	6000	1	PCT-US07-13803-75	Sequence 75, Appl
C 433	187.2	8.2	6433	7	US-11-490-374A-1951	Sequence 1951, App	C 506	183	8.0	6000	1	PCT-US07-13803-254	Sequence 254, App
C 434	187.2	8.2	6444	7	US-11-831-404-85	Sequence 85, Appl	C 507	182.8	8.0	425	7	US-11-881-406-3694	Sequence 3694, App
C 435	187	8.2	1430	7	US-11-781-665-1085	Sequence 1085, App	C 508	182.8	8.0	1162	7	US-11-781-665-2205	Sequence 2205, App
C 436	187	8.2	6000	1	PCT-US07-13803-264	Sequence 264, App	C 509	182.8	8.0	5019	8	US-60-970-396-7	Sequence 7, Appl
C 437	187	8.2	6883	7	US-11-490-374A-1494	Sequence 1494, App	C 510	182.6	8.0	1156	7	US-11-781-665-302	Sequence 302, App
C 438	186.8	8.2	420	7	US-11-881-406-1847	Sequence 1847, App	C 511	182.6	8.0	1158	7	US-11-781-665-367	Sequence 367, App
C 439	186.8	8.2	1227	7	US-11-781-665-2388	Sequence 2388, App	C 512	182.6	8.0	1718	7	US-11-781-665-920	Sequence 920, App
C 440	186.8	8.2	1278	7	US-11-781-665-551	Sequence 551, App	C 513	182.6	8.0	6000	1	PCT-US07-13803-57	Sequence 57, Appl
C 441	186.8	8.2	6000	1	PCT-US07-06371-92	Sequence 92, Appl	C 514	182.4	8.0	409	7	US-11-881-406-3993	Sequence 3993, App
C 442	186.8	8.2	13602	1	PCT-US07-06371-1	Sequence 1, Appl	C 515	182.4	8.0	706	7	US-11-781-665-2357	Sequence 2357, App
C 443	186.8	8.2	17534	1	PCT-US07-06371-16	Sequence 16, Appl	C 516	182.4	8.0	1141	7	US-11-781-665-1527	Sequence 1527, App
C 444	186.8	8.2	30756	1	PCT-US07-06371-16	Sequence 16, Appl	C 517	182.4	8.0	1158	7	US-11-781-665-1543	Sequence 1543, App
C 445	186.4	8.2	467	7	US-11-884-496-705	Sequence 705, App	C 518	182.4	8.0	5096	7	US-11-881-406-40	Sequence 40, Appl
C 446	186.4	8.2	2845	7	US-11-884-496-643	Sequence 643, App	C 519	182.4	8.0	6000	1	PCT-US07-13803-200	Sequence 200, App
C 447	186.2	8.2	953	7	US-11-781-665-2515	Sequence 2515, App	C 520	182.4	8.0	6000	1	PCT-US07-13803-227	Sequence 227, App
C 448	186.2	8.2	1256	7	US-11-781-665-1032	Sequence 1032, App	C 521	182.2	8.0	2168	7	US-11-781-665-160	Sequence 160, App
C 449	186.2	8.2	6000	1	PCT-US07-13803-147	Sequence 147, App	C 522	182.2	8.0	6000	1	PCT-US07-13803-11	Sequence 11, Appl
C 450	186.2	8.2	6000	1	PCT-US07-13803-187	Sequence 187, App	C 523	182.2	8.0	6000	1	PCT-US07-13803-502	Sequence 502, Appl
C 451	186	8.1	910	7	US-11-781-665-1438	Sequence 1438, App	C 524	182.2	8.0	7367	7	US-11-781-665-366	Sequence 366, App
C 452	186	8.1	1803	7	US-11-781-665-2824	Sequence 2824, App	C 525	182	8.0	1157	7	US-11-781-665-446	Sequence 446, App
C 453	185.8	8.1	6000	1	PCT-US07-13803-142	Sequence 142, App	C 526	182	8.0	1444	7	US-11-781-665-239	Sequence 239, App
C 454	185.6	8.1	379	7	US-11-881-406-1962	Sequence 1962, App	C 527	182	8.0	1842	7	US-11-781-665-439	Sequence 24, Appl
C 455	185.6	8.1	772	7	US-11-781-665-3009	Sequence 3009, App	C 528	182	8.0	2495	7	US-11-832-009-24	Sequence 24, Appl
C 456	185.6	8.1	1118	7	US-11-781-665-723	Sequence 723, App	C 529	182	8.0	2520	7	US-11-781-665-801	Sequence 801, App
C 457	185.6	8.1	1768	7	US-11-781-665-241	Sequence 241, App	C 530	182	8.0	2702	7	US-11-781-665-1686	Sequence 1686, App
C 458	185.6	8.1	6000	1	PCT-US07-13803-126	Sequence 126, App	C 531	181.8	8.0	430	7	US-11-881-406-3935	Sequence 3935, App
C 459	185.6	8.1	6000	1	PCT-US07-13803-188	Sequence 188, App	C 532	181.8	8.0	837	7	US-11-781-665-1440	Sequence 1440, App
C 460	185.4	8.1	422	7	US-11-881-406-1393	Sequence 1393, App	C 533	181.8	8.0	1288	7	US-11-781-665-2547	Sequence 2547, App
C 461	185.4	8.1	850	7	US-11-781-665-1280	Sequence 1280, App	C 534	181.8	8.0	1601	7	US-11-781-665-1708	Sequence 1708, App
C 462	185.4	8.1	6000	1	PCT-US07-13803-104	Sequence 104, App	C 535	181.8	8.0	6000	1	PCT-US07-13803-44	Sequence 44, Appl
C 463	185.4	8.1	6000	1	PCT-US07-13803-152	Sequence 152, App	C 536	181.6	8.0	800	7	US-11-881-406-1361	Sequence 1361, App
C 464	185.4	8.1	6000	1	PCT-US07-13803-204	Sequence 204, App	C 537	181.6	8.0	1076	7	US-11-781-665-60	Sequence 60, Appl

C 538	181.6	8.0	1181	7	US-11-781-665-228	Sequence 228, App	C 611	178	7.8	1262	7	US-11-832-009-30	Sequence 30, Appl
C 539	181.6	8.0	6000	1	PCT-US07-13803-49	Sequence 49, Appl	C 612	178	7.8	1262	7	US-11-781-665-3038	Sequence 3038, App
C 540	181.6	8.0	7468	1	PCT-US07-73799-2	Sequence 2, Appl	C 613	177.8	7.8	1200	7	US-11-781-665-465	Sequence 465, App
C 541	181.4	7.9	390	7	US-11-881-406-3065	Sequence 3065, App	C 614	177.8	7.8	1683	1	PCT-US07-13803-325	Sequence 325, App
C 542	181.4	7.9	430	7	US-11-881-406-2510	Sequence 2510, App	C 615	177.8	7.8	2007	7	US-11-781-665-230	Sequence 230, App
C 543	181.4	7.9	2043	7	US-11-781-665-2661	Sequence 2661, App	C 616	177.8	7.8	4015	7	US-11-851-267-8	Sequence 8, Appl
C 544	181.2	7.9	1633	7	US-11-781-665-407	Sequence 407, App	C 617	177.8	7.8	4015	7	US-11-851-267-15	Sequence 15, Appl
C 545	181.2	7.9	1693	7	US-11-781-665-1282	Sequence 1282, App	C 618	177.8	7.8	4356	7	US-11-852-912-10	Sequence 10, Appl
C 546	181.2	7.9	1790	7	US-11-781-665-1611	Sequence 1611, App	C 619	177.8	7.8	6000	1	PCT-US07-13803-75	Sequence 75, Appl
C 547	181.2	7.9	1797	7	US-11-781-665-2915	Sequence 2915, App	C 620	177.8	7.8	6000	1	PCT-US07-13803-261	Sequence 261, App
C 548	181	7.9	394	7	US-11-881-406-1032	Sequence 1032, App	C 621	177.6	7.8	410	7	US-11-881-406-2445	Sequence 2445, App
C 549	181	7.9	983	7	US-11-881-406-41	Sequence 41, Appl	C 622	177.6	7.8	2015	1	PCT-US07-13803-521	Sequence 521, App
C 550	181	7.9	1001	7	US-11-881-406-3751	Sequence 3751, App	C 623	177.6	7.8	2141	7	US-11-781-665-2001	Sequence 2001, App
C 551	180.8	7.9	1166	7	US-11-781-665-1983	Sequence 1983, App	C 624	177.4	7.8	358	7	US-11-781-665-670	Sequence 670, App
C 552	180.8	7.9	1302	7	US-11-682-135-1	Sequence 1, Appl	C 625	177.4	7.8	1901	7	US-11-781-665-1269	Sequence 1269, App
C 553	180.8	7.9	1566	7	US-11-781-665-1852	Sequence 1852, App	C 626	177.4	7.8	3271	7	US-11-816-601-123	Sequence 124, App
C 554	180.8	7.9	6000	1	PCT-US07-13803-136	Sequence 136, App	C 627	177.4	7.8	3271	7	US-11-816-601-124	Sequence 273, App
C 555	180.6	7.9	1384	7	US-11-781-665-1930	Sequence 1930, App	C 628	177.4	7.8	5001	7	US-11-885-002-23	Sequence 23, Appl
C 556	180.6	7.9	1535	7	US-11-781-665-1826	Sequence 1826, App	C 629	177.4	7.8	92384	7	US-11-328-881A-80	Sequence 80, Appl
C 557	180.6	7.9	1583	7	US-11-884-496-660	Sequence 660, App	C 630	177.2	7.8	1079	7	US-11-781-665-2781	Sequence 2781, App
C 558	180.6	7.9	6000	1	PCT-US07-13803-13	Sequence 13, Appl	C 631	177.2	7.8	2572	1	PCT-US07-13803-500	Sequence 500, App
C 559	180.6	7.9	6000	1	PCT-US07-13803-174	Sequence 174, App	C 632	177	7.7	1272	7	US-11-781-665-2259	Sequence 2259, App
C 560	180.6	7.9	6000	1	PCT-US07-13803-214	Sequence 214, App	C 633	177	7.7	1851	7	US-11-781-665-2960	Sequence 2960, App
C 561	180.6	7.9	17483	6	US-10-751-606A-1	Sequence 1, Appl	C 634	177	7.7	3382	7	US-11-781-665-2651	Sequence 2651, App
C 562	180.4	7.9	409	7	US-11-881-406-2557	Sequence 2657, App	C 635	177	7.7	3775	7	US-11-847-733-71	Sequence 71, Appl
C 563	180.4	7.9	7063	6	US-10-148-848D-1	Sequence 1, Appl	C 636	176.8	7.7	2001	7	US-11-881-406-3875	Sequence 3875, App
C 564	180.4	7.9	12050	1	PCT-US07-13803-347	Sequence 347, App	C 637	176.8	7.7	2001	7	US-11-881-406-3876	Sequence 3876, App
C 565	180.2	7.9	1725	7	US-11-781-665-1987	Sequence 1987, App	C 638	176.8	7.7	3708	1	PCT-US07-77281-17	Sequence 17, Appl
C 566	180.2	7.9	4868	7	US-11-490-374A-1594	Sequence 1594, App	C 639	176.8	7.7	5045	7	PCT-US07-77281-19	Sequence 19, Appl
C 567	180.2	7.9	5333	7	US-11-490-374A-1596	Sequence 1596, App	C 640	176.6	7.7	10240	8	US-60-970-396-5	Sequence 5, Appl
C 568	180.2	7.9	5441	7	US-11-490-374A-1595	Sequence 1595, App	C 641	176.4	7.7	6000	1	PCT-US07-13803-93	Sequence 93, Appl
C 569	180.2	7.9	6000	1	PCT-US07-13803-78	Sequence 78, Appl	C 642	176.2	7.7	3121	7	US-11-781-665-2419	Sequence 2419, App
C 570	180.2	7.9	6000	1	PCT-US07-13803-214	Sequence 214, App	C 643	176.2	7.7	6000	1	PCT-US07-13803-59	Sequence 59, Appl
C 571	180.2	7.9	6000	1	PCT-US07-13803-63	Sequence 63, App	C 644	176.2	7.7	6000	1	PCT-US07-13803-70	Sequence 70, Appl
C 572	180	7.9	1035	7	US-11-781-665-1881	Sequence 1881, App	C 645	176	7.7	788	7	US-11-781-665-363	Sequence 363, App
C 573	180	7.9	1472	7	US-11-781-665-2913	Sequence 2913, App	C 646	176	7.7	1750	7	US-11-781-665-2630	Sequence 2630, App
C 574	180	7.9	6000	1	PCT-US07-13803-197	Sequence 197, App	C 647	176	7.7	2001	7	US-11-881-406-2196	Sequence 2196, App
C 575	179.8	7.9	1491	7	US-11-781-665-1260	Sequence 1260, App	C 648	176	7.7	2521	7	US-11-235-701A-462	Sequence 462, App
C 576	179.8	7.9	1759	7	US-11-781-665-1684	Sequence 1684, App	C 649	176	7.7	3628	7	US-11-235-701A-463	Sequence 463, App
C 577	179.8	7.9	6000	1	PCT-US07-13803-72	Sequence 72, Appl	C 650	176	7.7	3856	7	US-11-235-701A-460	Sequence 460, App
C 578	179.8	7.9	6666	1	PCT-US07-13803-504	Sequence 504, App	C 651	175.8	7.7	390	7	US-11-881-406-2106	Sequence 2106, App
C 579	179.6	7.9	1520	7	US-11-781-665-131	Sequence 191, App	C 652	175.8	7.7	1305	7	US-11-490-374A-1810	Sequence 1810, App
C 580	179.6	7.9	6000	1	PCT-US07-13803-223	Sequence 222, App	C 653	175.8	7.7	2101	7	US-11-490-374A-1808	Sequence 1808, App
C 581	179.6	7.9	6000	1	PCT-US07-13803-223	Sequence 223, App	C 654	175.8	7.7	6000	1	PCT-US07-13803-146	Sequence 146, App
C 582	179.4	7.9	1102	7	US-11-781-665-535	Sequence 535, App	C 655	175.6	7.7	996	7	US-11-781-665-876	Sequence 876, App
C 583	179.4	7.9	1635	7	US-11-781-665-1064	Sequence 1064, App	C 656	175.6	7.7	1156	7	US-11-781-665-2437	Sequence 2437, App
C 584	179.4	7.9	2414	7	US-11-781-665-1355	Sequence 1255, App	C 657	175.6	7.7	1582	7	US-11-781-665-575	Sequence 575, App
C 585	179.4	7.9	3915	7	US-11-847-733-49	Sequence 49, Appl	C 658	175.6	7.7	2393	7	US-11-781-665-3062	Sequence 3062, App
C 586	179.4	7.9	6000	1	PCT-US07-13803-35	Sequence 35, Appl	C 659	175.6	7.7	6000	1	PCT-US07-13803-55	Sequence 55, Appl
C 587	179.4	7.9	6000	1	PCT-US07-13803-63	Sequence 63, Appl	C 660	175.6	7.7	6000	1	PCT-US07-13803-247	Sequence 247, App
C 588	179.2	7.8	1639	7	US-11-781-665-1680	Sequence 1680, App	C 661	175.4	7.7	1686	7	US-11-781-665-579	Sequence 579, App
C 589	179	7.8	636	7	US-11-781-665-2188	Sequence 2188, App	C 662	175.2	7.7	557	7	US-11-781-665-569	Sequence 569, App
C 590	179	7.8	4220	7	US-11-816-601-149	Sequence 149, App	C 663	175.2	7.7	974	7	US-11-781-665-2016	Sequence 2016, App
C 591	178.8	7.8	3234	7	US-11-816-601-13	Sequence 13, Appl	C 664	175.2	7.7	2288	7	US-11-781-665-2436	Sequence 2436, App
C 592	178.6	7.8	3234	7	US-11-816-601-293	Sequence 293, App	C 665	175.2	7.7	5518	7	US-11-884-496-547	Sequence 547, App
C 593	178.6	7.8	1104	7	US-11-781-665-2823	Sequence 2823, App	C 666	175.2	7.7	6000	1	PCT-US07-13803-145	Sequence 145, App
C 594	178.6	7.8	1162	7	US-11-781-665-754	Sequence 754, App	C 667	175	7.7	1450	7	US-11-781-665-2605	Sequence 2605, App
C 595	178.6	7.8	2001	7	US-11-881-406-901	Sequence 901, App	C 668	175	7.7	2280	7	US-11-781-665-884	Sequence 884, App
C 596	178.6	7.8	2001	7	US-11-881-406-3343	Sequence 3343, App	C 669	175	7.7	4964	7	US-11-884-496-680	Sequence 680, App
C 597	178.6	7.8	6000	1	PCT-US07-13803-45	Sequence 45, Appl	C 670	175	7.7	5508	1	PCT-US07-13803-1939	Sequence 1939, App
C 598	178.4	7.8	990	7	US-11-881-406-3842	Sequence 3842, App	C 671	175	7.7	6000	1	PCT-US07-13803-161	Sequence 161, App
C 599	178.4	7.8	1724	7	US-11-781-665-284	Sequence 284, App	C 672	175	7.7	6000	1	PCT-US07-13803-211	Sequence 211, App
C 600	178.4	7.8	1730	7	US-11-781-665-1921	Sequence 1921, App	C 673	175	7.7	18524	1	PCT-US07-06371-12	Sequence 12, Appl
C 601	178.4	7.8	6000	1	PCT-US07-13803-24	Sequence 24, Appl	C 674	174.8	7.7	1742	7	US-11-781-665-1488	Sequence 1488, App
C 602	178.4	7.8	6000	1	PCT-US07-13803-182	Sequence 182, App	C 675	174.8	7.7	2778	7	US-11-781-665-2904	Sequence 2904, App
C 603	178.4	7.8	6000	1	PCT-US07-13803-210	Sequence 210, App	C 676	174.8	7.7	3536	7	US-11-825-627-354	Sequence 354, App
C 604	178.4	7.8	6000	1	PCT-US07-13803-260	Sequence 260, App	C 677	174.8	7.7	10876	1	PCT-US07-16656-6	Sequence 6, Appl
C 605	178.4	7.8	9648	7	US-11-847-733-64	Sequence 64, Appl	C 678	174.6	7.6	1302	7	US-11-781-665-1478	Sequence 1478, App
C 606	178.2	7.8	898	7	US-11-781-665-2568	Sequence 2568, App	C 679	174.6	7.6	1626	7	US-11-781-665-2580	Sequence 2580, App
C 607	178.2	7.8	1230	7	US-11-781-665-852	Sequence 852, App	C 680	174.6	7.6	2157	7	US-11-781-665-627	Sequence 627, App
C 608	178.2	7.8	1295	7	US-11-781-665-1445	Sequence 1445, App	C 681	174.4	7.6	1461	7	US-11-781-665-844	Sequence 844, App
C 609	178.2	7.8	2085	7	US-11-781-665-503	Sequence 503, App	C 682	174.4	7.6	4122	1	PCT-US07-13803-280	Sequence 280, App
C 610	178.2	7.8	2284	7	US-11-781-665-1980	Sequence 1980, App	C 683	174.4	7.6	4122	1	PCT-US07-13803-365	Sequence 365, App

c 684	174.4	7.6	6221	7	US-11-908-114-27	Sequence 27, Appl	c 757	170.4	7.5	890	7	US-11-781-665-2820	Sequence 2820, Ap
c 685	174.2	7.6	1167	7	US-11-781-665-2199	Sequence 2799, Ap	c 758	170.4	7.5	2001	7	US-11-881-406-3890	Sequence 3890, Ap
c 686	174.2	7.6	1347	7	US-11-781-665-2131	Sequence 2131, Ap	c 759	170.4	7.5	3754	7	US-11-816-601-737	Sequence 737, App
c 687	174.2	7.6	6000	1	PCT-US07-13803-180	Sequence 180, App	c 760	170.4	7.5	3754	7	US-11-816-601-813	Sequence 813, App
c 688	174.2	7.6	6000	1	PCT-US07-13803-269	Sequence 269, App	c 761	170.4	7.5	6000	1	PCT-US07-13803-19	Sequence 19, Appl
c 689	174	7.6	1125	7	US-11-781-665-2572	Sequence 2572, Ap	c 762	170.4	7.5	6000	1	PCT-US07-13803-229	Sequence 229, App
c 690	174	7.6	1864	7	US-11-884-496-655	Sequence 655, App	c 763	170.2	7.5	2001	7	US-11-881-406-3382	Sequence 3382, Ap
c 691	173.8	7.6	978	7	US-11-881-406-3893	Sequence 3893, Ap	c 764	170.2	7.5	2001	7	US-11-881-406-3383	Sequence 3383, Ap
c 692	173.8	7.6	1255	7	US-11-781-665-1267	Sequence 1267, Ap	c 765	170.2	7.5	2001	7	US-11-881-406-3384	Sequence 3384, Ap
c 693	173.8	7.6	1311	7	US-11-781-665-1487	Sequence 1487, Ap	c 766	170.2	7.5	2001	7	US-11-881-406-3385	Sequence 3385, Ap
c 694	173.8	7.6	1369	7	US-11-781-665-2026	Sequence 2026, Ap	c 767	170.2	7.5	2001	7	US-11-881-406-3389	Sequence 3389, Ap
c 695	173.8	7.6	6000	1	PCT-US07-13803-192	Sequence 192, App	c 768	170.2	7.5	6000	1	PCT-US07-13803-105	Sequence 105, App
c 696	173.8	7.6	6000	1	PCT-US07-13803-230	Sequence 230, App	c 769	170	7.4	1598	7	US-11-781-665-2706	Sequence 2706, Ap
c 697	173.6	7.6	399	7	US-11-881-406-2276	Sequence 2276, Ap	c 770	170	7.4	1603	7	US-11-781-665-1481	Sequence 1481, Ap
c 698	173.6	7.6	416	7	US-11-881-406-2091	Sequence 2091, Ap	c 771	170	7.4	1877	7	US-11-781-665-2947	Sequence 2947, Ap
c 699	173.6	7.6	2272	7	US-11-794-690-22	Sequence 22, Appl	c 772	170	7.4	1927	7	US-11-825-627-246	Sequence 246, App
c 700	173.4	7.6	979	7	US-11-781-665-2631	Sequence 2631, Ap	c 773	170	7.4	1927	7	US-11-825-627-248	Sequence 248, App
c 701	173.2	7.6	1309	7	US-11-781-665-1967	Sequence 1967, Ap	c 774	170	7.4	2001	7	US-11-881-406-3389	Sequence 3389, Ap
c 702	173.2	7.6	1320	7	US-11-781-665-2387	Sequence 2387, Ap	c 775	170	7.4	6000	1	PCT-US07-13803-123	Sequence 123, App
c 703	173.2	7.6	1406	7	US-11-781-665-1486	Sequence 1486, Ap	c 776	169.8	7.4	1547	7	US-11-781-665-123	Sequence 123, App
c 704	173.2	7.6	1554	7	US-11-781-665-3024	Sequence 3024, Ap	c 777	169.8	7.4	2235	7	US-11-832-009-34	Sequence 34, Appl
c 705	173.2	7.6	2459	7	US-11-847-733-57	Sequence 57, Appl	c 778	169.8	7.4	4421	7	US-11-847-733-16	Sequence 16, Appl
c 706	173	7.6	2001	7	US-11-881-406-2280	Sequence 2280, Ap	c 779	169.6	7.4	4356	7	US-11-852-912-10	Sequence 10, Appl
c 707	173	7.6	2399	7	US-11-781-665-2071	Sequence 2071, Ap	c 780	169.6	7.4	4520	7	US-11-847-733-62	Sequence 62, Appl
c 708	173	7.6	6000	1	PCT-US07-13803-1	Sequence 1, Appl	c 781	169.6	7.4	6000	1	PCT-US07-13803-52	Sequence 52, Appl
c 709	173	7.6	6000	1	PCT-US07-13803-96	Sequence 96, Appl	c 782	169.6	7.4	6000	1	PCT-US07-13803-84	Sequence 84, Appl
c 710	173	7.6	6000	1	PCT-US07-13803-184	Sequence 184, Appl	c 783	169.4	7.4	3396	1	PCT-US07-13803-519	Sequence 519, App
c 711	172.8	7.6	824	7	US-11-781-665-1471	Sequence 1471, Ap	c 784	169.2	7.4	2014	7	US-11-781-665-1443	Sequence 1443, Ap
c 712	172.6	7.6	6000	1	PCT-US07-13803-97	Sequence 97, Appl	c 785	169.2	7.4	5182	6	US-10-910-811B-395	Sequence 395, App
c 713	172.6	7.6	6000	1	PCT-US07-13803-119	Sequence 119, App	c 786	169.2	7.4	5182	6	US-10-945-565B-395	Sequence 395, App
c 714	172.4	7.5	1998	7	US-11-832-009-47	Sequence 47, Appl	c 787	169.2	7.4	6000	1	PCT-US07-13803-115	Sequence 115, App
c 715	172.4	7.5	2001	7	US-11-881-406-3296	Sequence 3296, Ap	c 788	169.2	7.4	6000	1	PCT-US07-13803-209	Sequence 209, App
c 716	172.4	7.5	6000	1	PCT-US07-13803-168	Sequence 168, App	c 789	169.2	7.4	6000	1	PCT-US07-13803-223	Sequence 223, App
c 717	172.4	7.5	6004	7	US-11-235-701A-401	Sequence 401, Appl	c 790	169	7.4	411	7	US-11-881-406-2298	Sequence 2298, Ap
c 718	172.4	7.5	6004	7	US-11-235-701A-403	Sequence 403, Appl	c 791	169	7.4	2001	7	US-11-881-406-3562	Sequence 3562, Ap
c 719	172.4	7.5	6017	7	US-11-235-701A-402	Sequence 402, Appl	c 792	169	7.4	2001	7	US-11-881-406-3569	Sequence 3569, Ap
c 720	172.2	7.5	1692	7	US-11-781-665-2581	Sequence 2581, Ap	c 793	169	7.4	2251	7	US-11-852-219-13	Sequence 13, Appl
c 721	172.2	7.5	2001	7	US-11-881-406-3762	Sequence 3762, Ap	c 794	169	7.4	2587	7	US-11-852-219-3	Sequence 3, Appl
c 722	172.2	7.5	2001	7	US-11-881-406-3763	Sequence 3763, Ap	c 795	169	7.4	2587	7	US-11-852-219-3	Sequence 3, Appl
c 723	172.2	7.5	2001	7	US-11-881-406-3764	Sequence 3764, Ap	c 796	169	7.4	2587	7	US-11-852-219-5	Sequence 5, Appl
c 724	172.2	7.5	2893	7	US-11-881-406-1737	Sequence 1737, Ap	c 797	169	7.4	2587	7	US-11-852-219-9	Sequence 9, Appl
c 725	172.2	7.5	8122	7	US-11-847-733-87	Sequence 87, Appl	c 798	169	7.4	2587	7	US-11-852-219-9	Sequence 9, Appl
c 726	172	7.5	2783	7	US-11-781-665-3066	Sequence 3066, Ap	c 799	169	7.4	2587	7	US-11-852-219-11	Sequence 11, Appl
c 727	172	7.5	4220	7	US-11-816-601-149	Sequence 149, Appl	c 800	169	7.4	2593	7	US-11-852-219-17	Sequence 17, Appl
c 728	172	7.5	6000	1	PCT-US07-13803-84	Sequence 84, Appl	c 801	169	7.4	2623	7	US-11-852-219-15	Sequence 15, Appl
c 729	172	7.5	6000	1	PCT-US07-13803-207	Sequence 207, Appl	c 802	169	7.4	4978	6	US-10-571-511-19	Sequence 19, Appl
c 730	171.8	7.5	1899	7	US-11-881-406-1303	Sequence 1303, Ap	c 803	169	7.4	5631	1	PCT-US07-13803-390	Sequence 390, App
c 731	171.8	7.5	2001	7	US-11-881-406-3687	Sequence 3687, Ap	c 804	169	7.4	6000	1	PCT-US07-13803-157	Sequence 157, App
c 732	171.6	7.5	1276	7	US-11-781-665-1219	Sequence 1219, Ap	c 805	168.8	7.4	1332	7	US-11-781-665-1676	Sequence 1676, Ap
c 733	171.6	7.5	1502	7	US-11-781-665-1566	Sequence 1566, Ap	c 806	168.8	7.4	5184	7	US-11-235-701A-509	Sequence 509, App
c 734	171.4	7.5	1541	7	US-11-781-665-1963	Sequence 1963, Ap	c 807	168.8	7.4	6000	1	PCT-US07-13803-62	Sequence 62, Appl
c 735	171.4	7.5	2001	7	US-11-881-406-3366	Sequence 3366, Ap	c 808	168.6	7.4	421	7	US-11-881-406-1237	Sequence 1237, Ap
c 736	171.4	7.5	2036	7	US-11-781-665-148	Sequence 148, Appl	c 809	168.6	7.4	776	7	US-11-781-665-382	Sequence 382, App
c 737	171.4	7.5	6000	1	PCT-US07-13803-61	Sequence 61, Appl	c 810	168.6	7.4	853	7	US-11-781-665-827	Sequence 827, App
c 738	171.4	7.5	6000	1	PCT-US07-13803-97	Sequence 97, Appl	c 811	168.6	7.4	1316	7	US-11-781-665-195	Sequence 195, App
c 739	171.4	7.5	6000	1	PCT-US07-13803-98	Sequence 98, Appl	c 812	168.6	7.4	1907	7	US-11-781-665-1679	Sequence 1679, Ap
c 740	171.4	7.5	6683	1	PCT-US07-13803-493	Sequence 493, App	c 813	168.6	7.4	3337	7	US-11-832-009-51	Sequence 51, Appl
c 741	171.2	7.5	423	7	US-11-881-406-1097	Sequence 1097, Ap	c 814	168.6	7.4	6000	1	PCT-US07-13803-133	Sequence 133, App
c 742	171.2	7.5	429	7	US-11-881-406-2116	Sequence 2116, Ap	c 815	168.6	7.4	6000	1	PCT-US07-13803-225	Sequence 225, App
c 743	171.2	7.5	1195	7	US-11-781-665-2219	Sequence 2219, Ap	c 816	168.2	7.4	847	7	US-11-781-665-1231	Sequence 1231, Ap
c 744	171	7.5	416	7	US-11-881-406-3234	Sequence 3234, Ap	c 817	168.2	7.4	2001	7	US-11-881-406-3365	Sequence 3365, Ap
c 745	171	7.5	2945	7	US-11-781-665-282	Sequence 282, App	c 818	168.2	7.4	6000	1	PCT-US07-13803-99	Sequence 99, Appl
c 746	171	7.5	6000	1	PCT-US07-13803-247	Sequence 247, App	c 819	168	7.4	1605	7	US-11-832-009-42	Sequence 42, Appl
c 747	170.8	7.5	408	7	US-11-881-406-2710	Sequence 2710, Ap	c 820	168	7.4	2001	7	US-11-881-406-3798	Sequence 3798, Ap
c 748	170.8	7.5	2033	7	US-11-884-496-651	Sequence 651, App	c 821	168	7.4	2001	7	US-11-881-406-3799	Sequence 3799, Ap
c 749	170.8	7.5	6000	1	PCT-US07-13803-87	Sequence 87, Appl	c 822	167.8	7.3	2001	7	US-11-881-406-3787	Sequence 3787, Ap
c 750	170.6	7.5	427	7	US-11-881-406-2661	Sequence 2661, Ap	c 823	167.8	7.3	5312	7	US-11-816-601-740	Sequence 740, App
c 751	170.6	7.5	1586	7	US-11-781-665-2560	Sequence 2560, Ap	c 824	167.6	7.3	3655	7	US-11-490-374A-1818	Sequence 1818, Ap
c 752	170.6	7.5	1634	7	US-11-781-665-2313	Sequence 2313, Ap	c 825	167.6	7.3	3724	7	US-11-490-374A-1819	Sequence 1819, Ap
c 753	170.6	7.5	2141	7	US-11-781-665-1254	Sequence 1254, Ap	c 826	167.6	7.3	6000	1	PCT-US07-13803-212	Sequence 212, App
c 754	170.6	7.5	6000	1	PCT-US07-13803-30	Sequence 30, Appl	c 827	167.4	7.3	401	7	US-11-881-406-3793	Sequence 3793, Ap
c 755	170.6	7.5	6000	1	PCT-US07-13803-185	Sequence 185, App	c 828	167.4	7.3	793	7	US-11-781-665-2836	Sequence 2836, Ap
c 756	170.6	7.5	6000	1	PCT-US07-13803-195	Sequence 195, App	c 829	167.4	7.3	1141	7	US-11-781-665-1555	Sequence 1555, Ap

C 830	167.4	7.3	1514	7	US-11-781-665-2780	Sequence 2780, App	C 903	161.6	7.1	1887	7	US-11-781-665-142	Sequence 142, App
C 831	167.4	7.3	3455	7	US-11-829-279-154	Sequence 154, App	C 904	161.6	7.1	2604	7	US-11-781-665-2407	Sequence 2407, App
C 832	167.4	7.3	6000	1	PCT-US07-13803-192	Sequence 192, App	C 905	161.6	7.1	6000	1	PCT-US07-13803-190	Sequence 190, App
C 833	167.2	7.3	1726	7	US-11-781-665-2329	Sequence 2329, App	C 906	161.6	7.1	6000	1	PCT-US07-13803-222	Sequence 222, App
C 834	167.2	7.3	6000	1	PCT-US07-13803-263	Sequence 263, App	C 907	161.4	7.1	6000	1	PCT-US07-13803-9	Sequence 9, Appli
C 835	167	7.3	2511	7	US-11-884-496-624	Sequence 624, App	C 908	161.2	7.1	1029	7	US-11-781-665-2545	Sequence 2545, App
C 836	167	7.3	5667	7	US-11-847-733-84	Sequence 84, Appli	C 909	161	7.0	839	7	US-11-781-665-1750	Sequence 1750, App
C 837	166.8	7.3	811	7	US-11-781-665-656	Sequence 656, App	C 910	161	7.0	1241	7	US-11-781-665-2274	Sequence 2274, App
C 838	166.8	7.3	859	7	US-11-781-665-168	Sequence 168, App	C 911	161	7.0	1285	7	US-11-781-665-1950	Sequence 1950, App
C 839	166.8	7.3	888	7	US-11-781-665-767	Sequence 767, App	C 912	161	7.0	2030	6	US-10-788-318C-6	Sequence 6, Appli
C 840	166.8	7.3	1847	7	US-11-781-665-2049	Sequence 2049, App	C 913	161	7.0	6000	1	PCT-US07-13803-134	Sequence 134, App
C 841	166.8	7.3	6000	1	PCT-US07-13803-56	Sequence 56, Appli	C 914	161	7.0	6000	1	PCT-US07-13803-136	Sequence 136, App
C 842	166.8	7.3	6000	1	PCT-US07-13803-233	Sequence 233, App	C 915	161	7.0	6000	1	PCT-US07-13803-265	Sequence 265, App
C 843	166.6	7.3	1349	7	PCT-US07-13803-356	Sequence 356, App	C 916	160.8	7.0	960	7	US-11-781-665-2310	Sequence 2310, App
C 844	166.4	7.3	1714	7	US-11-781-665-866	Sequence 866, App	C 917	160.8	7.0	1145	8	US-60-970-858-73	Sequence 73, Appli
C 845	166.4	7.3	6000	1	PCT-US07-13803-115	Sequence 115, Appli	C 918	160.8	7.0	1344	6	US-10-433-238B-3	Sequence 3, Appli
C 846	166.2	7.3	2442	7	US-11-837-082-1	Sequence 1, Appli	C 919	160.8	7.0	1344	7	US-11-841-536-3	Sequence 3, Appli
C 847	166	7.3	6000	1	PCT-US07-13803-188	Sequence 188, App	C 920	160.8	7.0	2001	7	US-11-881-406-3385	Sequence 3385, App
C 848	165.8	7.3	1448	7	US-11-781-665-2040	Sequence 2040, App	C 921	160.8	7.0	2001	7	US-11-881-406-3389	Sequence 3389, App
C 849	165.8	7.3	1699	7	US-11-781-665-1414	Sequence 1414, App	C 922	160.8	7.0	4015	7	US-11-781-665-2565	Sequence 2565, App
C 850	165.6	7.3	924	7	US-11-781-665-2018	Sequence 2018, App	C 923	160.8	7.0	6000	1	PCT-US07-13803-77	Sequence 77, Appli
C 851	165.6	7.3	2625	7	US-11-781-665-114	Sequence 114, App	C 924	160.6	7.0	394	7	US-11-881-406-2138	Sequence 2138, App
C 852	165.6	7.3	6000	1	PCT-US07-13803-228	Sequence 228, App	C 925	160.6	7.0	676	7	US-11-781-665-1799	Sequence 1799, App
C 853	165.4	7.2	810	7	US-11-781-665-593	Sequence 593, App	C 926	160.6	7.0	2180	7	US-11-781-665-2510	Sequence 2510, App
C 854	165.4	7.2	3295	7	US-11-490-374A-1807	Sequence 1807, App	C 927	160.6	7.0	6000	1	PCT-US07-13803-10	Sequence 10, Appli
C 855	165.4	7.2	14123	7	US-11-569-756-6	Sequence 6, Appli	C 928	160.6	7.0	6000	1	PCT-US07-13803-131	Sequence 131, App
C 856	165.4	7.2	14177	7	US-11-569-756-4	Sequence 4, Appli	C 929	160.4	7.0	1124	7	US-11-781-665-1762	Sequence 1762, App
C 857	165.2	7.2	1363	7	US-11-781-665-1477	Sequence 1477, App	C 930	160.2	7.0	2099	7	US-11-781-665-1420	Sequence 1420, App
C 858	165.2	7.2	6000	1	PCT-US07-13803-87	Sequence 87, Appli	C 931	160	7.0	5001	7	US-11-885-002-23	Sequence 23, Appli
C 859	165	7.2	6000	1	PCT-US07-13803-151	Sequence 151, App	C 932	160	7.0	6000	1	PCT-US07-13803-66	Sequence 66, Appli
C 860	164.8	7.2	363	7	US-11-881-406-910	Sequence 910, App	C 933	160	7.0	6000	1	PCT-US07-13803-67	Sequence 67, Appli
C 861	164.8	7.2	374	7	US-11-881-406-2639	Sequence 2639, App	C 934	159.8	7.0	6000	1	PCT-US07-13803-191	Sequence 191, App
C 862	164.8	7.2	1380	7	US-11-781-665-894	Sequence 894, App	C 935	159.8	7.0	16015	7	US-11-885-002-74	Sequence 74, Appli
C 863	164.8	7.2	1552	7	US-11-781-665-341	Sequence 341, App	C 936	159.6	7.0	403	7	US-11-881-406-964	Sequence 964, App
C 864	164.8	7.2	6000	1	PCT-US07-13803-124	Sequence 124, App	C 937	159.6	7.0	6000	1	PCT-US07-13803-135	Sequence 135, App
C 865	164.6	7.2	2230	6	US-10-511-989B-25	Sequence 25, Appli	C 938	159.6	7.0	6000	1	PCT-US07-13803-148	Sequence 148, App
C 866	164.4	7.2	1610	7	US-11-781-665-2487	Sequence 2487, App	C 939	159.4	7.0	430	7	US-11-881-406-4108	Sequence 4108, App
C 867	164.4	7.2	6000	1	PCT-US07-13803-42	Sequence 42, Appli	C 940	159.4	7.0	6000	1	PCT-US07-13803-164	Sequence 164, App
C 868	164.2	7.2	1830	7	US-11-781-665-848	Sequence 848, App	C 941	159.4	7.0	10874	7	US-11-060-659A-63	Sequence 63, Appli
C 869	164.2	7.2	2001	7	US-11-881-406-3557	Sequence 3557, App	C 942	159.4	7.0	18524	1	PCT-US07-06371-12	Sequence 12, Appli
C 870	164.2	7.2	21001	1	PCT-US07-75297-3	Sequence 3, Appli	C 943	159.2	7.0	793	7	US-11-781-665-1429	Sequence 1429, App
C 871	164	7.2	1960	7	US-11-781-665-1103	Sequence 1103, App	C 944	159	7.0	1001	7	US-11-881-406-3472	Sequence 3472, App
C 872	163.8	7.2	1473	7	US-11-781-665-2159	Sequence 2159, App	C 945	159	7.0	1874	7	US-11-884-496-581	Sequence 581, App
C 873	163.6	7.2	773	7	US-11-781-665-2949	Sequence 2949, App	C 946	159	7.0	2001	7	US-11-881-406-3471	Sequence 3471, App
C 874	163.6	7.2	1262	7	US-11-781-665-784	Sequence 784, App	C 947	158.8	7.0	1472	7	US-11-781-665-2913	Sequence 2913, App
C 875	163.6	7.2	6000	1	PCT-US07-13803-239	Sequence 239, App	C 948	158.8	7.0	1861	7	US-11-781-665-487	Sequence 487, App
C 876	163.2	7.1	1679	7	US-11-881-406-3553	Sequence 3553, App	C 949	158.8	7.0	6000	1	PCT-US07-13803-61	Sequence 61, Appli
C 877	163.2	7.1	1832	7	US-11-781-665-1575	Sequence 1575, App	C 950	158.8	7.0	6000	1	PCT-US07-13803-153	Sequence 153, App
C 878	163.2	7.1	2640	7	US-11-885-002-45	Sequence 45, Appli	C 951	158.8	7.0	6000	1	PCT-US07-13803-159	Sequence 159, App
C 879	163.2	7.1	3534	6	US-10-699-597B-7	Sequence 7, Appli	C 952	158.6	6.9	722	7	US-11-781-665-1857	Sequence 1857, App
C 880	163.2	7.1	3534	6	US-10-699-597B-8	Sequence 8, Appli	C 953	158.4	6.9	686	7	US-11-781-665-1503	Sequence 1503, App
C 881	163.2	7.1	3534	6	US-10-699-597B-9	Sequence 9, Appli	C 954	158.2	6.9	793	7	US-11-781-665-2076	Sequence 2076, App
C 882	163.2	7.1	3534	6	US-10-699-597B-10	Sequence 10, Appli	C 955	158.2	6.9	1228	7	US-11-781-665-571	Sequence 571, App
C 883	163.2	7.1	3700	6	US-10-788-318C-5	Sequence 5, Appli	C 956	158.2	6.9	1959	7	US-11-781-665-2461	Sequence 2461, App
C 884	163.2	7.1	4874	7	US-11-825-627-373	Sequence 373, App	C 957	158	6.9	430	7	US-11-881-406-2346	Sequence 2346, App
C 885	162.8	7.1	690	7	US-11-781-665-45	Sequence 45, Appli	C 958	158	6.9	1301	7	US-11-781-665-2725	Sequence 2725, App
C 886	162.8	7.1	1009	7	US-11-781-665-678	Sequence 678, App	C 959	158	6.9	4316	6	US-10-580-107-3	Sequence 3, Appli
C 887	162.6	7.1	701	7	US-11-816-468-4	Sequence 4, Appli	C 960	158	6.9	6000	1	PCT-US07-13803-108	Sequence 108, App
C 888	162.6	7.1	1584	7	US-11-781-665-209	Sequence 209, App	C 961	157.8	6.9	625	7	US-11-881-406-1947	Sequence 1947, App
C 889	162.6	7.1	3675	1	PCT-US07-13803-283	Sequence 283, App	C 962	157.8	6.9	1092	7	US-11-781-665-2170	Sequence 2170, App
C 890	162.6	7.1	3675	1	PCT-US07-13803-330	Sequence 330, App	C 963	157.8	6.9	1710	7	US-11-781-665-2610	Sequence 2610, App
C 891	162.6	7.1	6000	1	PCT-US07-13803-199	Sequence 199, App	C 964	157.6	6.9	1277	7	US-11-781-665-1453	Sequence 1453, App
C 892	162.4	7.1	1120	7	US-11-781-665-550	Sequence 550, App	C 965	157.6	6.9	6000	1	PCT-US07-13803-125	Sequence 125, App
C 893	162.4	7.1	6000	1	PCT-US07-13803-136	Sequence 136, App	C 966	157.6	6.9	6000	1	PCT-US07-13803-258	Sequence 258, App
C 894	162.2	7.1	1536	7	US-11-781-665-2752	Sequence 2752, App	C 967	157.4	6.9	2001	7	US-11-881-406-3913	Sequence 3913, App
C 895	162.2	7.1	1876	7	US-11-816-601-773	Sequence 773, App	C 968	157.4	6.9	2001	7	US-11-881-406-3914	Sequence 3914, App
C 896	162.2	7.1	2212	7	US-11-884-496-723	Sequence 723, App	C 969	157.4	6.9	2001	7	US-11-881-406-3915	Sequence 3915, App
C 897	162	7.1	1063	7	US-11-781-665-1520	Sequence 1520, App	C 970	157.4	6.9	7932	1	PCT-US07-13803-397	Sequence 397, App
C 898	162	7.1	2001	7	US-11-881-406-3579	Sequence 3579, App	C 971	157.2	6.9	934	7	US-11-781-665-37	Sequence 37, Appli
C 899	162	7.1	6000	1	PCT-US07-13803-157	Sequence 157, App	C 972	157.2	6.9	1647	7	US-11-781-665-1482	Sequence 1482, App
C 900	162	7.1	7216	1	PCT-US07-13803-507	Sequence 507, App	C 973	157	6.9	1435	7	US-11-781-665-494	Sequence 494, App
C 901	161.6	7.1	1136	7	US-11-781-665-2532	Sequence 2532, App	C 974	157	6.9	1453	7	US-11-781-665-1469	Sequence 1469, App
C 902	161.6	7.1	1887	7	US-11-781-665-141	Sequence 141, App	C 975	157	6.9	5001	7	US-11-885-002-22	Sequence 22, Appli

c 976	156.8	6.9	423	7	US-11-881-406-4180	Sequence 4180, Ap	c1049	149.6	6.5	1904	7	US-11-781-665-2905	Sequence 2905, Ap
c 977	156.8	6.9	2220	1	US-11-781-665-1685	Sequence 1685, Ap	c1050	149.6	6.5	4421	7	US-11-847-733-16	Sequence 16, Appl
c 978	156.8	6.9	6000	1	PCT-US07-13803-133	Sequence 133, App	c1051	149.4	6.5	1280	7	US-11-781-665-565	Sequence 565, App
c 979	156.8	6.9	6000	1	PCT-US07-13803-193	Sequence 193, App	c1052	149.4	6.5	1485	7	US-11-781-665-2401	Sequence 2401, Ap
c 980	156.6	6.9	1074	1	US-11-781-665-2821	Sequence 2821, Ap	c1053	149.4	6.5	6000	1	PCT-US07-13803-81	Sequence 81, Appl
c 981	156.4	6.8	2001	7	US-11-881-406-3950	Sequence 3950, Ap	c1054	149.2	6.5	424	7	US-11-881-406-2937	Sequence 2937, Ap
c 982	156.2	6.8	6000	1	PCT-US07-13803-152	Sequence 152, App	c1055	149.2	6.5	559	7	US-11-881-406-3879	Sequence 3879, Ap
c 983	156.2	6.8	6000	1	PCT-US07-13803-198	Sequence 198, App	c1056	149.2	6.5	1236	7	US-11-781-665-189	Sequence 189, App
c 984	156	6.8	1520	7	US-11-781-665-2495	Sequence 2495, Ap	c1057	149.2	6.5	6000	1	PCT-US07-13803-151	Sequence 151, App
c 985	156	6.8	2001	7	US-11-881-406-3765	Sequence 3765, Ap	c1058	149	6.5	1149	7	US-11-781-665-2006	Sequence 2006, Ap
c 986	156	6.8	2001	7	US-11-881-406-3766	Sequence 3766, Ap	c1059	148.8	6.5	698	7	US-11-781-665-1732	Sequence 1732, Ap
c 987	156	6.8	2001	7	US-11-881-406-3767	Sequence 3767, Ap	c1060	148.4	6.5	1612	7	US-11-781-665-1415	Sequence 1415, Ap
c 988	156	6.8	2001	7	US-11-881-406-3768	Sequence 3768, Ap	c1061	148.4	6.5	6000	1	PCT-US07-13803-246	Sequence 246, App
c 989	155.8	6.8	360	7	US-11-757-860-12	Sequence 12, Appl	c1062	148.2	6.5	373	7	US-11-881-406-1002	Sequence 1002, Ap
c 990	155.8	6.8	1545	7	US-11-825-627-342	Sequence 342, App	c1063	148	6.5	2858	7	US-11-908-114-6	Sequence 6, Appl1
c 991	155.8	6.8	6000	1	PCT-US07-13803-220	Sequence 220, App	c1064	147.8	6.5	1058	7	US-11-781-665-1618	Sequence 1618, Ap
c 992	155.6	6.8	1316	7	US-11-781-665-1877	Sequence 1877, Ap	c1065	147.8	6.5	1160	7	US-11-781-665-452	Sequence 452, App
c 993	155.6	6.8	1383	7	US-11-781-665-2056	Sequence 2056, Ap	c1066	147.4	6.5	766	7	US-11-781-665-1937	Sequence 1937, Ap
c 994	155.6	6.8	2847	7	US-11-781-665-2494	Sequence 2494, Ap	c1067	147.4	6.5	2185	7	US-11-781-665-2344	Sequence 2344, Ap
c 995	155.6	6.8	6000	1	PCT-US07-13803-49	Sequence 49, Appl	c1068	147.4	6.5	6000	1	PCT-US07-13803-18	Sequence 18, Appl1
c 996	155.2	6.8	1455	7	US-11-781-665-2895	Sequence 2895, Ap	c1069	147.4	6.5	6000	1	PCT-US07-13803-130	Sequence 130, App
c 997	155.2	6.8	3590	7	US-11-884-496-683	Sequence 683, App	c1070	147.2	6.4	1419	7	US-11-781-665-2660	Sequence 2660, Ap
c 998	155	6.8	486	7	US-11-881-406-864	Sequence 864, App	c1071	147	6.4	1300	7	US-11-781-665-1037	Sequence 1037, Ap
c 999	155	6.8	2284	7	US-11-781-665-756	Sequence 756, App	c1072	147	6.4	1302	7	US-11-781-665-671	Sequence 671, App
c1000	155	6.8	6000	1	PCT-US07-13803-98	Sequence 98, Appl	c1073	147	6.4	1501	7	US-11-781-665-2604	Sequence 2604, Ap
c1001	155	6.8	6000	1	PCT-US07-13803-248	Sequence 248, App	c1074	147	6.4	1628	7	US-11-781-665-2973	Sequence 2973, Ap
c1002	154.8	6.8	781	7	US-11-781-665-714	Sequence 714, App	c1075	147	6.4	6000	1	PCT-US07-13803-64	Sequence 64, Appl
c1003	154.8	6.8	969	7	US-11-881-406-2016	Sequence 2016, Ap	c1076	147	6.4	6000	1	PCT-US07-13803-231	Sequence 231, App
c1004	154.8	6.8	1798	7	US-11-881-406-2015	Sequence 2015, Ap	c1077	146.8	6.4	386	7	US-11-881-406-2763	Sequence 2763, App
c1005	154.8	6.8	6000	1	PCT-US07-13803-199	Sequence 199, App	c1078	146.8	6.4	589	7	US-11-781-665-2128	Sequence 2128, Ap
c1006	154.6	6.8	1359	7	US-11-781-665-88	Sequence 88, Appl	c1079	146.8	6.4	1668	7	US-11-781-665-902	Sequence 902, App
c1007	154.4	6.8	2063	7	US-11-490-374A-2179	Sequence 2179, Ap	c1080	146.8	6.4	1669	7	US-11-781-665-901	Sequence 901, App
c1008	154.4	6.8	6000	1	PCT-US07-13803-145	Sequence 145, App	c1081	146.8	6.4	2708	7	US-11-490-374A-1814	Sequence 1814, Ap
c1009	154.4	6.8	6000	1	PCT-US07-13803-241	Sequence 241, App	c1082	146.6	6.4	1913	7	US-11-781-665-1214	Sequence 1214, Ap
c1010	154.2	6.8	1237	7	US-11-781-665-27	Sequence 27, Appl	c1083	146.4	6.4	1659	7	US-11-881-406-3497	Sequence 3497, Ap
c1011	154.2	6.8	17483	6	US-10-751-606A-1	Sequence 1, Appl1	c1084	146	6.4	5688	7	US-11-733-861-17	Sequence 17, Appl1
c1012	153.8	6.7	805	7	US-11-781-665-2735	Sequence 2735, Ap	c1085	145.8	6.4	1030	7	US-11-781-665-1519	Sequence 1519, Ap
c1013	153.8	6.7	5399	7	US-11-884-496-692	Sequence 692, App	c1086	145.4	6.4	1684	7	US-11-490-374A-1637	Sequence 1637, Ap
c1014	153.6	6.7	6000	1	PCT-US07-13803-169	Sequence 169, App	c1087	145.4	6.4	3470	7	US-11-272-833C-3	Sequence 3, Appl1
c1015	153.4	6.7	11779	8	US-60-970-396-3	Sequence 3, Appl1	c1088	145.4	6.4	4828	7	US-11-725-402A-7	Sequence 7, Appl1
c1016	153	6.7	1127	7	US-11-781-665-3008	Sequence 3008, Ap	c1089	145.2	6.4	674	7	US-11-781-665-699	Sequence 699, App
c1017	153	6.7	6926	7	US-11-490-374A-1345	Sequence 1345, Ap	c1090	145.2	6.4	1647	7	US-11-781-665-167	Sequence 167, App
c1018	153	6.7	6980	7	US-11-490-374A-1338	Sequence 1338, Ap	c1091	145.2	6.4	2001	7	US-11-881-406-3747	Sequence 3747, Ap
c1019	153	6.7	6980	7	US-11-490-374A-1342	Sequence 1342, Ap	c1092	145.2	6.4	2001	7	US-11-881-406-3748	Sequence 3748, Ap
c1020	152.8	6.7	231	6	US-10-587-791-653	Sequence 653, App	c1093	145.2	6.4	2001	7	US-11-881-406-3749	Sequence 3749, Ap
c1021	152.8	6.7	782	7	US-11-781-665-1704	Sequence 1704, Ap	c1094	145.2	6.4	2001	7	US-11-881-406-3750	Sequence 3750, Ap
c1022	152.8	6.7	3852	7	US-11-781-665-2406	Sequence 2406, Ap	c1095	144.8	6.3	637	7	US-11-881-406-3148	Sequence 3148, Ap
c1023	152.6	6.7	334	7	US-11-881-406-4183	Sequence 4183, Ap	c1096	144.8	6.3	2207	7	US-11-781-665-868	Sequence 868, App
c1024	152.6	6.7	1893	7	US-11-781-665-850	Sequence 850, App	c1097	144.8	6.3	2281	7	US-11-490-374A-1965	Sequence 1965, Ap
c1025	152.6	6.7	6000	1	PCT-US07-13803-91	Sequence 91, Appl	c1098	144.6	6.3	624	7	US-11-781-665-2563	Sequence 2563, Ap
c1026	152.4	6.7	419	7	US-11-881-406-2323	Sequence 2323, Ap	c1099	144.6	6.3	999	7	US-11-881-406-3109	Sequence 3109, Ap
c1027	152	6.7	1545	7	US-11-781-665-1001	Sequence 1001, Ap	c1100	144.6	6.3	1162	7	US-11-781-665-1688	Sequence 1688, Ap
c1028	151.8	6.6	1551	7	US-11-781-665-812	Sequence 812, App	c1101	144.6	6.3	2204	7	US-11-832-009-46	Sequence 46, Appl1
c1029	151.6	6.6	1076	7	US-11-781-665-1646	Sequence 1646, Ap	c1102	144.4	6.3	1392	7	US-11-881-406-2522	Sequence 2522, Ap
c1030	151.4	6.6	1645	7	US-11-781-665-1973	Sequence 1973, Ap	c1103	144.2	6.3	1267	7	US-11-781-665-1114	Sequence 1114, Ap
c1031	151.4	6.6	2001	7	US-11-881-406-3786	Sequence 3786, Ap	c1104	144.2	6.3	2719	7	US-11-781-665-1199	Sequence 1199, Ap
c1032	151.4	6.6	2521	7	US-11-781-665-2173	Sequence 2173, Ap	c1105	144.2	6.3	6000	1	PCT-US07-13803-162	Sequence 162, App
c1033	151.4	6.6	5871	1	PCT-US07-13803-405	Sequence 405, App	c1106	144	6.3	810	7	US-11-781-665-1031	Sequence 1031, App
c1034	151.2	6.6	424	7	US-11-881-406-4156	Sequence 4156, Ap	c1107	144	6.3	2212	7	US-11-884-496-723	Sequence 723, App
c1035	151.2	6.6	2075	1	US-11-781-665-574	Sequence 574, App	c1108	143.8	6.3	428	7	US-11-881-406-2122	Sequence 2122, Ap
c1036	151.2	6.6	6000	1	PCT-US07-13803-162	Sequence 162, App	c1109	143.8	6.3	1063	7	US-11-781-665-120	Sequence 120, App
c1037	151	6.6	3161	7	US-11-781-665-1295	Sequence 1295, Ap	c1110	143.8	6.3	1309	7	US-11-781-665-2351	Sequence 2351, Ap
c1038	150.8	6.6	1305	7	US-11-781-665-1941	Sequence 1941, Ap	c1111	143.8	6.3	2689	7	US-11-781-665-1818	Sequence 1818, Ap
c1039	150.8	6.6	2390	7	US-11-781-665-2490	Sequence 2490, Ap	c1112	143.8	6.3	2778	7	US-11-781-665-2904	Sequence 2904, Ap
c1040	150.8	6.6	3633	7	US-11-884-496-678	Sequence 678, App	c1113	143.8	6.3	2945	7	US-11-781-665-282	Sequence 282, App
c1041	150.8	6.6	4290	7	US-11-884-496-653	Sequence 653, App	c1114	143.8	6.3	4284	1	PCT-US07-13803-444	Sequence 444, App
c1042	150.6	6.6	1479	7	US-11-781-665-2838	Sequence 2838, Ap	c1115	143.6	6.3	1174	7	US-11-781-665-2111	Sequence 2111, Ap
c1043	150.2	6.6	879	7	US-11-831-468-73	Sequence 73, Appl	c1116	143.4	6.3	1541	7	US-11-781-665-2434	Sequence 2434, Ap
c1044	150.2	6.6	2324	7	US-11-781-665-1612	Sequence 1612, Ap	c1117	143.4	6.3	1577	7	US-11-781-665-1666	Sequence 1666, Ap
c1045	150	6.6	971	7	US-11-781-665-2854	Sequence 2854, App	c1118	143	6.3	2048	7	US-11-781-665-279	Sequence 279, App
c1046	150	6.6	6000	1	PCT-US07-13803-119	Sequence 119, App	c1119	142.8	6.3	754	7	US-11-781-665-617	Sequence 617, App
c1047	150	6.6	6000	1	PCT-US07-13803-150	Sequence 150, App	c1120	142.6	6.2	6000	1	PCT-US07-13803-114	Sequence 114, App
c1048	149.6	6.5	1647	7	US-11-781-665-2355	Sequence 2355, Ap	c1121	142.6	6.2	6000	1	PCT-US07-13803-155	Sequence 155, App

c1122	142.4	6.2	1467	7	US-11-781-665-3552	Sequence 2552, Ap	c1195	135.4	5.9	1026	7	US-11-781-665-2846	Sequence 2846, Ap
c1123	142.2	6.2	915	7	US-11-781-665-2011	Sequence 301, App	c1196	135.4	5.9	1055	7	US-11-781-665-1022	Sequence 1022, Ap
c1124	142	6.2	1061	7	US-11-781-665-1800	Sequence 1800, Ap	c1197	135.4	5.9	2180	7	US-11-781-665-2510	Sequence 2510, Ap
c1125	142	6.2	1344	7	US-11-235-701A-373	Sequence 373, App	c1198	135.2	5.9	2075	7	US-11-781-665-574	Sequence 574, App
c1126	141.8	6.2	936	7	US-11-781-665-1731	Sequence 1731, Ap	c1199	135.2	5.9	6000	1	PCT-US07-13803-171	Sequence 171, App
c1127	141.8	6.2	1501	7	US-11-781-665-2604	Sequence 2604, Ap	c1200	135	5.9	2957	7	US-11-781-665-2659	Sequence 2659, Ap
c1128	141.8	6.2	6000	1	PCT-US07-13803-95	Sequence 95, Appl	c1201	135	5.9	6000	1	PCT-US07-13803-26	Sequence 26, Appl
c1129	141.8	6.2	6000	1	PCT-US07-13803-226	Sequence 226, App	c1202	135	5.9	6000	1	PCT-US07-13803-177	Sequence 177, App
c1130	141.6	6.2	1120	7	US-11-781-665-2135	Sequence 2135, Ap	c1203	134.6	5.9	2001	7	US-11-881-406-3381	Sequence 3381, Ap
c1131	141.6	6.2	5727	7	US-11-490-374A-1306	Sequence 1306, Ap	c1204	134.4	5.9	1539	7	US-11-490-374A-1346	Sequence 1346, Ap
c1132	141.6	6.2	5947	7	US-11-490-374A-1305	Sequence 1305, Ap	c1205	134.4	5.9	1539	7	US-11-490-374A-1351	Sequence 1351, Ap
c1133	141.2	6.2	876	7	US-11-781-665-626	Sequence 626, App	c1206	134.4	5.9	1539	7	US-11-490-374A-1352	Sequence 1352, Ap
c1134	141.2	6.2	3644	7	US-11-847-733-25	Sequence 25, Appl	c1207	134.4	5.9	1562	7	US-11-490-374A-1350	Sequence 1350, Ap
c1135	141	6.2	1125	7	US-11-884-496-636	Sequence 636, App	c1208	134.4	5.9	1614	7	US-11-781-665-1222	Sequence 1222, Ap
c1136	141	6.2	1138	7	US-11-781-665-2248	Sequence 2248, Ap	c1209	134.4	5.9	1842	7	US-11-781-665-2921	Sequence 2921, Ap
c1137	141	6.2	2001	7	US-11-881-406-3771	Sequence 3771, Ap	c1210	134.2	5.9	583	7	US-11-781-665-2653	Sequence 2653, Ap
c1138	141	6.2	2001	7	US-11-881-406-3772	Sequence 3772, Ap	c1211	134.2	5.9	1552	7	US-11-781-665-341	Sequence 341, App
c1139	141	6.2	2001	7	US-11-881-406-3773	Sequence 3773, Ap	c1212	134	5.9	410	7	US-11-881-406-1984	Sequence 1984, Ap
c1140	140.8	6.2	1075	7	US-11-781-665-2542	Sequence 2542, Ap	c1213	134	5.9	18997	7	US-11-835-336-32	Sequence 32, Appl
c1141	140.8	6.2	1544	7	US-11-781-665-2971	Sequence 2971, Ap	c1214	133.8	5.9	6000	1	PCT-US07-13803-28	Sequence 28, Appl
c1142	140.8	6.2	6000	1	PCT-US07-13803-191	Sequence 191, App	c1215	133.8	5.9	6000	1	PCT-US07-13803-136	Sequence 136, App
c1143	140.4	6.1	1020	7	US-11-781-665-1923	Sequence 1923, Ap	c1216	133.8	5.9	6000	1	PCT-US07-13803-268	Sequence 268, App
c1144	140.2	6.1	883	7	US-11-781-665-1024	Sequence 1024, Ap	c1217	133.4	5.8	283	7	US-11-831-404-98	Sequence 98, Appl
c1145	140.2	6.1	4232	7	US-11-781-905-1	Sequence 1, Appli	c1218	133.4	5.8	1304	7	US-11-781-665-157	Sequence 157, App
c1146	140.2	6.1	5775	7	US-11-839-314-6	Sequence 6, Appli	c1219	133.4	5.8	6074	7	US-11-835-336-76	Sequence 76, Appl
c1147	140.2	6.1	6641	7	US-11-816-601-718	Sequence 718, App	c1220	133.2	5.8	3760	1	PCT-US07-13803-340	Sequence 340, App
c1148	140.2	6.1	6641	7	US-11-235-701A-328	Sequence 328, App	c1221	133	5.8	1422	7	US-11-781-665-1083	Sequence 1083, Ap
c1149	140	6.1	428	7	US-11-881-406-1656	Sequence 1656, Ap	c1222	132.8	5.8	1193	7	US-11-781-665-545	Sequence 545, App
c1150	140	6.1	813	7	US-11-781-665-1942	Sequence 1942, Ap	c1223	132.8	5.8	6000	1	PCT-US07-13803-17	Sequence 17, Appl
c1151	139.8	6.1	1679	7	US-11-881-406-3553	Sequence 3553, Ap	c1224	132.8	5.8	6000	1	PCT-US07-13803-251	Sequence 251, App
c1152	139.8	6.1	1698	7	US-11-781-665-1493	Sequence 1493, Ap	c1225	132.6	5.8	1504	7	US-11-781-665-563	Sequence 563, App
c1153	139.8	6.1	1865	7	US-11-881-406-3556	Sequence 3556, Ap	c1226	132.4	5.8	420	7	US-11-881-406-3355	Sequence 3355, Ap
c1154	139.8	6.1	2001	7	US-11-881-406-3557	Sequence 3557, Ap	c1227	132.4	5.8	831	7	US-11-781-665-3068	Sequence 3068, Ap
c1155	139.6	6.1	917	7	US-11-781-665-2234	Sequence 2234, Ap	c1228	132.2	5.8	774	7	US-11-781-665-1769	Sequence 1769, Ap
c1156	139.4	6.1	1050	7	US-11-781-665-2934	Sequence 2934, Ap	c1229	132	5.8	699	7	US-11-781-665-1137	Sequence 1137, Ap
c1157	139.4	6.1	2166	7	US-11-781-665-1235	Sequence 1235, Ap	c1230	131.8	5.8	379	7	US-11-881-406-2141	Sequence 2141, Ap
c1158	139.4	6.1	6000	1	PCT-US07-13803-9	Sequence 9, Appli	c1231	131.8	5.8	998	7	US-11-781-665-1715	Sequence 1715, Ap
c1159	139.2	6.1	6000	1	PCT-US07-13803-117	Sequence 117, App	c1232	131.8	5.8	3564	7	US-11-814-954-2	Sequence 2, Appli
c1160	139	6.1	410	7	US-11-881-406-2400	Sequence 2400, Ap	c1233	131.6	5.8	7787	7	US-11-490-374A-1234	Sequence 1234, Ap
c1161	139	6.1	10240	8	US-60-970-396-5	Sequence 5, Appli	c1234	131.6	5.8	7787	7	US-11-490-374A-1236	Sequence 1236, Ap
c1162	138.8	6.1	1035	7	US-11-781-665-1590	Sequence 1590, Ap	c1235	131.6	5.8	7787	7	US-11-490-374A-1237	Sequence 1237, Ap
c1163	138.4	6.1	2251	7	US-11-781-665-1072	Sequence 1072, Ap	c1236	131.6	5.8	7787	7	US-11-490-374A-1238	Sequence 1238, Ap
c1164	138	6.0	1830	7	US-11-781-665-848	Sequence 848, App	c1237	131.4	5.8	1086	7	US-11-781-665-1218	Sequence 1218, Ap
c1165	138	6.0	2486	7	US-11-781-665-1081	Sequence 1081, Ap	c1238	131.4	5.8	1560	7	US-11-781-665-2953	Sequence 2953, Ap
c1166	137.8	6.0	814	7	US-11-781-665-1567	Sequence 1567, Ap	c1239	131.4	5.8	60401	1	PCT-US06-25800-36	Sequence 36, Appl
c1167	137.6	6.0	1827	7	US-11-781-665-1824	Sequence 1824, Ap	c1240	131.2	5.7	1041	7	US-11-781-665-2750	Sequence 2750, Ap
c1168	137.6	6.0	2050	7	US-11-781-665-1824	Sequence 1824, Ap	c1241	131	5.7	1373	7	US-11-816-601-275	Sequence 275, App
c1169	137.4	6.0	2001	7	US-11-881-406-3843	Sequence 615, App	c1242	131	5.7	2001	7	US-11-881-406-1328	Sequence 1328, Ap
c1170	137.4	6.0	2001	7	US-11-881-406-3843	Sequence 3843, Ap	c1243	131	5.7	5659	7	US-11-835-336-13	Sequence 13, Appl
c1171	137.4	6.0	2203	7	US-11-781-665-2421	Sequence 2421, Ap	c1244	130.8	5.7	761	7	US-11-781-665-1411	Sequence 1411, Ap
c1172	137.2	6.0	1786	7	US-11-781-665-890	Sequence 890, App	c1245	130.4	5.7	396	7	US-11-881-406-3972	Sequence 3972, Ap
c1173	137.2	6.0	2105	7	US-11-781-665-1259	Sequence 1259, Ap	c1246	130.4	5.7	807	7	US-11-781-665-755	Sequence 755, App
c1174	137	6.0	1795	7	US-11-781-665-1080	Sequence 1080, Ap	c1247	130.2	5.7	1828	7	US-11-781-665-1975	Sequence 1975, App
c1175	137	6.0	1808	7	US-11-781-665-1473	Sequence 1473, Ap	c1248	130	5.7	1061	7	US-11-781-665-388	Sequence 388, App
c1176	136.8	6.0	844	7	US-11-781-665-2512	Sequence 2512, Ap	c1249	130	5.7	6000	1	PCT-US07-13803-238	Sequence 238, App
c1177	136.8	6.0	1535	7	US-11-781-665-2847	Sequence 2847, Ap	c1250	129.8	5.7	712	7	US-11-781-665-1885	Sequence 1885, Ap
c1178	136.8	6.0	2208	7	US-11-702-018-1	Sequence 1, Appli	c1251	129.8	5.7	1234	7	US-11-781-665-763	Sequence 763, App
c1179	136.8	6.0	3600	7	US-11-847-733-6	Sequence 6, Appli	c1252	129.8	5.7	1724	7	US-11-781-665-1097	Sequence 1097, Ap
c1180	136.8	6.0	4827	7	US-11-816-601-70	Sequence 70, Appl	c1253	129.8	5.7	1801	7	US-11-781-665-229	Sequence 229, App
c1181	136.8	6.0	7086	7	US-11-847-733-5	Sequence 5, Appli	c1254	129.8	5.7	1874	7	US-11-781-665-584	Sequence 584, App
c1182	136.6	6.0	713	7	US-11-781-665-2254	Sequence 2254, Ap	c1255	129.8	5.7	3775	7	US-11-847-733-71	Sequence 71, Appl
c1183	136.6	6.0	2366	7	US-11-781-665-2254	Sequence 2254, Ap	c1256	129.8	5.7	5310	7	US-11-835-336-17	Sequence 17, Appl
c1184	136.4	6.0	1782	7	US-11-781-665-1475	Sequence 1475, Ap	c1257	129.6	5.7	3644	7	US-11-847-733-25	Sequence 25, Appl
c1185	136.4	6.0	3590	7	US-11-884-496-683	Sequence 683, App	c1258	129.6	5.7	4130	7	US-11-884-496-670	Sequence 670, App
c1186	136.2	6.0	8017	7	US-11-781-665-2252	Sequence 2252, Ap	c1259	129.6	5.7	5376	7	US-11-835-336-94	Sequence 94, Appl
c1187	136.2	6.0	1095	7	US-11-781-665-2772	Sequence 2772, Ap	c1260	129.4	5.7	9021	7	US-11-835-336-74	Sequence 74, Appl
c1188	136.2	6.0	1633	7	US-11-781-665-2819	Sequence 2819, Ap	c1261	129.2	5.7	1067	7	US-11-781-665-1776	Sequence 1776, Ap
c1189	136.2	6.0	2472	7	US-11-884-496-647	Sequence 647, App	c1262	129.2	5.7	1067	7	US-11-781-665-1580	Sequence 1580, Ap
c1190	136.2	6.0	3591	7	US-11-490-374A-1815	Sequence 1815, Ap	c1263	129.2	5.7	3536	7	US-11-825-627-354	Sequence 354, App
c1191	136.2	6.0	3591	7	US-11-490-374A-1816	Sequence 1816, Ap	c1264	128.8	5.6	1114	7	US-11-781-665-2562	Sequence 2562, Ap
c1192	136.2	6.0	3591	7	US-11-490-374A-1817	Sequence 1817, Ap	c1265	128.6	5.6	1114	7	US-11-881-406-2807	Sequence 2807, Ap
c1193	136	6.0	997	7	US-11-881-406-2195	Sequence 2195, Ap	c1266	128.4	5.6	1445	7	US-11-781-665-1329	Sequence 1329, Ap
c1194	136	6.0	3080	7	US-11-832-009-45	Sequence 45, Appl	c1267	128.4	5.6	6000	1	PCT-US07-13803-143	Sequence 143, App

cl268	128.2	5.6	623	7	US-11-881-406-1779	Sequence 1779, Ap	cl341	117.8	5.2	18997	7	US-11-835-336-31	Sequence 31, Appl
cl269	128.2	5.6	802	7	US-11-781-665-938	Sequence 938, App	cl342	117.2	5.1	1003	7	US-11-781-665-1330	Sequence 1330, Ap
cl270	128.2	5.6	1485	7	US-11-781-665-2091	Sequence 2091, Ap	cl343	117.2	5.1	3647	7	US-11-835-336-42	Sequence 42, Appl
cl271	128.2	5.6	1935	7	US-11-883-496-3	Sequence 3, Appl	cl344	117.2	5.1	5477	7	US-11-835-336-108	Sequence 108, App
cl272	128.2	5.6	2001	7	US-11-881-406-3769	Sequence 3769, Ap	cl345	117	5.1	6000	1	PCT-US07-13803-78	Sequence 78, Appl
cl273	128	5.6	5659	7	US-11-835-336-14	Sequence 14, Appl	cl346	116.8	5.1	2249	7	US-11-781-665-285	Sequence 285, App
cl274	127.8	5.6	429	7	US-11-881-406-2593	Sequence 2593, Ap	cl347	116.6	5.1	386	7	US-11-881-406-4081	Sequence 4081, Ap
cl275	127.8	5.6	2001	7	US-11-881-406-2594	Sequence 2594, Ap	cl348	116.6	5.1	1576	7	US-11-781-665-1524	Sequence 1524, Ap
cl276	127.4	5.6	6271	7	US-11-835-336-61	Sequence 61, Appl	cl349	116.6	5.1	2764	7	US-11-781-665-1547	Sequence 1547, Ap
cl277	127.2	5.6	1631	7	US-11-781-665-2650	Sequence 2650, Ap	cl350	116.4	5.1	619	7	US-11-744-695-17	Sequence 17, Appl
cl278	126.8	5.6	3548	7	US-11-884-496-721	Sequence 721, App	cl351	116.4	5.1	1936	7	US-11-781-665-2656	Sequence 2656, Ap
cl279	126.4	5.5	6246	7	US-11-835-336-50	Sequence 50, Appl	cl352	116	5.1	1391	7	US-11-781-665-1463	Sequence 1463, Ap
cl280	126	5.5	637	7	US-11-781-665-2486	Sequence 2486, Ap	cl353	116	5.1	2001	7	US-11-881-406-2107	Sequence 2107, Ap
cl281	125.8	5.5	1293	7	US-11-781-665-2392	Sequence 2392, Ap	cl354	115.8	5.1	228	6	US-10-587-791-432	Sequence 432, App
cl282	125.8	5.5	2345	7	US-11-781-665-786	Sequence 786, App	cl355	115.8	5.1	4001	7	US-11-835-336-10	Sequence 10, Appl
cl283	125.8	5.5	6000	1	PCT-US07-13803-7	Sequence 7, Appl	cl356	115.6	5.1	1112	7	US-11-781-665-1091	Sequence 1091, Ap
cl284	125.8	5.5	6000	1	PCT-US07-13803-186	Sequence 186, App	cl357	115.4	5.1	1300	7	US-11-781-665-2911	Sequence 2911, Ap
cl285	125.8	5.5	7432	7	US-11-835-336-5	Sequence 5, Appl	cl358	115.4	5.1	1904	7	US-11-781-665-2905	Sequence 2905, Ap
cl286	125.8	5.5	14147	7	US-11-835-336-39	Sequence 39, Appl	cl359	115.2	5.0	5477	7	US-11-835-336-107	Sequence 107, App
cl287	125.6	5.5	2001	7	US-11-881-406-1366	Sequence 1366, Ap	cl360	114.6	5.0	1453	7	US-11-781-665-1469	Sequence 1469, Ap
cl288	125.4	5.5	4613	7	US-11-816-601-108	Sequence 108, App	cl361	114.6	5.0	2001	7	US-11-881-406-3752	Sequence 3752, Ap
cl289	125.2	5.5	402	7	US-11-881-406-1324	Sequence 1324, Ap	cl362	114.6	5.0	2001	7	US-11-881-406-3753	Sequence 3753, Ap
cl290	125.2	5.5	1377	7	US-11-781-665-794	Sequence 794, App	cl363	114.2	5.0	2244	7	US-11-847-733-46	Sequence 46, Appl
cl291	125.2	5.5	1544	7	US-11-781-665-2371	Sequence 2371, Ap	cl364	113.8	5.0	1879	7	US-11-781-665-800	Sequence 800, App
cl292	125.2	5.5	1625	7	US-11-781-665-1965	Sequence 1965, Ap	cl365	113.6	5.0	1504	7	US-11-781-665-1972	Sequence 1972, Ap
cl293	125	5.5	1084	7	US-11-781-665-1850	Sequence 1850, Ap	cl366	113.2	5.0	1317	7	US-11-781-665-2500	Sequence 2500, Ap
cl294	125	5.5	1610	7	US-11-781-665-1592	Sequence 1592, Ap	cl367	113.2	5.0	9884	7	US-11-835-336-8	Sequence 8, Appl
cl295	124.8	5.5	798	7	US-11-881-406-2523	Sequence 2523, Ap	cl368	113	4.9	413	7	US-11-881-406-1439	Sequence 1439, Ap
cl296	124.8	5.5	955	7	US-11-781-665-1424	Sequence 1424, Ap	cl369	113	4.9	933	7	US-11-831-468-103	Sequence 103, App
cl297	124.6	5.5	1345	7	US-11-781-665-2399	Sequence 2399, Ap	cl370	113	4.9	4001	7	US-11-835-336-9	Sequence 9, Appl
cl298	124.6	5.5	6771	7	US-11-908-114-12	Sequence 12, Appl	cl371	112.8	4.9	758	7	US-11-831-404-91	Sequence 91, Appl
cl299	124.4	5.4	1759	7	US-11-781-665-792	Sequence 792, App	cl372	112.8	4.9	2099	7	US-11-781-665-2198	Sequence 2198, Ap
cl300	124.2	5.4	1367	7	US-11-235-701A-353	Sequence 353, App	cl373	112.6	4.9	415	7	US-11-881-406-3022	Sequence 3022, Ap
cl301	124.2	5.4	9021	7	US-11-835-336-73	Sequence 73, Appl	cl374	112.4	4.9	7432	7	US-11-835-336-5	Sequence 5, Appl
cl302	123.8	5.4	6803	7	US-11-884-496-514	Sequence 514, App	cl375	112.2	4.9	701	8	US-60-916-036-7	Sequence 7, Appl
cl303	123.6	5.4	1157	7	US-11-781-665-180	Sequence 180, Appl	cl376	112	4.9	849	7	US-11-781-665-2505	Sequence 2505, Ap
cl304	123.6	5.4	5976	7	US-11-835-336-93	Sequence 93, Appl	cl377	112	4.9	4271	7	US-11-816-601-101	Sequence 101, App
cl305	123	5.4	6000	1	PCT-US07-13803-79	Sequence 79, Appl	cl378	112	4.9	4271	7	US-11-816-601-294	Sequence 294, App
cl306	122.8	5.4	1224	7	US-11-781-665-294	Sequence 294, App	cl379	112	4.9	6050	7	US-11-835-336-20	Sequence 20, Appl
cl307	122.6	5.4	818	7	US-11-781-665-2683	Sequence 2683, Ap	cl380	112	4.9	7001	7	US-11-835-336-2	Sequence 2, Appl
cl308	122.6	5.4	1219	7	US-11-781-665-73	Sequence 73, Appl	cl381	111.8	4.9	3647	7	US-11-835-336-41	Sequence 41, Appl
cl309	122.6	5.4	1492	7	US-11-781-665-2548	Sequence 2548, Ap	cl382	111.4	4.9	2153	7	US-11-781-665-1969	Sequence 1969, Ap
cl310	122.6	5.4	8693	7	US-11-835-336-70	Sequence 70, Appl	cl383	111.4	4.9	8666	7	US-11-835-336-93	Sequence 93, Appl
cl311	122.4	5.4	1535	7	US-11-781-665-2847	Sequence 2847, Ap	cl384	111	4.9	5976	7	US-11-835-336-95	Sequence 95, Appl
cl312	122.2	5.4	1939	7	US-11-781-665-2112	Sequence 2112, Ap	cl385	110.4	4.8	657	7	US-11-781-665-1026	Sequence 1026, Ap
cl313	122.2	5.4	6074	7	US-11-835-336-75	Sequence 75, Appl	cl386	110.4	4.8	1241	7	US-11-781-665-2951	Sequence 2951, Ap
cl314	122	5.3	1229	7	US-11-781-665-83	Sequence 83, Appl	cl387	110.4	4.8	2001	7	US-11-881-406-3837	Sequence 3837, Ap
cl315	121.4	5.3	4964	7	US-11-884-496-680	Sequence 680, App	cl388	110.4	4.8	8093	7	US-11-835-336-58	Sequence 58, Appl
cl316	121.4	5.3	7432	7	US-11-835-336-6	Sequence 6, Appl	cl389	110.2	4.8	327	7	US-11-881-406-358	Sequence 358, App
cl317	121	5.3	3138	7	US-11-781-665-1492	Sequence 1492, Ap	cl390	110.2	4.8	1686	7	US-11-781-665-1968	Sequence 1968, Ap
cl318	121	5.3	6000	1	PCT-US07-13803-26	Sequence 26, Appl	cl391	110.2	4.8	14147	7	US-11-835-336-40	Sequence 40, Appl
cl319	121	5.3	6000	1	PCT-US07-13803-177	Sequence 177, App	cl392	110	4.8	1131	7	US-11-781-665-717	Sequence 717, App
cl320	120.8	5.3	1694	7	US-11-781-665-1943	Sequence 1943, Ap	cl393	110	4.8	1855	7	US-11-881-406-3556	Sequence 3556, Ap
cl321	120.8	5.3	6621	7	US-11-835-336-16	Sequence 16, Appl	cl394	110	4.8	8666	7	US-11-835-336-95	Sequence 95, Appl
cl322	120.6	5.3	1424	7	US-11-781-665-2503	Sequence 2503, Ap	cl395	109.8	4.8	4724	7	US-11-490-374A-2082	Sequence 2082, Ap
cl323	120.6	5.3	1720	7	US-11-781-665-846	Sequence 846, App	cl396	109.6	4.8	1629	7	US-11-781-665-2996	Sequence 2996, Ap
cl324	120.6	5.3	2001	7	US-11-881-406-3436	Sequence 3436, Ap	cl397	109.4	4.8	1352	7	US-11-781-665-1767	Sequence 1767, Ap
cl325	120.4	5.3	7001	7	US-11-835-336-1	Sequence 1, Appl	cl398	109.2	4.8	9884	7	US-11-835-336-7	Sequence 7, Appl
cl326	120.2	5.3	5969	7	US-11-835-336-84	Sequence 84, Appl	cl399	109	4.8	6621	7	US-11-835-336-15	Sequence 15, Appl
cl327	120.2	5.3	6000	1	PCT-US07-13803-249	Sequence 249, App	cl400	109	4.8	9021	7	US-11-835-336-73	Sequence 73, Appl
cl328	120.2	5.3	11779	8	US-60-970-396-3	Sequence 3, Appl	cl401	108.8	4.8	5976	7	US-11-835-336-94	Sequence 94, Appl
cl329	119.8	5.2	374	7	US-11-881-406-1259	Sequence 1259, Ap	cl402	108.6	4.8	1003	7	US-11-781-665-2868	Sequence 2868, Ap
cl330	119.6	5.2	1200	7	US-11-835-336-101	Sequence 101, App	cl403	108.4	4.7	359	7	US-11-881-406-1873	Sequence 1873, Ap
cl331	119.4	5.2	412	7	US-11-881-406-4129	Sequence 4129, Ap	cl404	108.2	4.7	1167	7	US-11-781-665-2799	Sequence 2799, Ap
cl332	119.4	5.2	1049	7	US-11-781-665-232	Sequence 232, App	cl405	108.2	4.7	7309	7	US-11-835-336-97	Sequence 97, Appl
cl333	119.4	5.2	8666	7	US-11-835-336-96	Sequence 96, Appl	cl406	107.8	4.7	616	7	US-11-781-665-1928	Sequence 1928, Ap
cl334	119.2	5.2	1361	7	US-11-781-665-479	Sequence 479, App	cl407	107.8	4.7	2136	7	US-11-832-009-20	Sequence 20, Appl
cl335	118.6	5.2	7040	7	US-11-835-336-47	Sequence 47, Appl	cl408	107.6	4.7	1117	7	US-11-781-665-2914	Sequence 81, Appl
cl336	118.4	5.2	2001	7	US-11-881-406-3715	Sequence 3715, Ap	cl409	107.6	4.7	3107	7	US-11-835-336-81	Sequence 81, Appl
cl337	118.4	5.2	2001	7	US-11-881-406-3716	Sequence 3716, Ap	cl410	107.6	4.7	6000	1	PCT-US07-13803-172	Sequence 172, App
cl338	118.4	5.2	7309	7	US-11-835-336-98	Sequence 98, Appl	cl411	107.2	4.7	1243	7	US-11-781-665-251	Sequence 251, App
cl339	118.2	5.2	1348	7	US-11-781-665-2504	Sequence 2504, Ap	cl412	107	4.7	608	7	US-11-781-665-1953	Sequence 1953, Ap
cl340	117.8	5.2	287	7	US-11-881-406-1944	Sequence 1944, Ap	cl413	106.8	4.7	362	7	US-11-881-406-4174	Sequence 4174, Ap

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OM nucleic - nucleic search, using sw model

Run on: September 19, 2007, 19:55:18 ; Search time 25012 Seconds
(without alignments)
5665.349 Million cell updates/sec

Title: US-09-944-929-82

Perfect score: 2284

Sequence: 1 gcggagatccgcgcggtc.....ataaatctttgttactcaa 2284

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hic:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_est13:*

12: gb_est12:*

13: gb_est11:*

14: gb_est10:*

15: gb_gss1:*

16: gb_gss2:*

17: gb_gss3:*

18: gb_gss4:*

19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131.2	93.3	4613	6	CR58919 Pongo pyg
2	1802.6	78.9	1965	6	CR621081
3	1291.2	56.5	1296	19	AY401136 Homo sapi
4	1272.6	55.7	1296	19	AY401137
5	921.6	40.4	1050	1	AL525434
6	917.6	40.2	1057	1	AL525390
7	826.6	36.2	884	5	BX350141
8	797.2	34.9	853	4	BQ424639
9	719.8	31.5	1036	1	AL549886
10	718.2	31.4	839	8	CF593691
11	708.4	31.0	785	14	DA581021
12	702	30.7	728	3	BM480136
13	700.4	30.7	717	13	DR004375
14	700.4	30.7	729	3	BM480099

15	690.6	30.2	870	2	BF312571
16	689.6	30.2	940	2	BF683169
17	687.8	30.1	753	14	CK759847
18	676.6	29.6	2265	6	AK046837
19	676.2	29.6	759	14	DA732539
20	675	29.6	697	9	CN365249
21	674.8	29.5	2175	6	AK033557
22	670.6	29.4	2286	6	AK018660
23	669.8	29.3	699	2	BG720669
24	666.2	29.2	2265	6	AK018635
25	665.6	29.1	865	14	DA735624
26	661.8	29.0	805	7	AU138119
27	646.2	28.3	753	8	CF595929
28	646	28.3	1051	1	AL573909
29	644.4	28.2	2235	6	AK033526
30	634.2	27.8	807	14	DA733100
31	633.6	27.7	2284	6	AK171842
32	630.4	27.6	646	9	CN485040
33	630.2	27.6	796	4	BU930526
34	626.8	27.4	687	5	BX953184
35	615	27.1	668	13	DN993870
36	613.8	26.9	623	10	CV024215
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54	563	24.6	592	14	DB031358
55	561.4	24.6	596	14	DA542297
56	560	24.5	594	4	BP247838
57	559.4	24.5	589	14	DB197257
58	558	24.4	587	14	DA748744
59	557.4	24.4	603	14	DB264701
60	556	24.3	584	14	DB201117
61	555.4	24.3	591	14	DA529624
62	555	24.3	584	14	DB261530
63	554	24.3	590	14	DA583643
64	553	24.2	591	3	BM828071
65	552.4	24.2	583	14	DA769469
66	552	24.2	585	14	DA293619
67	552	24.2	592	14	DA527373
68	551	24.1	580	14	DA925055
69	550	24.1	583	14	DA303353
70	550	24.1	583	14	DA354352
71	549.2	24.0	610	4	BP272379
72	549	24.0	578	14	DB107700
73	548.4	24.0	592	14	DB264705
74	547.4	24.0	589	14	DB112866
75	545.4	23.9	583	14	DA207426
76	545	23.9	576	14	DA706884
77	545	23.9	577	14	DA866073
78	545	23.9	578	14	DB202346
79	545	23.9	601	14	DB263168
80	544	23.8	577	14	DA711645
81	544	23.8	584	14	DA001661
82	543	23.8	570	14	DA750655
83	543	23.8	576	14	DB201861
84	543	23.8	579	14	DA090848
85	543	23.8	583	14	DA346289
86	543	23.8	585	14	DB265991
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BF313571	601897547
BF683169	602139129
CK759847	AGENCOURT
AK046837	Mus muscu
DA732539	DA732539
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CF595929	AGENCOURT
AL573909	AL573909
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AK171842	Mus muscu
CN485040	hx22c11.Y
BU930526	AGENCOURT
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DA748744	DA748744
DB264701	DB264701
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DA001661	DA001661
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DA346289	DA346289
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90	542	23.7	583	14	DA590234	DA590234 DA590234	163	521.4	22.8	564	14	DA886089	DA886089
91	541.8	23.7	574	4	BP375859	BP375859 BP375859	164	521.4	22.8	571	14	DA494871	DA494871
92	541.4	23.7	584	3	BM828163	BM828163 K-EST0100	165	521	22.8	553	14	DB207522	DB207522
93	541	23.7	574	14	DA873470	DA873470 DA873470	166	521	22.8	561	14	DB257489	DB257489
94	541	23.7	574	14	DB201824	DB201824 DB201824	167	521	22.8	562	14	DA009313	DA009313
95	541	23.7	582	4	BP256186	BP256186 BP256186	168	520.4	22.8	558	14	DA916870	DA916870
96	540.4	23.7	563	14	DA879194	DA879194 DA879194	169	520.4	22.8	567	14	DB008431	DB008431
97	540	23.6	573	14	DA172736	DA172736 DA172736	170	520	22.8	549	14	DA885250	DA885250
98	539.4	23.6	576	14	DB009591	DB009591 DB009591	171	520	22.8	561	14	DA749318	DA749318
99	539.4	23.6	570	14	DA766877	DA766877 DA766877	172	520	22.8	584	14	DB256983	DB256983
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105	537.4	23.5	567	14	DA485280	DA485280 DA485280	178	518	22.7	551	14	DA882853	DA882853
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108	536.4	23.5	567	14	DA583585	DA583585 DA583585	181	517	22.6	547	14	DA060573	DA060573
109	536.4	23.5	571	14	DA744872	DA744872 DA744872	182	516.6	22.6	562	14	DA452998	DA452998
110	536	23.5	569	14	DB270706	DB270706 DB270706	183	516.4	22.6	551	14	DB105348	DB105348
111	535	23.4	575	14	DB204597	DB204597 DB204597	184	516.4	22.6	559	14	DA950526	DA950526
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114	534	23.4	574	14	DA299483	DA299483 DA299483	187	516	22.6	569	14	DA711490	DA711490
115	533.4	23.4	573	14	DA016588	DA016588 DA016588	188	515.8	22.6	559	14	DA932819	DA932819
116	533.4	23.4	575	14	DA278922	DA278922 DA278922	189	515.4	22.6	544	14	DA850355	DA850355
117	533	23.3	566	14	DA486096	DA486096 DA486096	190	515	22.5	551	14	DA103576	DA103576
118	533	23.3	573	14	DA063309	DA063309 DA063309	191	514.8	22.5	557	14	DA590549	DA590549
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122	532	23.3	561	14	DA017673	DA017673 DA017673	195	514	22.5	559	14	DA041769	DA041769
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129	529.8	23.2	573	14	DA942667	DA942667 DA942667	202	511.4	22.4	566	14	DA513506	DA513506
130	529	23.2	558	14	DA885677	DA885677 DA885677	203	511.2	22.4	527	3	BM790877	BM790877
131	529	23.2	562	14	DB173161	DB173161 DA173161	204	511	22.4	540	14	DB212308	DB212308
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141	528	23.1	827	13	DN371075	DN371075 LIB3733-0	214	509	22.3	557	14	DA171315	DA171315
142	527.4	23.1	569	14	DA075629	DA075629 DA075629	215	508	22.2	549	14	DA888887	DA888887
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153	524	22.9	557	14	DA715919	DA715919 DA715919	226	506	22.2	546	14	DA753698	DA753698
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157	523	22.9	555	14	DA747951	DA747951 DA747951	230	504	22.1	537	14	DA516958	DA516958
158	522	22.9	555	14	DA884221	DA884221 DA884221	231	504	22.1	560	14	DA349567	DA349567
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235	499.4	21.9	542	14	DB059714	DB059714	308	412.6	18.1	420	14	DB509363	DB509363
236	499	21.8	528	14	DB255096	DB255096	309	411.2	18.0	580	4	BP291358	BP291358
237	499	21.8	539	14	DB256521	DB256521	310	411	18.0	441	3	BI031052	BI031052
238	499	21.8	540	14	DB001639	DB001639	311	410.4	18.0	424	3	AW008237	AW008237
239	499	21.8	571	14	DA890033	DA890033	312	406.8	17.8	412	3	BM820174	BM820174
240	498	21.8	540	14	DB244134	DB244134	313	405	17.7	817	12	DV905318	DV905318
241	497	21.8	537	14	DA489229	DA489229	314	405	17.7	853	11	BE234595	BE234595
242	496	21.7	568	14	DA706892	DA706892	315	401	17.6	542	14	DA653625	DA653625
C 243	495.8	21.7	588	14	DB364984	DB364984	316	398.4	17.4	539	14	DA689777	DA689777
244	495	21.7	566	14	DB265802	DB265802	317	395.4	17.3	766	12	DY497041	DY497041
245	494	21.6	552	14	DA158656	DA158656	318	393.6	17.2	469	14	DB262059	DB262059
246	493.4	21.6	566	14	DA693173	DA693173	319	382	16.7	534	14	DA625746	DA625746
247	492	21.5	507	5	BA100624	BA100624	320	382	16.7	559	14	DA632196	DA632196
248	491	21.5	571	14	DA656346	DA656346	321	381.8	16.7	549	14	DA347002	DA347002
249	490	21.5	530	3	BM753270	BM753270	322	379.8	16.6	555	14	DA710837	DA710837
250	489.8	21.4	920	12	DV928382	DV928382	323	375.6	16.4	534	14	DB263443	DB263443
251	489	21.4	560	14	DA022777	DA022777	324	363.8	15.9	439	11	H50932	H50932
252	488.8	21.4	566	14	DA453539	DA453539	325	362	15.8	362	7	AW057870	AW057870
253	488	21.4	559	14	DB249814	DB249814	326	361.4	15.8	734	10	CO879641	CO879641
254	487.6	21.3	584	14	DB364075	DB364075	327	360.8	15.8	364	3	BI031814	BI031814
255	487	21.3	528	14	DA761447	DA761447	328	358.4	15.7	373	4	BQ325584	BQ325584
256	486.8	21.3	561	14	DA884160	DA884160	329	358.4	15.7	534	14	DA149350	DA149350
257	485	21.2	557	14	DA275399	DA275399	330	356.2	15.6	880	10	CR851889	CR851889
C 258	482.2	21.1	550	7	AU152691	AU152691	331	355	15.5	601	4	BP239336	BP239336
259	482	21.1	547	14	DA999982	DA999982	332	352.8	15.4	464	2	BG899200	BG899200
260	480.4	21.0	568	14	DA999605	DA999605	333	347.4	15.2	514	14	DA701250	DA701250
261	479.4	21.0	869	12	DV932206	DV932206	334	345.4	15.1	707	9	CK974547	CK974547
262	479	21.0	521	14	DB248037	DB248037	335	344.8	15.1	362	1	AI979095	AI979095
263	478	20.9	518	14	DB208478	DB208478	336	344	15.1	828	13	DN870441	DN870441
264	478	20.9	543	14	DA688482	DA688482	337	340.4	14.9	342	11	F12992	F12992
265	477.4	20.9	520	14	DA624843	DA624843	338	339.8	14.9	1015	5	BY703150	BY703150
266	476.4	20.9	526	14	DB207283	DB207283	339	338.8	14.8	961	5	BY720875	BY720875
267	476.4	20.9	569	14	DA149179	DA149179	340	335.8	14.7	567	3	BI682666	BI682666
268	476	20.8	516	14	DA008487	DA008487	341	335	14.7	533	3	BM087304	BM087304
269	476	20.8	517	3	BM838896	BM838896	342	334.8	14.7	562	12	DY048683	DY048683
C 270	470.2	20.6	522	7	AU157477	AU157477	343	331.8	14.5	1036	3	BI410030	BI410030
C 271	469.6	20.6	504	14	DB319107	DB319107	344	330.4	14.4	805	13	DT833902	DT833902
C 272	469.4	20.6	472	2	BE301806	BE301806	345	328.2	14.4	764	13	DT848580	DT848580
C 273	468	20.5	496	14	DB195696	DB195696	346	328.2	14.4	790	13	DT848455	DT848455
C 274	465	20.4	478	1	AI207832	AI207832	347	327.8	14.4	886	4	BQ922735	BQ922735
275	461.8	20.2	880	8	CB959572	CB959572	348	325.2	14.2	1018	3	BI416048	BI416048
276	460.4	20.2	503	14	DA604196	DA604196	349	323	14.1	947	5	BY720818	BY720818
277	458.8	20.1	533	14	DA624540	DA624540	350	317	13.9	496	14	DA703232	DA703232
278	452.4	19.8	506	14	DB208508	DB208508	C 351	315.6	13.8	424	11	H51595	H51595
279	451.6	19.8	583	4	BP248346	BP248346	352	309.6	13.6	806	5	BX920338	BX920338
280	451	19.7	564	14	DA014288	DA014288	353	309.4	13.5	821	5	BX920277	BX920277
281	450.6	19.7	697	13	DT891744	DT891744	354	301.4	13.2	364	3	BI029201	BI029201
282	448.6	19.6	528	14	DA698278	DA698278	355	297.4	13.0	631	8	CF746243	CF746243
283	447.6	19.6	692	13	DT895274	DT895274	356	296.2	13.0	439	14	DB444501	DB444501
284	447	19.6	479	14	DA739541	DA739541	357	291	12.7	701	4	BP147701	BP147701
285	447	19.6	488	14	DA699749	DA699749	358	289.8	12.7	673	7	BB661915	BB661915
286	445.4	19.5	475	14	DA129582	DA129582	359	288.6	12.6	784	9	CJ462354	CJ462354
287	444.4	19.5	515	14	DA129582	DA129582	360	285.8	12.5	727	10	CN793285	CN793285
C 288	443.4	19.4	445	1	AI612764	AI612764	361	281.8	12.3	439	14	DB442366	DB442366
289	443	19.4	571	14	DA707669	DA707669	362	279.8	12.3	663	7	BB645954	BB645954
290	443	19.4	595	14	DA672973	DA672973	363	278.6	12.2	323	2	BE710389	BE710389
291	439	19.2	572	14	DA130511	DA130511	364	274.2	12.0	668	11	EE216707	EE216707
292	436	19.1	564	14	DA269140	DA269140	365	273.8	12.0	691	14	DN117286	DN117286
293	435.4	19.1	668	9	CB834065	CB834065	366	272.2	12.0	691	14	DN117635	DN117635
294	434	19.0	500	14	DA835136	DA835136	367	273.8	11.9	641	7	BB624968	BB624968
295	433	19.0	581	14	DA750536	DA750536	368	269.4	11.8	683	13	DN280755	DN280755
296	432.4	18.9	751	12	DY492741	DY492741	369	268.6	11.8	710	2	BG964611	BG964611
297	429	18.8	557	14	DA278002	DA278002	370	268	11.7	762	13	DN870440	DN870440
298	429	18.8	557	14	DA707706	DA707706	C 371	267.2	11.7	862	14	DN132822	DN132822
299	427	18.7	472	14	DA017137	DA017137	372	266.6	11.7	671	8	CF789259	CF789259
300	426	18.7	559	14	DA130901	DA130901	373	266.6	11.7	862	9	CN164398	CN164398
301	426	18.7	571	14	DA873110	DA873110	374	265.2	11.6	314	4	BP224438	BP224438
302	425.6	18.6	447	4	BP246319	BP246319	375	262.8	11.5	574	2	BE533293	BE533293
303	424	18.6	569	14	DB241748	DB241748	376	262	11.5	295	14	DA446001	DA446001
304	418.4	18.3	456	14	DB204351	DB204351	377	261.8	11.5	560	2	BF046016	BF046016
305	416.4	18.2	457	7	AW752992	AW752992	C 378	261.6	11.5	630	9	CK963012	CK963012
306	415.2	18.2	718	9	CK971151	CK971151	C 379	261.6	11.5	630	9	CK971129	CK971129

380	261.6	11.5	771	10	C0809298	C0809298 AGENCOURT	453	229	10.0	1988	6	HSMB02962	AL7113640 Homo sapi
381	257	11.3	826	5	CR926783	CR926783 BX926783	454	229	10.0	2194	6	CR610806	CR610806 full-leng
382	255.6	11.2	848	9	CK449279	CK449279 892833 MA	455	229	10.0	2195	6	CR622984	CR622984 full-leng
383	253.2	11.1	388	3	BI024344	BI024344 CM3-MT029	456	228.8	10.0	2195	14	DB353009	DB353009 AGENCOURT
384	250.2	11.0	587	13	DN279685	DN279685 1160739 M	C 457	228.8	10.0	911	4	BQ676349	BQ676349 AGENCOURT
385	245.2	10.8	447	17	CG620426	CG620426 OST3117492	C 458	228.8	10.0	941	4	BQ678783	BQ678783 AGENCOURT
386	245.6	10.8	323	14	D25954	D25954 HUMGS06728	C 459	228.8	10.0	956	4	BQ900958	BQ900958 AGENCOURT
387	245.4	10.7	555	13	DN339203	DN339203 LIB3523-0	460	228.6	10.0	497	7	AW974932	AW974932 EST187037
388	244	10.6	620	5	FX926593	FX926593 BX926593	C 461	228.6	10.0	1023	5	BX356060	BX356060 BX356060
389	243	10.7	269	11	F10587	F10587 HSC3HC052 n	462	228.6	10.0	2971	15	AF101960	AF101960 AF101960
390	241.4	10.6	251	10	CR555844	CR555844 DKF2p469A	C 463	228.4	10.0	512	3	BI494531	BI494531 df110h01.
391	239.4	10.5	341	7	AW478661	AW478661 21466 MAR	C 464	228.4	10.0	641	14	DB117312	DB117312 DB117312
392	237.6	10.4	436	3	BI497377	BI497377 df135g02.	465	228.4	10.0	755	4	BQ615930	BQ615930 UI-H-DF0-
393	237	10.4	253	7	AW087232	AW087232 XBP7B03.x	C 466	228.4	10.0	981	4	BQ707985	BQ707985 AGENCOURT
394	236.4	10.4	579	7	AU145055	AU145055 AUI45055	C 467	228.2	10.0	598	17	CG696805	CG696805 MUGQ_CH25
395	236	10.3	504	14	DA798480	DA798480 DA798480	C 468	228.2	10.0	714	18	CZ459896	CZ459896 MCF748H06
396	236	10.3	594	14	DA192037	DA192037 DA192037	C 469	228.2	10.0	1073	16	BZ610713	BZ610713 WHAC155TR
397	236	10.3	614	15	AQ055703	AQ055703 CIT-HSP-2	C 470	228	10.0	618	8	CD369000	CD369000 UI-H-F11-
398	236	10.3	676	18	AG075207	AG075207 Pan trog1	C 471	228	10.0	1042	5	BX338157	BX338157 BX338157
399	235.2	10.3	735	9	CK963207	CK963207 Pan trog1	C 472	227.8	10.0	486	15	AQ939756	AQ939756 NR5-102R
400	235	10.3	598	7	AW913757	AW913757 uF56G09.Y	473	227.6	10.0	556	7	AU152561	AU152561 AUI52561
401	234.6	10.3	405	7	AW855803	AW855803 RCL-CT027	474	227.6	10.0	562	14	DA283098	DA283098 DA283098
402	234.6	10.3	547	18	CZ464372	CZ464372 MCF755E09	475	227.6	10.0	641	9	CK979245	CK979245 411113 B
403	234.2	10.3	708	7	AW955633	AW955633 EST367763	C 476	227.6	10.0	658	15	AQ357800	AQ357800 CITBI-E1-
404	233.8	10.2	1028	3	BM564754	BM564754 AGENCOURT	C 477	227.6	10.0	680	15	AQ317036	AQ317036 CITBI-E1-
405	233.6	10.2	287	2	BF361648	BF361648 CM1-NN000	C 478	227.6	10.0	816	18	CZ450800	CZ450800 MCF755356
406	233.4	10.2	771	12	EB528550	EB528550 303150 P1	C 479	227.6	10.0	1106	5	BX355356	BX355356 BX355356
407	233.2	10.2	318	4	BU531754	BU531754 AGENCOURT	C 480	227.4	10.0	306	2	BF681619	BF681619 602155887
408	233.2	10.2	786	4	BU954286	BU954286 AGENCOURT	C 481	227.4	10.0	512	7	AV740009	AV740009 AV740009
409	233	10.2	569	14	DA777850	DA777850 DA777850	C 482	227.4	10.0	668	8	CD517214	CD517214 AGENCOURT
410	233	10.2	572	14	DA524408	DA524408 DA524408	C 483	227.2	9.9	358	2	BG236628	BG236628 nai46b07.
411	233	10.2	1329	2	BF984807	BF984807 602308054	C 484	227.2	9.9	433	7	AW819125	AW819125 RC3-ST028
412	232.8	10.2	376	1	AA579179	AA579179 nF28A09.s	C 485	227.2	9.9	429	15	AQ090219	AQ090219 HS 3009 A
413	232.8	10.2	695	3	BI146784	BI146784 602911863	C 486	227.2	9.9	558	14	DB019422	DB019422 DB019422
414	232.4	10.2	472	7	AW855730	AW855730 RCL-CT027	C 487	227.2	9.9	566	14	DA900739	DA900739 DA900739
415	232.2	10.2	548	14	DB273413	DB273413 DB273413	C 488	227.2	9.9	531	14	DA303160	DA303160 DA303160
416	231.6	10.1	551	14	DB269889	DB269889 DB269889	C 489	227.2	9.9	515	18	AG050659	AG050659 Pan trog1
417	231.6	10.1	655	18	DX813762	DX813762 MUGQ_CH25	C 490	227	9.9	552	4	BQ017601	BQ017601 UI-H-D10-
418	231.6	10.1	914	5	BX435087	BX435087 BX435087	C 491	227	9.9	679	9	CN304238	CN304238 170004247
419	231.6	10.1	951	5	BX463923	BX463923 BX463923	C 492	227	9.9	4697	6	CR859207	CR859207 Pongo PVG
420	231.6	10.1	990	5	BX345245	BX345245 BX345245	C 493	226.8	9.9	544	14	DB344021	DB344021 DB344021
421	231.6	10.1	1207	15	AF102031	AF102031 AF102031	C 494	226.8	9.9	680	2	BG924866	BG924866 HNC38-1-C
422	231.6	10.1	1216	15	AF101533	AF101533 AF101533	C 495	226.8	9.9	779	15	AZ517787	AZ517787 RPCI-11-1
423	231.4	10.1	446	13	DN384707	DN384707 LIB3892-0	C 496	226.6	9.9	339	7	AW270258	AW270258 xp43e01.x
424	231.4	10.1	530	14	DN133295	DN133295 997137 MA	C 497	226.6	9.9	349	2	BF477463	BF477463 nac61e07.
425	231.2	10.1	588	14	DA100593	DA100593 DA100593	C 498	226.6	9.9	546	15	AQ548438	AQ548438 RPCI-11-4
426	230.8	10.1	340	7	AW855736	AW855736 RCL-CT027	C 499	226.6	9.9	574	14	DA090879	DA090879 DA090879
427	230.8	10.1	1009	5	BX344308	BX344308 BX344308	C 500	226.6	9.9	772	7	AU121695	AU121695 AUI21695
428	230.6	10.1	317	4	BU602934	BU602934 AGENCOURT	C 501	226.6	9.9	792	8	CD655541	CD655541 AGENCOURT
429	230.6	10.1	518	2	BG577022	BG577022 602599429	C 502	226.6	9.9	820	8	CD653272	CD653272 AGENCOURT
430	230.6	10.1	955	2	BG029224	BG029224 602292436	C 503	226.6	9.9	894	15	AQ787773	AQ787773 HS 3072 A
431	230.6	10.1	1029	16	BZ610725	BZ610725 WHACK01TF	C 504	226.4	9.9	445	4	BQ008264	BQ008264 UI-H-E10-
432	230.4	10.1	354	5	BX480821	BX480821 DKF2p686F	C 505	226.4	9.9	473	15	AQ242916	AQ242916 HS-2061 A
433	230.2	10.1	315	9	CN275226	CN275226 170006000	C 506	226.4	9.9	567	15	AQ546141	AQ546141 CITBI-E1-
434	230.2	10.1	534	7	AW500029	AW500029 UI-HF-BN0	C 507	226.4	9.9	685	18	ED009913	ED009913 MUGQ_CH25
435	230.2	10.1	543	14	DB231425	DB231425 DB231425	C 508	226.4	9.9	694	19	AG172896	AG172896 Pan trog1
436	230.2	10.1	667	9	CN392067	CN392067 170005998	C 509	226.4	9.9	761	5	CA426986	CA426986 UI-H-DF0-
437	230	10.1	510	2	BF965775	BF965775 602277404	C 510	226.4	9.9	1346	18	DUR00579	DUR00579 lv01 fp00
438	230	10.1	513	3	BI494511	BI494511 df110g02.	C 511	226.2	9.9	376	15	B78953	B78953 CIT-HSP-456
439	229.8	10.1	900	5	AX407077	AX407077 BX407077	C 512	226.2	9.9	547	5	BX472351	BX472351 DKF2p686K
440	229.8	10.1	340	7	AW468372	AW468372 hb37a08.x	C 513	226.2	9.9	557	3	BM742596	BM742596 K-EST0015
441	229.6	10.1	648	15	AQ547540	AQ547540 RPCI-11-4	C 514	226.2	9.9	620	1	AL042635	AL042635 DKF2p434M
442	229.4	10.0	738	5	CA428400	CA428400 UI-H-DF0-	C 515	226.2	9.9	632	5	BX953656	BX953656 DKF2p7810
443	229.2	10.0	394	1	AA613627	AA613627 noi8D06.s	C 516	226.2	9.9	642	18	CZ454001	CZ454001 MCF735022
444	229.2	10.0	487	5	BX954470	BX954470 DKF2p781N	C 517	226	9.9	516	1	AL449689	AL449689 DA449689
445	229.2	10.0	542	14	DB305045	DB305045 DB305045	C 518	226	9.9	560	14	DB264370	DB264370 DB264370
446	229.2	10.0	585	9	CK825907	CK825907 ik35a09.Y	C 519	226	9.9	566	14	DB349252	DB349252 DB349252
447	229.2	10.0	675	3	BM994911	BM994911 UI-H-D10-	C 520	226	9.9	635	8	CB216644	CB216644 NISC nq07
448	229.2	10.0	1890	6	CR624170	CR624170 full-leng	C 521	226	9.9	652	3	BM992081	BM992081 UI-H-DF1-
449	229	10.0	571	3	BM757793	BM757793 K-EST0037	C 522	226	9.9	741	15	AQ376674	AQ376674 RPCI11-16
450	229	10.0	626	3	BM750039	BM750039 K-EST0025	C 523	226	9.9	807	13	DR761844	DR761844 HESC4_133
451	229	10.0	791	8	CD104542	CD104542 AGENCOURT	C 524	225.8	9.9	451	3	BM853062	BM853062 K-EST0134
452	229	10.0	1925	6	CR602031	CR602031 full-leng	C 525	225.8	9.9	559	14	DA016896	DA016896 DA016896

c 526	225.8	9.9	665	18	AG049305	AG049305 Pan trogl	c 599	223.6	9.8	514	2	BF814446	BF814446 MR2-CI018
c 527	225.8	9.9	765	16	BZ604837	BZ604837 WHABV91TR	c 600	223.6	9.8	645	10	CR752070	CR752070 DKFZp469F
c 528	225.8	9.9	769	19	AG123414	AG123414 Pan trogl	c 601	223.6	9.8	742	2	BG431052	BG431052 602498667
c 529	225.6	9.9	427	1	A1821044	A1821044 yb96f10.y	c 602	223.6	9.8	848	19	CR961389	CR961389 Homo sapi
c 530	225.6	9.9	438	1	AA584489	AA584489 n011f12.s	c 603	223.4	9.8	463	14	DA087633	DA087633 DA087633
c 531	225.6	9.9	735	1	AL042756	AL042756 DKFZp434C	c 604	223.4	9.8	477	8	CB067450	CB067450 IG37a09.x
c 532	225.6	9.9	780	14	CR866374	CR866374 HESCA_10	c 605	223.4	9.8	497	15	AO635538	AO635538 RPCI-11-4
c 533	225.6	9.9	5417	6	HS0803282	AL831975 Homo sapi	c 606	223.4	9.8	520	15	AQ877271	AQ877271 HS_2142_B
c 534	225.4	9.9	477	14	DA621338	DA621338 Homo sapi	c 607	223.4	9.8	522	1	AL708846	AL708846 DKFZp686J
c 535	225.4	9.9	767	16	BZ606672	BZ606672 WHAAO22TR	c 608	223.4	9.8	528	15	AQ377485	AQ377485 RPCI11-16
c 536	225.2	9.9	481	15	AO244348	AO244348 HS_2064_B	c 609	223.4	9.8	543	14	DB348633	DB348633 DB348633
c 537	225.2	9.9	561	14	DA067793	DA067793 DA067793	c 610	223.4	9.8	546	14	DB279941	DB279941 DB279941
c 538	225.2	9.9	700	7	AU253657	AU253657 AU253657	c 611	223.4	9.8	566	4	BP262254	BP262254 BP262254
c 539	225.2	9.9	740	8	CB963410	CB963410 AGENCOURT	c 612	223.4	9.8	578	14	DB371589	DB371589 DB371589
c 540	225.2	9.9	788	2	BG108021	BG108021 602279942	c 613	223.4	9.8	583	4	BP261956	BP261956 BP261956
c 541	225.2	9.9	917	8	CD359746	CD359746 AGENCOURT	c 614	223.4	9.8	584	7	AV721886	AV721886 AV721886
c 542	225.2	9.9	2940	6	CR858431	CR858431 Pongo pyg	c 615	223.4	9.8	635	7	AV711430	AV711430 AV711430
c 543	225	9.9	499	15	AQ380362	AQ380362 RPCI11-15	c 616	223.4	9.8	782	1	AL598828	AL598828 DKFZp313L
c 544	225	9.9	512	10	CR543116	CR543116 DKFZp470I	c 617	223.4	9.8	927	1	AL536665	AL536665 AL536665
c 545	225	9.9	623	7	AV762741	AV762741 AV762741	c 618	223.4	9.8	1708	6	CR596492	CR596492 full-leng
c 546	224.8	9.8	309	4	BU940813	BU940813 AGENCOURT	c 619	223.4	9.8	2334	6	BC018303	BC018303 Homo sapi
c 547	224.8	9.8	435	14	DA224227	DA224227 DA224227	c 620	223.2	9.8	431	9	CA413118	CA413118 170005326
c 548	224.8	9.8	440	7	AW408643	AW408643 UI-HF-BM0	c 621	223.2	9.8	457	8	CF788452	CF788452 860404 MA
c 549	224.8	9.8	565	4	BP264321	BP264321 BP264321	c 622	223.2	9.8	624	19	AG098912	AG098912 Pan trogl
c 550	224.8	9.8	585	15	AQ668477	AQ668477 HS_5422_A	c 623	223.2	9.8	631	4	BU874105	BU874105 UI-CF-DU0
c 551	224.8	9.8	631	5	BA496221	BA496221 DKFZp779N	c 624	223.2	9.8	651	7	AU131834	AU131834 AU131834
c 552	224.8	9.8	642	7	AV759557	AV759557 AV759557	c 625	223.2	9.8	669	19	AG182560	AG182560 Pan trogl
c 553	224.8	9.8	680	16	BZ772360	BZ772360 mcV35e11.	c 626	223	9.8	223	2	BF793997	BF793997 602254640
c 554	224.8	9.8	979	3	BM468648	BM468648 AGENCOURT	c 627	223	9.8	424	8	CD238242	CD238242 ENPAXG05
c 555	224.8	9.8	3820	6	HS0803830	AL832522 Homo sapi	c 628	223	9.8	546	14	DA516684	DA516684 DA516684
c 556	224.8	9.8	3820	6	HS0803831	AL831957 Homo sapi	c 629	223	9.8	576	14	DA615550	DA615550 DA615550
c 557	224.6	9.8	440	15	AQ593063	AQ593063 HS_5457_A	c 630	223	9.8	583	15	AQ391722	AQ391722 CITBI-E1-
c 558	224.6	9.8	447	1	AL596543	AL596543 DKFZp451G	c 631	223	9.8	693	19	AG111039	AG111039 Pan trogl
c 559	224.6	9.8	456	15	AQ122741	AQ122741 HS_3088_A	c 632	222.8	9.8	301	12	DW420151	DW420151 HHAGE0198
c 560	224.6	9.8	504	15	BH001309	BH001309 UP_391-8J	c 633	222.8	9.8	474	14	DB3232036	DB3232036 DB3232036
c 561	224.6	9.8	536	15	AQ391735	AQ391735 CITBI-E1-	c 634	222.8	9.8	495	5	BR356614	BR356614 DKFZp781C
c 562	224.6	9.8	604	15	AQ262198	AQ262198 CITBI-E1-	c 635	222.8	9.8	534	15	AQ282060	AQ282060 RPCI11-81
c 563	224.6	9.8	795	18	DU797114	DU797114 fv01.fp00	c 636	222.8	9.8	600	15	AQ075668	AQ075668 CIT-HSP-2
c 564	224.6	9.8	878	5	BA431169	BA431169 BA431169	c 637	222.8	9.8	643	18	AG052500	AG052500 Pan trogl
c 565	224.6	9.8	2320	6	CR860114	CR860114 Pongo pyg	c 638	222.8	9.8	649	14	DA326552	DA326552 DA326552
c 566	224.4	9.8	572	7	AU145224	AU145224 AU145224	c 639	222.8	9.8	661	14	DA570357	DA570357 DA570357
c 567	224.4	9.8	651	1	AL707137	AL707137 DKFZp686C	c 640	222.8	9.8	688	4	BQ447037	BQ447037 UI-H-EUL-
c 568	224.4	9.8	660	5	BA484570	BA484570 DKFZp686I	c 641	222.8	9.8	719	18	DX582587	DX582587 MUQO_CH25
c 569	224.4	9.8	1130	2	BE888786	BE888786 601513704	c 642	222.8	9.8	748	18	ED017328	ED017328 MUQO_CH25
c 570	224.4	9.8	3577	8	CB617708	CB617708 OX-TES-2	c 643	222.8	9.8	750	18	C2459718	C2459718 MCF748C12
c 571	224.2	9.8	332	1	AA574442	AA574442 nf45g11.s	c 644	222.8	9.8	909	8	CD299999	CD299999 AGENCOURT
c 572	224.2	9.8	339	3	BU564846	BU564846 AGENCOURT	c 645	222.8	9.8	1983	6	CR861149	CR861149 Pongo pyg
c 573	224.2	9.8	456	7	AW021917	AW021917 df30a07.y	c 646	222.6	9.7	337	12	DW409824	DW409824 HHAGE0105
c 574	224.2	9.8	491	9	CK902916	CK902916 ip33g03.x	c 647	222.6	9.7	376	1	AI623764	AI623764 ts23a08.x
c 575	224.2	9.8	559	14	DA341077	DA341077 DA341077	c 648	222.6	9.7	514	9	CA414996	CA414996 328801351
c 576	224.2	9.8	602	2	BF030641	BF030641 601560021	c 649	222.6	9.7	540	15	AO415039	AO415039 RPCI-11-2
c 577	224.2	9.8	629	9	CK003458	CK003458 AGENCOURT	c 650	222.6	9.7	556	7	AU152964	AU152964 AU152964
c 578	224.2	9.8	671	19	AG164586	AG164586 Pan trogl	c 651	222.6	9.7	558	4	BU681086	BU681086 AU152964
c 579	224.2	9.8	685	9	CN274874	CN274874 170006000	c 652	222.6	9.7	565	14	DA137218	DA137218 DA137218
c 580	224.2	9.8	694	13	DT892500	DT892500 1474931.M	c 653	222.6	9.7	642	14	DA771719	DA771719 DA771719
c 581	224.2	9.8	723	5	BA642407	BA642407 DKFZp686C	c 654	222.6	9.7	642	9	CN483194	CN483194 hw29d11.y
c 582	224.2	9.8	942	2	BG287829	BG287829 602384191	c 655	222.6	9.7	667	2	BG577280	BG577280 602595473
c 583	224	9.8	463	1	AA563770	AA563770 nk18c10.s	c 656	222.6	9.7	687	5	CA445710	CA445710 UI-H-ED0-
c 584	224	9.8	529	1	AA680243	AA680243 ac86a01.s	c 657	222.6	9.7	765	18	ED014316	ED014316 MUQO_CH25
c 585	224	9.8	553	15	AQ246228	AQ246228 HS_2063_B	c 658	222.6	9.7	768	5	BA327610	BA327610 BX327610
c 586	224	9.8	561	8	CB549179	CB549179 NMPL0003	c 659	222.6	9.7	792	7	AU118852	AU118852 AU118852
c 587	224	9.8	636	18	ED007091	ED007091 MUQO_CH25	c 660	222.6	9.7	818	14	CA871639	CA871639 HESCA_59
c 588	224	9.8	960	5	BA407738	BA407738 BX407738	c 661	222.6	9.7	867	4	BQ232704	BQ232704 AGENCOURT
c 589	224	9.8	963	3	BA1862349	BA1862349 603389135	c 662	222.6	9.7	882	8	CD516256	CD516256 AGENCOURT
c 590	224	9.8	4635	6	CR857664	CR857664 Pongo pyg	c 663	222.6	9.7	917	8	CD558585	CD558585 AGENCOURT
c 591	223.8	9.8	500	15	AQ194178	AQ194178 RPCI11-65	c 664	222.6	9.7	941	4	BQ711583	BQ711583 AGENCOURT
c 592	223.8	9.8	503	14	DB306267	DB306267 DB306267	c 665	222.6	9.7	1601	6	BC015184	BC015184 Homo sapi
c 593	223.8	9.8	665	19	AG107938	AG107938 Pan trogl	c 666	222.4	9.7	507	18	DX563314	DX563314 MUQO_CH25
c 594	223.8	9.8	750	19	AG184338	AG184338 Pan trogl	c 667	222.4	9.7	580	2	BE392138	BE392138 601308007
c 595	223.8	9.8	841	2	BG256457	BG256457 602370182	c 668	222.4	9.7	583	4	BP249631	BP249631 BP249631
c 596	223.6	9.8	310	8	CD518028	CD518028 AGENCOURT	c 669	222.4	9.7	717	19	AG177220	AG177220 Pan trogl
c 597	223.6	9.8	329	8	CD559092	CD559092 AGENCOURT	c 670	222.2	9.7	356	15	B70864	B70864 CIT-HSP-206
c 598	223.6	9.8	450	14	DB459908	DB459908 DB459908	c 671	222.2	9.7	389	7	AW271904	AW271904 xr42e04.x

672	222.2	9.7	498	5	BX645799	BX645799 DKF2p781E	C 745	221.2	9.7	703	2	BG429978	BG429978 602495040
673	222.2	9.7	579	18	DX815132	DX815132 MUGQ_CH25	746	221.2	9.7	1003	3	BM450614	BM450614 AGENCOURT
674	222.2	9.7	611	15	AQ585842	AQ585842 RPTC1-11-4	C 747	221.2	9.7	1077	1	AL524675	AL524675 ALS24675
675	222.2	9.7	656	18	AG059506	AG059506 Pan trogl	748	221.2	9.7	1926	6	BR859560	BR859560 Pongo pyg
676	222	9.7	344	12	DM467706	DM467706 HHAGE0089	749	221	9.7	518	5	BX952917	BX952917 DKF2p781C
677	222	9.7	461	1	AA225406	AA225406 AC2402.r	750	221	9.7	526	10	CR556387	CR556387 DKF2p459P
678	222	9.7	513	3	BI494510	BI494510 df110502.	751	221	9.7	537	15	AZ254548	AZ254548 HSC 00142
679	222	9.7	513	3	BI494510	BI494510 df110501.	C 752	221	9.7	547	14	DA696294	DA696294 DA696294
680	222	9.7	556	4	BU658064	BU658064 cl131f08.z	753	221	9.7	582	14	DA172599	DA172599 DA172599
681	222	9.7	566	14	DA3330565	DA3330565 DA330565	C 754	221	9.7	664	2	BE395137	BE395137 601310764
682	222	9.7	570	4	BO086265	BO086265 ij20604.Y	755	221	9.7	692	18	AG065442	AG065442 Pan trogl
683	222	9.7	571	9	CR822946	CR822946 ij20604.Y	756	221	9.7	748	5	BX501280	BX501280 DKF2p7790
684	222	9.7	623	5	XA489100	XA489100 DKF2p686E	C 757	221	9.7	754	14	CR870603	CR870603 HSC4_47
685	222	9.7	629	19	AG139479	AG139479 Pan trogl	758	221	9.7	785	18	ED013960	ED013960 MUGQ_CH25
686	222	9.7	640	8	CF128614	CF128614 UI-HF-ET0	759	221	9.7	823	16	BZ608535	BZ608535 WHACQ30TR
687	222	9.7	659	19	AG148163	AG148163 Pan trogl	760	221	9.7	827	5	BM414525	BM414525 BX414525
688	222	9.7	694	8	CF124970	CF124970 UI-HF-EL0	C 761	221	9.7	1010	3	BM465334	BM465334 AGENCOURT
689	222	9.7	727	12	EB388118	EB388118 nbj40b07.	C 762	221	9.7	4360	6	CR749270	CR749270 Homo sapi
690	222	9.7	858	15	AQ742838	AQ742838 HS_5482.B	763	221	9.7	5957	6	HSM800277	HSM800277 Homo sapi
691	222	9.7	910	4	BU850247	BU850247 AGENCOURT	C 764	220.8	9.7	365	2	BF751949	BF751949 RC4-BN053
692	222	9.7	915	4	BU149187	BU149187 AGENCOURT	C 765	220.8	9.7	392	1	AI246796	AI246796 qx72a01.x
693	222	9.7	924	2	BG697612	BG697612 602660853	766	220.8	9.7	470	14	DA107367	DA107367 DA107367
694	222	9.7	1035	4	BQ217751	BQ217751 AGENCOURT	C 767	220.8	9.7	547	4	BU600474	BU600474 AGENCOURT
695	221.8	9.7	377	14	DB787367	DB787367 DB787367	768	220.8	9.7	643	19	AG169898	AG169898 Pan trogl
696	221.8	9.7	404	7	AW504224	AW504224 UI-HF-BN0	769	220.8	9.7	669	14	CR866917	CR866917 HSC4_14_
697	221.8	9.7	447	15	AQ242689	AQ242689 HS_2058.B	770	220.8	9.7	678	5	CA413435	CA413435 UI-H-E20-
698	221.8	9.7	452	9	CN275878	CN275878 170006000	771	220.8	9.7	711	18	AG010148	AG010148 Homo sapi
699	221.8	9.7	484	1	AI017251	AI017251 ov03005.x	C 772	220.8	9.7	729	18	DX822465	DX822465 MUGQ_CH25
700	221.8	9.7	554	14	DA105249	DA105249 DA105249	C 773	220.8	9.7	803	16	BZ601931	BZ601931 WHADQ92TR
701	221.8	9.7	554	18	D0638051	D0638051 Ciuiffi-HI	774	220.8	9.7	911	2	BG618992	BG618992 602616510
702	221.8	9.7	578	14	DA933755	DA933755 DA933755	775	220.8	9.7	3143	6	HSM805999	HSM805999 Homo sapi
703	221.8	9.7	586	15	AG196559	AG196559 CIT-HSP-2	776	220.6	9.7	401	1	AI358384	AI358384 qw20d04.x
704	221.8	9.7	637	5	CA428427	CA428427 UI-H-DF0-	C 777	220.6	9.7	416	2	BE062476	BE062476 QV4-BT025
705	221.8	9.7	709	4	BQ181930	BQ181930 UI-H-EU0-	C 778	220.6	9.7	444	4	BU429807	BU429807 UI-HF-BN0
706	221.8	9.7	5940	6	CR627133	CR627133 Homo sapi	C 779	220.6	9.7	454	16	BZ892950	BZ892950 UP_508-19
707	221.6	9.7	432	1	AI003611	AI003611 zF99B04.s	780	220.6	9.7	455	15	AQ167232	AQ167232 HS_3171.A
708	221.6	9.7	447	2	BE147833	BE147833 RC3-HT023	781	220.6	9.7	459	1	AI598003	AI598003 ts05d01.x
709	221.6	9.7	482	4	BU735500	BU735500 UI-E-DW0-	782	220.6	9.7	479	15	AQ225492	AQ225492 HS_2007.B
710	221.6	9.7	562	5	BX481151	BX481151 DKF2p686N	C 783	220.6	9.7	481	8	CB147163	CB147163 K-EST0202
711	221.6	9.7	572	14	DB046356	DB046356 DB046356	C 784	220.6	9.7	553	14	DB104990	DB104990 DKF2p686C
712	221.6	9.7	596	7	AW962298	AW962298 EST374371	785	220.6	9.7	673	1	AL696209	AL696209 Pan trogl
713	221.6	9.7	625	5	CA430874	CA430874 UI-H-FLI-	786	220.6	9.7	675	19	AG176894	AG176894 Pan trogl
714	221.6	9.7	662	18	AG074486	AG074486 Pan trogl	C 787	220.6	9.7	1039	3	BM914519	BM914519 AGENCOURT
715	221.6	9.7	689	19	AG092596	AG092596 Pan trogl	C 788	220.4	9.6	305	3	BM732188	BM732188 ba06f05.x
716	221.6	9.7	748	15	AA226022	AA226022 CITBI-EI-	C 789	220.4	9.6	434	10	CR976138	CR976138 CR976138
717	221.6	9.7	1071	5	BX402079	BX402079 BX402079	C 790	220.4	9.6	548	14	DA101825	DA101825 DA101825
718	221.6	9.7	5440	5	HSW803133	HSW803133 Homo sapi	C 791	220.4	9.6	583	14	DB153528	DB153528 DB153528
719	221.4	9.7	389	5	BA484792	BA484792 DKF2p686H	C 792	220.4	9.6	592	14	DA102631	DA102631 DA102631
720	221.4	9.7	434	1	AA610509	AA610509 np93007.s	C 793	220.4	9.6	593	14	DB161277	DB161277 DB161277
721	221.4	9.7	439	2	BF760919	BF760919 CM0-CS004	C 794	220.4	9.6	599	4	BU676947	BU676947 UI-CF-DU1
722	221.4	9.7	466	4	BU617568	BU617568 UI-H-DF0-	795	220.4	9.6	658	15	AQ393450	AQ393450 CITBI-E1-
723	221.4	9.7	492	5	BX280214	BX280214 BX280214	C 796	220.4	9.6	671	12	EB386691	EB386691 nbj19f09.
724	221.4	9.7	515	15	BH634642	BH634642 TAR-CH5-N	C 797	220.4	9.6	682	19	AG148469	AG148469 Pan trogl
725	221.4	9.7	566	15	AQ274827	AQ274827 RPTC1-1-21	C 798	220.4	9.6	797	15	AY758761	AY758761 RP43-99B9
726	221.4	9.7	575	7	AW574976	AW574976 UI-HF-BN0	799	220.2	9.6	392	2	BG944147	BG944147 ax47a10.x
727	221.4	9.7	622	2	BG476240	BG476240 602521795	C 800	220.2	9.6	411	9	CK816169	CK816169 AGENCOURT
728	221.4	9.7	622	2	BG476396	BG476396 602521910	C 801	220.2	9.6	447	14	DB107238	DB107238 DB107238
729	221.4	9.7	697	15	AQ054805	AQ054805 CIT-HSP-2	C 802	220.2	9.6	458	1	AI733856	AI733856 zo19c03.Y
730	221.4	9.7	698	5	CA431502	CA431502 UI-H-FPT0-	803	220.2	9.6	480	15	AQ415807	AQ415807 RPTC1-11-2
731	221.4	9.7	760	18	DX818101	DX818101 MUGQ_CH25	804	220.2	9.6	500	15	AQ428772	AQ428772 CITBI-E1-
732	221.4	9.7	807	8	CD643859	CD643859 AGENCOURT	C 805	220.2	9.6	508	12	DM525942	DM525942 CYLA_3622
733	221.4	9.7	967	4	BQ707517	BQ707517 AGENCOURT	C 806	220.2	9.6	537	10	CR544001	CR544001 DKF2p470G
734	221.4	9.7	1016	4	BQ707142	BQ707142 Homo sapi	C 807	220.2	9.6	560	4	BQ287748	BQ287748 ik35a09.x
735	221.4	9.7	1400	6	BC016013	BC016013 Homo sapi	C 808	220.2	9.6	675	4	BU664420	BU664420 cl116d07.
736	221.2	9.7	369	1	AA528390	AA528390 nb83902.s	C 809	220.2	9.6	695	9	CN277620	CN277620 170006001
737	221.2	9.7	514	7	AW190505	AW190505 xl63a09.x	C 810	220.2	9.6	830	18	DX415865	DX415865 MUGQ_CH25
738	221.2	9.7	515	15	AQ658589	AQ658589 HS_5318.A	811	220.2	9.6	835	18	CZ457689	CZ457689 MCF745c16
739	221.2	9.7	572	14	DB236781	DB236781 DB236781	C 812	220	9.6	220	11	HG0061	HG0061 yr19f06.s1
740	221.2	9.7	596	15	B95532	B95532 CIT-HSP-216	C 813	220	9.6	441	1	AI732120	AI732120 ac86a01.x
741	221.2	9.7	622	4	BU158469	BU158469 AGENCOURT	814	220	9.6	441	1	AI732180	AI732180 ac86a01.x
742	221.2	9.7	663	18	CZ464233	CZ464233 MCF755c03	815	220	9.6	498	1	AA579566	AA579566 nfi17d09.s
743	221.2	9.7	664	19	AG173858	AG173858 Pan trogl	816	220	9.6	528	1	AA572685	AA572685 nfi18h09.s
744	221.2	9.7	674	18	AG068517	AG068517 Pan trogl	C 817	220	9.6	574	14	DA311459	DA311459 DA311459

818	220	9.6	604	12	EC327580	EC327580	GUTR09168	891	219	9.6	547	15	AQ381396	AQ381396	AQ381396	RPC11-13
819	220	9.6	617	10	CV574570	CV574570	oe26a09.y	892	219	9.6	551	7	AW971243	AW971243	AW971243	EST383332
820	220	9.6	649	14	DB527805	DB527805	DB527805	893	219	9.6	552	15	AQ240624	AQ240624	AQ240624	CIT-HSP-2
C 821	220	9.6	687	10	CR772263	CR772263	DKFPZ468P	894	219	9.6	554	14	DA882749	DA882749	DA882749	DA882749
822	220	9.6	858	18	CZ451896	CZ451896	MCF733b24	895	219	9.6	563	14	DA209580	DA209580	DA209580	DA209580
823	220	9.6	2193	6	CR596399	CR596399	full-1-1eng	896	219	9.6	567	14	DA357821	DA357821	DA357821	DA357821
824	219.8	9.6	359	1	AA304275	AA304275	oq01b11.s	897	219	9.6	572	18	CZ455724	CZ455724	MCF738F08	CZ455724
825	219.8	9.6	436	5	EX957111	EX957111	DKFPZ781A	C 898	219	9.6	576	8	CB141188	CB141188	K-EST0194	CB141188
826	219.8	9.6	466	15	AQ178343	AQ178343	HS-2219.B	C 899	219	9.6	579	14	DA011940	DA011940	DA011940	DA011940
C 827	219.8	9.6	527	14	DB323215	DB323215	DB323215	C 900	219	9.6	581	14	DA387076	DA387076	DA387076	DA387076
828	219.8	9.6	542	1	AI302242	AI302242	q017a08.x	C 901	219	9.6	585	8	CB146604	CB146604	K-EST0202	CB146604
829	219.8	9.6	543	14	DB297838	DB297838	DB297838	C 902	219	9.6	589	8	CB148826	CB148826	K-EST0205	CB148826
C 830	219.8	9.6	543	15	AQ514325	AQ514325	HS-5194.B	903	219	9.6	601	1	AL597814	AL597814	DKFPZ313A	AL597814
C 831	219.8	9.6	579	14	DA302868	DA302868	DA302868	C 904	219	9.6	613	8	CB135613	CB135613	K-EST0187	CB135613
C 832	219.8	9.6	655	18	AG044137	AG044137	Pan trogl	C 905	219	9.6	616	8	CB141203	CB141203	K-EST0194	CB141203
C 833	219.8	9.6	665	2	BG770830	BG770830	602719019	C 906	219	9.6	655	15	AQ538235	AQ538235	RPC11-11-3	AQ538235
C 834	219.8	9.6	666	19	AG183601	AG183601	Pan trogl	C 907	219	9.6	658	5	BA457079	BA457079	BA457079	BA457079
C 835	219.8	9.6	683	9	CN255502	CN255502	170006001	C 908	219	9.6	692	18	AQ081865	AQ081865	Pan trogl	AQ081865
C 836	219.8	9.6	760	16	BZ599728	BZ599728	WHABO11TF	C 909	219	9.6	702	15	AQ026964	AQ026964	CIT-HSP-2	AQ026964
C 837	219.8	9.6	850	14	DA646717	DA646717	DA646717	C 910	219	9.6	733	3	BM454752	BM454752	AGENCOURT	BM454752
C 838	219.8	9.6	852	4	BU164937	BU164937	AGENCOURT	911	219	9.6	735	5	AX506443	AX506443	DKFPZ779B	AX506443
C 839	219.8	9.6	919	2	BG389578	BG389578	602414303	C 912	219	9.6	737	8	CD365151	CD365151	UI-H-FT2	CD365151
840	219.8	9.6	1389	18	BU799614	BU799614	lv01 fp00	913	219	9.6	739	3	BM665558	BM665558	UI-E-CL1	BM665558
C 841	219.6	9.6	316	5	EX479256	EX479256	DKFPZ686M	914	219	9.6	768	14	CX784339	CX784339	HESC3-33	CX784339
C 842	219.6	9.6	318	4	BUS88322	BUS88322	AGENCOURT	C 915	219	9.6	874	14	DA568957	DA568957	DA568957	DA568957
843	219.6	9.6	509	2	BF720424	BF720424	MAF54b05.	C 916	218.8	9.6	329	7	AW504435	AW504435	UI-HF-ENO	AW504435
844	219.6	9.6	538	1	AL041450	AL041450	DKFPZ434E	917	218.8	9.6	371	7	AW191886	AW191886	UI-76f10.x	AW191886
845	219.6	9.6	555	9	CN418755	CN418755	170005326	918	218.8	9.6	492	3	BM993628	BM993628	UI-H-DHO-	BM993628
846	219.6	9.6	558	14	DB120388	DB120388	DB120388	919	218.8	9.6	514	9	CN346214	CN346214	170004177	CN346214
847	219.6	9.6	575	15	AQ269005	AQ269005	RPC111-75	920	218.8	9.6	537	15	AQ390912	AQ390912	CITBI-E1-	AQ390912
C 848	219.6	9.6	602	15	AQ316912	AQ316912	RPC111-96	C 921	218.8	9.6	544	15	B65955	B65955	CIT-HSP-202	B65955
C 849	219.6	9.6	622	7	AW963565	AW963565	EST375638	922	218.8	9.6	569	15	AQ490878	AQ490878	RPC11-11-2	AQ490878
C 850	219.6	9.6	645	19	AG095095	AG095095	Pan trogl	C 923	218.8	9.6	578	4	BU952135	BU952135	in74a13.y	BU952135
C 851	219.6	9.6	647	2	BG283918	BG283918	602407672	924	218.8	9.6	635	16	BZ602392	BZ602392	WHAAR59TR	BZ602392
C 852	219.6	9.6	729	8	CD219732	CD219732	FNPBXH08	925	218.8	9.6	660	3	BM823453	BM823453	K-EST0094	BM823453
C 853	219.6	9.6	807	14	CX786783	CX786783	HESC3-64-	C 926	218.8	9.6	676	4	BU685838	BU685838	UI-CF-DU1	BU685838
854	219.6	9.6	1592	6	BC015057	BC015057	Homo sapi	927	218.8	9.6	732	19	AG183158	AG183158	Pan trogl	AG183158
855	219.4	9.6	374	7	AW500250	AW500250	UI-HF-BNO	C 928	218.8	9.6	762	16	BZ602401	BZ602401	WHAAR60TR	BZ602401
856	219.4	9.6	418	15	AQ078001	AQ078001	CIT-HSP-2	929	218.8	9.6	768	5	CA448487	CA448487	UI-H-E10-	CA448487
857	219.4	9.6	463	5	CA427660	CA427660	UI-H-DF0-	930	218.8	9.6	1129	5	BA404719	BA404719	BA404719	BA404719
C 858	219.4	9.6	467	5	BX955596	BX955596	DKFPZ781H	C 931	218.6	9.6	383	2	BE139267	BE139267	XR68a06.x	BE139267
C 859	219.4	9.6	501	7	BE019467	BE019467	hb56c01.y	C 932	218.6	9.6	384	15	B91064	B91064	CIT-HSP-216	B91064
C 860	219.4	9.6	526	5	CA771412	CA771412	1070912.y	933	218.6	9.6	424	14	DA327318	DA327318	DA327318	DA327318
861	219.4	9.6	529	8	CB133928	CB133928	K-EST0185	C 934	218.6	9.6	457	10	CR774476	CR774476	DKFPZ459G	CR774476
C 862	219.4	9.6	547	7	AW963117	AW963117	EST375190	935	218.6	9.6	466	14	DA222896	DA222896	DA222896	DA222896
C 863	219.4	9.6	570	9	CN358099	CN358099	170005321	C 936	218.6	9.6	483	7	AV737931	AV737931	AV737931	AV737931
C 864	219.4	9.6	573	2	BG654402	BG654402	ib39g11.y	937	218.6	9.6	541	14	DA803349	DA803349	DA803349	DA803349
865	219.4	9.6	577	14	DA219587	DA219587	DA219587	938	218.6	9.6	545	14	DA405230	DA405230	DA405230	DA405230
C 866	219.4	9.6	634	4	BU952192	BU952192	in74h06.y	939	218.6	9.6	547	14	DA625579	DA625579	DA625579	DA625579
867	219.4	9.6	685	5	BX497635	BX497635	DKFPZ779N	940	218.6	9.6	554	14	DA436188	DA436188	DA436188	DA436188
C 868	219.4	9.6	733	16	BZ611870	BZ611870	WHAAR73TR	C 941	218.6	9.6	560	14	DB320019	DB320019	DB320019	DB320019
C 869	219.4	9.6	736	18	AG011968	AG011968	Homo sapi	942	218.6	9.6	604	13	DN994475	DN994475	TC110312	DN994475
C 870	219.4	9.6	757	8	CD511672	CD511672	AGENCOURT	C 943	218.6	9.6	608	7	AV761106	AV761106	AV761106	AV761106
C 871	219.4	9.6	826	16	BZ600333	BZ600333	WHAAR46TR	C 944	218.6	9.6	624	2	BF854308	BF854308	MR2-ENO09	BF854308
C 872	219.4	9.6	854	18	C2448805	C2448805	MCF728p07	945	218.6	9.6	675	18	DX569934	DX569934	MUGQ-CH25	DX569934
873	219.2	9.6	432	1	AI753365	AI753365	cr09b12.x	C 946	218.6	9.6	733	14	DA647137	DA647137	DA647137	DA647137
874	219.2	9.6	539	15	B15409	B15409	345A19.TV C	947	218.6	9.6	759	7	AW976010	AW976010	EST388119	AW976010
C 875	219.2	9.6	548	14	DB272897	DB272897	DB272897	948	218.6	9.6	763	15	AQ528690	AQ528690	RPC11-11-3	AQ528690
876	219.2	9.6	571	18	DX417035	DX417035	MUGQ-CH25	949	218.6	9.6	832	18	CZ445986	CZ445986	MCF725c08	CZ445986
877	219.2	9.6	573	14	DA752064	DA752064	DA752064	950	218.6	9.6	925	18	DU710536	DU710536	aaav01.fpo	DU710536
C 878	219.2	9.6	667	4	BQ183124	BQ183124	UI-H-EU0-	951	218.4	9.6	325	1	AI689019	AI689019	tx10f10.x	AI689019
879	219.2	9.6	717	19	AG099865	AG099865	Pan trogl	952	218.4	9.6	373	7	AW167154	AW167154	xg71f10.x	AW167154
C 880	219.2	9.6	732	8	CD357649	CD357649	AGENCOURT	C 953	218.4	9.6	403	7	AV710482	AV710482	AV710482	AV710482
881	219.2	9.6	893	5	BX431127	BX431127	BX431127	C 954	218.4	9.6	407	1	AA634837	AA634837	ab28f04.x	AA634837
882	219.2	9.6	971	4	BQ720778	BQ720778	AGENCOURT	C 955	218.4	9.6	445	5	CA867048	CA867048	ir56f02.x	CA867048
C 883	219.2	9.6	1820	6	HSW808590	HSW808590	Homo sapi	C 956	218.4	9.6	456	2	BF814327	BF814327	BF814327	BF814327
C 884	219	9.6	320	4	BUE861095	BUE861095	AGENCOURT	C 957	218.4	9.6	473	14	DB016498	DB016498	DB016498	DB016498
C 885	219	9.6	486	15	AQ395336	AQ395336	CITBI-E1-	958	218.4	9.6	517	5	CA868535	CA868535	ir81a07.x	CA868535
C 886	219	9.6	488	8	CB147333	CB147333	K-EST0203	959	218.4	9.6	541	3	BM876405	BM876405	ij58d11.y	BM876405
C 887	219	9.6	497	15	B65584	B65584	CIT-HSP-200	960	218.4	9.6	565	14	DA146497	DA146497	DA146497	DA146497
C 888	219	9.6	511	14	DA643514	DA643514	DA643514	961	218.4	9.6	576	15	AQ546229	AQ546229	CITBI-E1-	AQ546229
C 889	219	9.6	534	14	DA103534	DA103534	DA103534	962	218.4	9.6	695	15	AQ387117	AQ387117	RPC11-11-15	AQ387117
C 890	219	9.6	545	14	DB301440	DB301440	DB301440	963	218.4	9.6	849	18	CZ452536	CZ452536	MCF733p11	CZ452536

964	218.4	9.6	854	15	AQ747026	HS_5538_A	C1037	217.8	9.5	866	6	CR590505	full-leng
965	218.4	9.6	1345	15	AV762220	AV762220	1038	217.8	9.5	894	4	BU189287	AGENCOURT
966	218.2	9.6	317	15	AQ035006	CIT-HSP-2	1039	217.8	9.5	964	16	BZ600930	WHAC184TF
967	218.2	9.6	322	4	BU289333	AGENCOURT	C1040	217.8	9.5	988	8	CR518499	AGENCOURT
968	218.2	9.6	351	2	BF974756	602245404	1041	217.8	9.5	1598	6	CR611538	full-leng
969	218.2	9.6	351	2	BG684452	602636211	1042	217.8	9.5	1973	6	AF289611	Homo sapi
970	218.2	9.6	351	2	BG685274	602637184	C1043	217.6	9.5	360	15	B91708	CIT-HSP-217
971	218.2	9.6	351	2	BG685533	602637504	C1044	217.6	9.5	364	12	DM463025	HHAGE0057
972	218.2	9.6	400	14	DB317789	DB317789	1045	217.6	9.5	445	1	AI570943	to24c10.x
973	218.2	9.6	412	2	BF809041	PM4-CI015	1046	217.6	9.5	466	14	DA222202	DA222202
974	218.2	9.6	425	1	AI471691	l199611.x	1047	217.6	9.5	513	14	DA990685	DA990685
975	218.2	9.6	464	4	BQ775040	UT-H-PHO-	C1048	217.6	9.5	518	1	AL036282	DKFZ0564M
976	218.2	9.6	464	4	BQ775040	UT-H-PHO-	C1049	217.6	9.5	530	10	CR548390	DKFZ0564M
977	218.2	9.6	509	2	BE294700	601173920	1050	217.6	9.5	533	15	AZ517333	RPCI-11-2
978	218.2	9.6	524	14	DB361653	DB361653	C1051	217.6	9.5	534	14	DA622364	DA622364
979	218.2	9.6	530	5	BX512983	BX512983	C1052	217.6	9.5	536	14	DB305212	DB305212
980	218.2	9.6	622	7	AV761862	AV761862	C1053	217.6	9.5	539	14	DA311387	DA311387
981	218.2	9.6	647	5	CA428170	UT-H-PHO-	C1054	217.6	9.5	570	18	CZ457323	MCF740K16
982	218.2	9.6	690	5	BX484572	DKFZ06861	C1055	217.6	9.5	576	14	DB164758	DB164758
983	218.2	9.6	734	8	CB998641	CB998641	C1056	217.6	9.5	602	14	DA334765	DA334765
984	218.2	9.6	746	18	DU840729	MUGQ_CH25	C1057	217.6	9.5	607	7	AV761714	AV761714
985	218.2	9.6	771	4	BQ776208	UT-H-PHO-	1058	217.6	9.5	654	14	DB636697	DB636697
986	218.2	9.6	818	16	BZ598824	WHARF56TR	C1059	217.6	9.5	656	2	BG546809	602574182
987	218.2	9.6	868	4	BQ933326	BQ933326	C1060	217.6	9.5	773	18	CZ450219	MCF730n19
988	218.2	9.6	889	18	CZ446098	CZ446098	1061	217.6	9.5	777	2	BG193279	RST12407
989	218	9.5	407	5	BX480830	DKFZ0686F	1062	217.6	9.5	789	18	CZ460194	MCF748015
990	218	9.5	451	4	BQ181691	UT-H-EUO-	1063	217.6	9.5	841	18	ED010990	MUGQ_CH25
991	218	9.5	497	15	AO569975	HS_5354_A	1064	217.6	9.5	978	8	BM554734	AGENCOURT
992	218	9.5	548	14	DB280345	DB280345	1065	217.6	9.5	1058	3	BM554734	AGENCOURT
993	218	9.5	550	14	DA123991	DA123991	C1066	217.4	9.5	438	15	AQ695967	HS_2160_A
994	218	9.5	550	15	AO202021	AO202021	C1067	217.4	9.5	498	15	AQ487770	RPCI-11-2
995	218	9.5	559	14	DA905220	DA905220	C1068	217.4	9.5	507	15	AQ169564	AQ169564
996	218	9.5	570	9	CN346228	170006000	C1069	217.4	9.5	538	16	BZ610864	WHADJ62TF
997	218	9.5	570	14	DB290617	DB290617	C1070	217.4	9.5	539	8	CD683597	EST117_hu
998	218	9.5	572	14	DA995619	DA995619	C1071	217.4	9.5	552	4	BQ613908	il01a04.x
999	218	9.5	589	14	BU069957	im19409.x	1072	217.4	9.5	560	14	DA398384	DA398384
1000	218	9.5	634	4	BU069957	im19409.x	1073	217.4	9.5	584	15	B56203	CIT-HSP-200
1001	218	9.5	655	19	AG119935	Pan trogl	1074	217.4	9.5	594	14	DA440810	DA440810
1002	218	9.5	675	5	BX954661	DKFZ0781P	1075	217.4	9.5	597	15	AQ112406	CIT-HSP-2
1003	218	9.5	679	19	AG158317	Pan trogl	1076	217.4	9.5	607	15	B01406	CSRL-131c10
1004	218	9.5	696	9	CN417713	170004240	C1077	217.4	9.5	635	9	CK820306	il01a04.x
1005	218	9.5	698	19	AG183302	AG183302	C1078	217.4	9.5	656	19	AG158221	Pan trogl
1006	218	9.5	773	1	AL040663	DKFZ0434N	1079	217.4	9.5	686	2	BE888976	601513907
1007	218	9.5	791	8	CD652079	AGENCOURT	C1080	217.4	9.5	720	18	DX569157	MUGQ_CH25
1008	218	9.5	844	15	AO747032	HS_5538_A	C1081	217.4	9.5	726	19	AG142182	AG142182
1009	218	9.5	853	4	BU177236	AGENCOURT	C1082	217.4	9.5	731	19	AG186212	Pan trogl
1010	218	9.5	3057	6	CR749632	Homo sapi	C1083	217.4	9.5	739	7	AU117276	AU117276
1011	218	9.5	3180	6	HSW800699	HSW800699	C1084	217.4	9.5	739	18	AG031712	Pan trogl
1012	217.8	9.5	373	1	AA828047	Homo sapi	C1085	217.4	9.5	746	4	BU741907	UI-B-EOL-
1013	217.8	9.5	387	1	AI061313	an32907.x	C1086	217.4	9.5	795	2	BG115239	602316160
1014	217.8	9.5	416	2	BG474043	602516603	1087	217.4	9.5	815	18	DU797002	DU797002
1015	217.8	9.5	459	14	DA183796	DA183796	C1088	217.4	9.5	878	19	CR958416	Homo sapi
1016	217.8	9.5	478	15	B67141	CIT-HSP-201	1089	217.4	9.5	937	18	DU799058	fv01 fp00
1017	217.8	9.5	500	14	DB276848	DB276848	1090	217.2	9.5	937	15	B88989	CIT-HSP-216
1018	217.8	9.5	501	5	BX485916	DKFZ0686E	1091	217.2	9.5	347	7	AW768489	AW768489
1019	217.8	9.5	539	3	BM091137	lq22907.y	C1092	217.2	9.5	388	15	AQ125184	HS_2163_B
1020	217.8	9.5	565	7	AW979033	EST391203	1093	217.2	9.5	389	2	BG014630	IL5-GN023
1021	217.8	9.5	572	14	DA707826	DA707826	C1094	217.2	9.5	444	1	AL692023	DKFZ0313J
1022	217.8	9.5	575	14	DB165721	DB165721	1095	217.2	9.5	448	1	AI653515	lq95c08.x
1023	217.8	9.5	582	2	BE252421	BE252421	C1096	217.2	9.5	467	14	DA818169	DA818169
1024	217.8	9.5	588	14	DA755991	DA755991	1097	217.2	9.5	501	10	CR546841	CR546841
1025	217.8	9.5	593	14	DA115493	DA115493	C1098	217.2	9.5	547	3	BM831490	K-EST0105
1026	217.8	9.5	595	5	BX099082	BX099082	C1099	217.2	9.5	554	14	DB350072	DB350072
1027	217.8	9.5	600	14	DA237284	DA237284	C1100	217.2	9.5	572	16	BZ610254	WHADRA3TR
1028	217.8	9.5	627	10	CV571026	oe08a10.y	C1101	217.2	9.5	716	19	AG101592	AG101592
1029	217.8	9.5	667	19	AG150197	Pan trogl	1102	217.2	9.5	724	19	AG166111	Pan trogl
1030	217.8	9.5	677	18	AG068925	AG068925	C1103	217.2	9.5	770	5	BX953657	BX953657
1031	217.8	9.5	715	18	AG010149	Homo sapi	1104	217.2	9.5	783	5	BX093341	EX093341
1032	217.8	9.5	738	2	BF527070	BF527070	C1105	217.2	9.5	800	10	CX164763	HESC2_20
1033	217.8	9.5	751	15	CA745128	HS_5501_A	C1106	217.2	9.5	866	8	CD643421	CD643421
1034	217.8	9.5	761	5	CA430359	UT-H-PHO-	1107	217.2	9.5	972	8	CD359175	AGENCOURT
1035	217.8	9.5	839	4	BQ429058	BQ429058	1108	217.2	9.5	2273	6	CR933698	Homo sapi
	217.8	9.5	864	1	AL574059	AL574059	C1109	217	9.5	357	2	BE139358	BE139358

1110	217	9.5	364	2	BF891585	BF891585 PM3-WT011	CI183	216.6	9.5	589	8	CD236861	FNPADE10
1111	217	9.5	419	15	AQ585850	AQ585850 RPCI-11-4	1184	216.6	9.5	604	14	CX868054	CX868054 HSC4_25
1112	217	9.5	426	15	AQ118480	AQ118480 HS_3011.B	CI185	216.6	9.5	634	7	AU118200	AU118200
1113	217	9.5	433	14	DB539313	DB539313 DB539313	CI186	216.6	9.5	661	2	BG566535	BG566535 602585562
1114	217	9.5	462	3	BM314942	BM314942 i94502.x	CI187	216.6	9.5	703	7	AU121536	AU121536
1115	217	9.5	497	15	B46795	B46795 HS-1066-A1-	CI188	216.6	9.5	753	2	BG535663	BG535663 602563373
1116	217	9.5	502	15	AQ675962	AQ675962 HS_2162.A	CI189	216.6	9.5	757	14	DA197171	DA197171
1117	217	9.5	515	14	DB075662	DB075662 DB075662	CI190	216.6	9.5	791	18	CZ449503	CZ449503 MCF729009
1118	217	9.5	535	5	CA843882	CA843882 i95301.x	CI191	216.6	9.5	808	18	BU835835	BU835835 MUCQ_CH25
1119	217	9.5	538	18	C2454853	C2454853 MCF737C20	CI192	216.6	9.5	819	4	BU565560	BU565560 AGENCOURT
1120	217	9.5	543	4	BU078086	BU078086 i96702.x	CI193	216.4	9.5	387	5	BA485020	BA485020 DKF2p686H
1121	217	9.5	548	5	CA952530	CA952530 i913C05.x	CI194	216.4	9.5	395	15	AQ135782	AQ135782 HS_3059.A
1122	217	9.5	548	14	DA102913	DA102913 DA102913	CI195	216.4	9.5	407	1	AA651639	AA651639 ns99b02.s
1123	217	9.5	558	5	CA949783	CA949783 i925C05.y	CI196	216.4	9.5	412	2	BE062478	BE062478 QV4-BT025
1124	217	9.5	558	14	DB371674	DB371674 DB371674	CI197	216.4	9.5	416	7	AW117740	AW117740 xe5sall.x
1125	217	9.5	564	14	DA327363	DA327363 DA327363	CI198	216.4	9.5	489	3	BI438864	BI438864 IC27f05.x
1126	217	9.5	574	3	BM310737	BM310737 i947h04.y	CI199	216.4	9.5	510	5	CA441782	CA441782 UI-H-ED0-
1127	217	9.5	575	14	DA727243	DA727243 DA727243	CI200	216.4	9.5	519	14	DA083484	DA083484 DA083484
1128	217	9.5	598	4	BQ417003	BQ417003 i940e05.y	CI201	216.4	9.5	520	1	AI859280	AI859280 wm09d08.x
1129	217	9.5	621	4	BQ777011	BQ777011 i142C04.y	CI202	216.4	9.5	543	14	DB281213	DB281213 DB281213
1130	217	9.5	648	4	BQ072917	BQ072917 i136D06.y	CI203	216.4	9.5	551	15	AQ528700	AQ528700 RPCI-11-3
1131	217	9.5	649	4	BQ631821	BQ631821 i122G02.y	CI204	216.4	9.5	554	2	BE207719	BE207719 bb12h08.x
1132	217	9.5	665	18	AG079274	AG079274 Pan trogl	CI205	216.4	9.5	556	14	DB225618	DB225618 DB225618
1133	217	9.5	669	5	BX953552	BX953552 DKF2p781E	CI206	216.4	9.5	561	14	DA856475	DA856475 DA856475
1134	217	9.5	682	4	BQ477320	BQ477320 i984d10.x	CI207	216.4	9.5	563	14	DA757036	DA757036 DA757036
1135	217	9.5	708	15	AQ530231	AQ530231 RPCI-11-3	CI208	216.4	9.5	564	4	BU674339	BU674339 UI-CF-DU0
1136	217	9.5	718	5	CA771728	CA771728 i082a05.x	CI209	216.4	9.5	564	7	DA449860	DA449860 DA449860
1137	217	9.5	719	18	DX383004	DX383004 AGENCOURT	CI210	216.4	9.5	564	14	DA449860	DA449860 DA449860
1138	217	9.5	719	18	ED033615	ED033615 AGENCOURT	CI211	216.4	9.5	571	7	AU153445	AU153445 AU153445
1139	217	9.5	3230	6	CR860761	CR860761 Pongo PV9	CI212	216.4	9.5	572	14	DB188245	DB188245 DB188245
1140	216.8	9.5	317	4	BUS39891	BUS39891 AGENCOURT	CI213	216.4	9.5	576	14	DB11585	DB11585 DB11585
1141	216.8	9.5	318	4	BUS36666	BUS36666 AGENCOURT	CI214	216.4	9.5	580	14	DA127342	DA127342 DA127342
1142	216.8	9.5	346	12	DA646741	DA646741 HHAGE0086	CI215	216.4	9.5	622	1	BM0718317	BM0718317 UI-E-E01-
1143	216.8	9.5	432	1	AI336480	AI336480 Q061d11.x	CI216	216.4	9.5	623	1	AL041749	AL041749 DKF2p434P
1144	216.8	9.5	432	15	B68858	B68858 CIT-HSP-202	CI217	216.4	9.5	648	3	BM991131	BM991131 UI-H-D10-
1145	216.8	9.5	446	15	AQ593034	AQ593034 HS_5457.A	CI218	216.4	9.5	651	3	BM993430	BM993430 UI-H-D10-
1146	216.8	9.5	468	8	CD704230	CD704230 EST20757	CI219	216.4	9.5	672	18	AG086117	AG086117 Pan trogl
1147	216.8	9.5	513	14	DB327136	DB327136 DB327136	CI220	216.4	9.5	697	5	CA446017	CA446017 UI-H-E10-
1148	216.8	9.5	516	15	AQ205872	AQ205872 HS_3239.A	CI221	216.4	9.5	702	5	BA645944	BA645944 DKF2p781F
1149	216.8	9.5	562	14	DB325222	DB325222 DB325222	CI222	216.4	9.5	716	18	AG029392	AG029392 Pan trogl
1150	216.8	9.5	572	14	DB094885	DB094885 DB094885	CI223	216.4	9.5	726	10	CV814284	CV814284 AGENCOURT
1151	216.8	9.5	585	14	DA436716	DA436716 DA436716	CI224	216.4	9.5	793	4	BU616465	BU616465 UI-H-D10-
1152	216.8	9.5	597	7	AV762633	AV762633 AV762633	CI225	216.4	9.5	825	5	BX335093	BX335093 BX335093
1153	216.8	9.5	603	8	CF122917	CF122917 UI-HF-CB0	CI226	216.4	9.5	1085	3	BM555966	BM555966 AGENCOURT
1154	216.8	9.5	631	9	CN479775	CN479775 UI-H-EU0-	CI227	216.4	9.5	1365	6	CR859576	CR859576 Pongo PV9
1155	216.8	9.5	635	8	CF146577	CF146577 UI-HF-CB0	CI228	216.2	9.5	298	15	AQ322208	AQ322208 RPCI11-97
1156	216.8	9.5	662	8	CF146555	CF146555 UI-HF-CB0	CI229	216.2	9.5	308	12	DA416528	DA416528 HHAGE0172
1157	216.8	9.5	683	5	BX644054	BX644054 DKF2p781N	CI230	216.2	9.5	330	9	CN285372	CN285372 170004245
1158	216.8	9.5	692	8	CB958092	CB958092 AGENCOURT	CI231	216.2	9.5	341	3	BM709383	BM709383 UI-E-CQ1-
1159	216.8	9.5	692	15	AG09792	AG09792 Pan trogl	CI232	216.2	9.5	435	7	AW975095	AW975095 EST387201
1160	216.8	9.5	692	19	AG09792	AG09792 Pan trogl	CI233	216.2	9.5	436	14	DB518072	DB518072 DB518072
1161	216.8	9.5	698	3	BM671318	BM671318 UI-E-CQ1-	CI234	216.2	9.5	459	10	CR538925	CR538925 DKF2p4591
1162	216.8	9.5	717	4	BQ228105	BQ228105 AGENCOURT	CI235	216.2	9.5	466	15	AQ590440	AQ590440 HS_5388.A
1163	216.8	9.5	769	15	AQ491214	AQ491214 RPCI-11-2	CI236	216.2	9.5	475	10	CR538946	CR538946 DKF2p459J
1164	216.8	9.5	801	7	AU118632	AU118632 AU118632	CI237	216.2	9.5	498	7	AW996821	AW996821 QV3-BN004
1165	216.8	9.5	829	18	C2461839	C2461839 MCF751g13	CI238	216.2	9.5	500	5	BX643503	BX643503 DKF2p781B
1166	216.8	9.5	847	2	BG574144	BG574144 602596021	CI239	216.2	9.5	505	14	DB313673	DB313673 DB313673
1167	216.8	9.5	884	4	BQ230527	BQ230527 AGENCOURT	CI240	216.2	9.5	529	3	BM857649	BM857649 i969c01.x
1168	216.8	9.5	936	15	AQ749045	AQ749045 HS_5575.A	CI241	216.2	9.5	533	3	BM565593	BM565593 i927e03.x
1169	216.8	9.5	3539	6	HSN801977	AL137304 Homo sapi	CI242	216.2	9.5	534	3	BM505548	BM505548 i913e09.x
1170	216.6	9.5	338	1	AA779783	AA779783 af4q08-s	CI243	216.2	9.5	543	15	AQ799687	AQ799687 HS_5270.A
1171	216.6	9.5	350	18	DU639641	DU639641 Ciuiffi-HI	CI244	216.2	9.5	548	14	DA912844	DA912844 DA912844
1172	216.6	9.5	405	1	AI270476	AI270476 GU88e12.x	CI245	216.2	9.5	549	5	BA493137	BA493137 DKF2p781E
1173	216.6	9.5	426	7	AV701116	AV701116 AV701116	CI246	216.2	9.5	570	14	DB238325	DB238325 DB238325
1174	216.6	9.5	427	12	DAW18436	DAW18436 HHAGE0011	CI247	216.2	9.5	574	15	AQ625117	AQ625117 RPCI11-E1-
1175	216.6	9.5	506	7	AW970877	AW970877 EST382960	CI248	216.2	9.5	578	15	AQ378179	AQ378179 RPCI11-15
1176	216.6	9.5	512	3	BM721982	BM721982 UI-E-E00-	CI249	216.2	9.5	586	4	BQ581762	BQ581762 i112g08.x
1177	216.6	9.5	535	7	AW608051	AW608051 RC3-LT002	CI250	216.2	9.5	588	5	BA488003	BA488003 DKF2p686H
1178	216.6	9.5	538	1	AI377413	AI377413 C35C05.x	CI251	216.2	9.5	615	9	CN263622	CN263622 170004241
1179	216.6	9.5	548	14	DA188705	DA188705 DA188705	CI252	216.2	9.5	622	8	BM510895	BM510895 i944f10.x
1180	216.6	9.5	555	15	AQ267940	AQ267940 RPCI11-72	CI253	216.2	9.5	628	8	CD366995	CD366995 UI-H-F12-
1181	216.6	9.5	564	14	DA955389	DA955389 DA955389	CI254	216.2	9.5	639	15	AZ516496	AZ516496 RPCI11-11
1182	216.6	9.5	570	14	DA676786	DA676786 DA676786	CI255	216.2	9.5	640	4	BU787662	BU787662 i036g06.x

c1256	216.2	9.5	654	18	AG087678	Pan trogl	1329	215.8	9.4	582	14	DA166100
1257	216.2	9.5	681	1	AI561116	tq26609.x	c1330	215.8	9.4	596	2	BF681607
1258	216.2	9.5	682	19	AG165798	Pan trogl	c1331	215.8	9.4	597	2	CF122892
c1259	216.2	9.5	730	5	CA417963	UI-H-FHO-	1332	215.8	9.4	600	5	AX951315
1260	216.2	9.5	739	18	C2463661	MCF754e14	c1333	215.8	9.4	602	9	CK430039
1261	216.2	9.5	760	15	BH732787	BOMHX25TF	1334	215.8	9.4	611	14	DB372780
1262	216.2	9.5	772	5	CA420894	UI-H-FGO-	c1335	215.8	9.4	613	8	CD709038
1263	216.2	9.5	799	18	ED006469	MUGQ_CH25	1336	215.8	9.4	641	18	DX414988
1264	216.2	9.5	802	18	C2453257	MCF734o17	1337	215.8	9.4	652	3	BM999045
c1265	216.2	9.5	811	8	CD511251	AGENCOURT	c1338	215.8	9.4	664	15	AQ343449
c1266	216.2	9.5	826	4	BO221186	AGENCOURT	c1339	215.8	9.4	666	18	AQ084334
c1267	216.2	9.5	851	10	CR788530	KDF2p459C	c1340	215.8	9.4	712	8	CD237852
1268	216.2	9.5	853	15	AQ747124	HS_5339.A	c1341	215.8	9.4	729	19	AG175633
1269	216.2	9.5	895	16	DU797653	fv01 fp01	c1342	215.8	9.4	738	4	BUS61758
c1270	216.2	9.5	1335	6	BC071992	Homo sapi	c1343	215.8	9.4	740	8	CD512317
c1271	216.2	9.5	1808	6	CR858461	Pongo pyg	1344	215.8	9.4	742	8	CF127609
1272	216.2	9.5	2177	15	AQ0839825	h02h08.x	c1345	215.8	9.4	751	4	BQ772858
1273	216.2	9.5	4042	6	HS8801427	Homo sapi	c1346	215.8	9.4	751	4	BUS53245
c1274	216	9.5	303	14	DB270104		c1347	215.8	9.4	781	4	BUS53986
1275	216	9.5	309	1	AA720732		c1348	215.8	9.4	791	4	BUS67220
1276	216	9.5	367	1	AA601986	h088912.s	c1349	215.8	9.4	815	4	BUS30469
1277	216	9.5	376	7	AW503420	UI-HF-BNO	c1350	215.8	9.4	819	4	BUI65654
1278	216	9.5	389	7	BE049229	h02h08.x	c1351	215.8	9.4	838	4	BUS70932
1279	216	9.5	390	15	B79179	CR7978SK-14	c1352	215.8	9.4	839	4	BQ434443
1280	216	9.5	406	1	AL708766	KDF2p686C	c1353	215.8	9.4	964	15	AQ747314
1281	216	9.5	407	1	AI753113	CR05G11.x	c1354	215.8	9.4	968	2	BG499561
c1282	216	9.5	443	9	CN274447		1355	215.8	9.4	3775	6	CR627381
1283	216	9.5	455	1	AA904211	q088e02.s	c1356	215.6	9.4	352	5	AX485943
c1284	216	9.5	486	3	BM993751	UI-H-DHO-	c1357	215.6	9.4	376	7	AV735495
c1285	216	9.5	497	3	EX480039	KDF2p686F	c1358	215.6	9.4	398	15	AQ122574
c1286	216	9.5	521	8	CF130229	UI-HF-ESO	c1359	215.6	9.4	417	5	AX953071
1287	216	9.5	530	14	DB115431		c1360	215.6	9.4	448	15	AQ634562
1288	216	9.5	549	14	DB302670	DA360031	c1361	215.6	9.4	520	2	BE674881
c1289	216	9.5	568	14	DA360031		c1362	215.6	9.4	549	14	DA399272
1290	216	9.5	572	14	DA493918	DA493918	c1363	215.6	9.4	550	10	CR545302
1291	216	9.5	580	14	DB051141		c1364	215.6	9.4	555	14	DA813919
c1292	216	9.5	582	7	AV764329	AV764329	1365	215.6	9.4	563	14	DA083096
c1293	216	9.5	596	15	AQ323805	RPC111-11	c1366	215.6	9.4	564	14	DA547902
c1294	216	9.5	630	15	AQ239777		c1367	215.6	9.4	576	4	BU078633
c1295	216	9.5	657	7	AV701234	AV701234	c1368	215.6	9.4	593	14	DB291492
1296	216	9.5	661	13	CR004361	DR004361	c1369	215.6	9.4	611	15	AQ554801
1297	216	9.5	665	10	CR750680	KDF2p470B	c1370	215.6	9.4	612	9	CK817709
c1298	216	9.5	666	18	DX104772	MUGQ_CH25	c1371	215.6	9.4	620	10	CR750555
c1299	216	9.5	668	18	AG050903	Pan trogl	1372	215.6	9.4	624	7	AW973777
1300	216	9.5	677	18	AG083690	AG083690	c1373	215.6	9.4	637	19	AG160849
1301	216	9.5	684	15	AQ554303	RPC1-11-4	c1374	215.6	9.4	652	18	AG038075
c1302	216	9.5	714	9	CN426512		c1375	215.6	9.4	666	18	DX927459
c1303	216	9.5	714	16	B2611771	BZ611771	c1376	215.6	9.4	692	18	CZ463785
c1304	216	9.5	714	19	AG177522	WHAAO64TR	c1377	215.6	9.4	714	12	DY751486
c1305	216	9.5	746	2	BF675678	602083577	1378	215.6	9.4	720	15	AQ588993
1306	216	9.5	814	5	CA771920	io93a10.x	c1379	215.6	9.4	724	18	AG051798
1307	216	9.5	857	18	CZ464602		c1380	215.6	9.4	758	4	BQ708090
1308	216	9.5	932	4	BQ716029	AGENCOURT	c1381	215.6	9.4	769	15	AQ900076
c1309	216	9.5	967	15	AQ744206	AG744206	c1382	215.6	9.4	799	7	AV755512
1310	216	9.5	1428	15	AZ124375	Cg122.25	c1383	215.6	9.4	803	4	BUS70156
1311	216	9.5	2983	6	BC082988	Homo sapi	1384	215.6	9.4	842	15	AQ748478
c1312	215.8	9.4	319	7	AW021116	df19a04.y	c1385	215.6	9.4	844	16	BZ597986
c1313	215.8	9.4	329	4	BUS65543	AGENCOURT	c1386	215.6	9.4	873	18	CZ447157
1314	215.8	9.4	330	7	AW189068	xx99d12.x	c1387	215.6	9.4	900	4	BQ710544
1315	215.8	9.4	357	14	DB325522	DB325522	1388	215.6	9.4	917	4	BUI53359
c1316	215.8	9.4	421	1	AA631497	np83h03.s	c1389	215.6	9.4	981	3	BM468639
1317	215.8	9.4	427	1	A1338426	qg92a01.x	c1390	215.6	9.4	3005	6	BC111052
1318	215.8	9.4	452	1	AD041894	AL041894	c1391	215.6	9.4	310	4	BUS933518
c1319	215.8	9.4	455	8	CD702830	KDF2p434I	c1392	215.4	9.4	344	4	BUS603545
1320	215.8	9.4	471	4	BQ286229	BQ286229	c1393	215.4	9.4	350	7	AV764259
c1321	215.8	9.4	488	4	BUR45939	AGENCOURT	1394	215.4	9.4	510	15	AQ284649
1322	215.8	9.4	489	2	BG941830	ax17h04.x	1395	215.4	9.4	522	3	BM993791
c1323	215.8	9.4	496	7	AW512196	xx71e04.x	1396	215.4	9.4	523	9	CN479672
1324	215.8	9.4	516	8	CB147131	K-EST0202	1397	215.4	9.4	531	14	DA516868
c1325	215.8	9.4	541	14	DA496138	DA496138	1398	215.4	9.4	537	1	AL120343
1326	215.8	9.4	544	14	DA801008	DA801008	1399	215.4	9.4	539	14	DB341486
c1327	215.8	9.4	557	15	B85764	B85764	1400	215.4	9.4	541	15	AQ529925
1328	215.8	9.4	567	14	DA261198	DA261198	c1401	215.4	9.4	546	7	AW007759

1402	215.4	9.4	548	3	BI792342	BI792342 ic29d04.x	1475	215	9.4	670	18	AG084044	AG084044 Pan trogl
1403	215.4	9.4	557	14	DA224868	DA224868 DA224868	1476	215	9.4	680	5	BM900097	BM900097 UI-H-DIO-
1404	215.4	9.4	558	14	DB180245	DB180245 DB180245	1477	215	9.4	691	3	BM900097	BM900097 UI-H-DIO-
1405	215.4	9.4	562	8	CF124579	CF124579 UI-H-CHO	1478	215	9.4	700	7	AU252665	AU252665 AU252665
1406	215.4	9.4	575	15	AZ521417	AZ521417 RPCI-11-3	1479	215	9.4	703	19	AG141722	AG141722 Pan trogl
1407	215.4	9.4	589	14	DA043357	DA043357 MCF736B22	1480	215	9.4	703	19	AG141722	AG141722 Pan trogl
1408	215.4	9.4	646	18	CZ454140	CZ454140 MCF736B22	1481	215	9.4	703	19	AG141722	AG141722 Pan trogl
1409	215.4	9.4	648	14	DA224349	DA224349 DA224349	1482	215	9.4	703	19	AG141722	AG141722 Pan trogl
1410	215.4	9.4	671	2	BG289041	BG289041 602383913	1483	215	9.4	703	19	AG141722	AG141722 Pan trogl
1411	215.4	9.4	678	18	CZ458639	CZ458639 MCF746116	1484	215	9.4	703	19	AG141722	AG141722 Pan trogl
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1418	215.4	9.4	3238	6	CR861250	CR861250 Pongo pyg	1491	215	9.4	703	19	AG141722	AG141722 Pan trogl
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1420	215.2	9.4	296	4	BQ023663	BQ023663 UI-1-BB0	1493	215	9.4	703	19	AG141722	AG141722 Pan trogl
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1424	215.2	9.4	428	1	A1040051	A1040051 ox24a11.x	1497	215	9.4	703	19	AG141722	AG141722 Pan trogl
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1429	215.2	9.4	515	10	CR546036	CR546036 DKF2p4701							
1430	215.2	9.4	516	2	BE143634	BE143634 MR0-HT016							
1431	215.2	9.4	530	14	DA961685	DA961685 DA961685							
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1460	215	9.4	477	14	DB572332	DB572332 DB572332							
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ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

CONSTRM

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

source

source

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Db 1945 CCTTCCAAATTAATATTTGAA 1965

RESULT 3
LOCUS AY401136 1296 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY401136
VERSION AY401136.1 GI:39757125
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
Gene trios
Science 302 (5652), 1960-1963 (2003)
REFERENCE 2 (bases 1 to 1296)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..1296
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1296
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Query Match 56.5%; Score 1291.2; DB 19; Length 1296;
Best Local Similarity 99.8%; Pred. No. 5.1e-197;
Matches 1293; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 226 ATGTTCTTCGGGGAGAGGGAGCTTCGACTTACACTTTGGTAATAAATTTGCTTCTGTACA 285
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Qy 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCGATATATATCTCAACTCAA 405
Db 121 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCGATATATATCTCAACTCAA 180
Qy 406 GAAGACTGCAATTAATCTCTGCTGTTCAACAAAAAATATCAGGGGACAAAGCATGTAAAC 465
Db 181 GAAGACTGCAATTAATCTCTGCTGTTCAACAAAAAATATCAGGGGACAAAGCATGTAAAC 240
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Db 301 CCNACAGGAAGCTGTCCATTGAACCCAGCAAGGACTTATGAGTTACAGGATAAT 360
Qy 586 ACAGATTTTCCATCTTTGACGAGAAATTTGCCAAGCCAAAGATTACCCCGAGAGATTCT 645
Db 361 ACAGATTTTCCATCTTTGACGAGAAATTTGCCAAGCCAAAGATTACCCCGAGAGATTCT 420
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Qy 706 TCAAGCCCAACCGATATCTCATGGAGAGACACATTTTCTCAGAAAGTTGGATTCCTCAGAT 765
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Qy 766 CACCTGAGAACTATTTTAAGATGATGAACAGTGCAGCTCCCTGCTTATTAAGAA 825
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Qy 826 AAAGGCCATTTCTCAGAGTTTCAAAATTTTCTCTCATCAAGAAATAGCTCATCTGCTGCT 885
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Db 661 GAAATGTGAGTGCCTCCAGCTACGTGGGAGTGTCTCTCCACATACCACTCGGCT 720
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 Db 721 ACTCAAAGCCGCGCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 780
 QY 1006 GAGCCACAGCTGGCCACACAGCTCCACTGTAACCACTGTCTCTCAGGCTCCAGG 1065
 Db 781 CAGCCACAGCTGGCCACACAGCTCCACTGTAACCACTGTCTCTCAGGCTCCAGG 840
 QY 1066 ACCCTCATTTCTACAGTTTTTACAGGCTGGGCTTACACTCAAGCAATGCTTCAACA 1125
 Db 841 ACCCTCATTTCTACAGTTTTTACAGGCTGGGCTTACACTCAAGCAATGCTTCAACA 900
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 Db 1261 GATTATTTGATCAATGGGATCTATGTGGACATCTAA 1296

RESULT 4
 LOCUS AY401137
 DEFINITION Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY401137
 VERSION AY401137.1 GI:39757126
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 1296)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1296)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 Query Match 55.7%; Score 1272.6; DB 19; Length 1296;
 Best Local Similarity 98.8%; Pred. No. 4.9e-194;
 Matches 1281; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 226 ATGTTCTTCGGGGAGAGGGAGCTTGCATTTACATCTTTGGTAAATAATTTGCTTCTCTGACA 285
 Db 1 ATGTTCTTTGGGGAGAGGGAGCTTGCATTTACCTTATCTTTGGTAAATAATTTGCTTCTCTGACA 60
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 QY 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACCAACCACTGCTACTATTTTCTGT 525
 Db 241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACCAACCACTGCTACTATTTTCTGT 300
 QY 526 CCCAAGGAGAGCCCTGCTCAATTTGAAAACAGGAAAGGACTTATGAGTTACAGATTAAT 585
 Db 301 CCCAATGAGGAGCCCTGCTCAATTTGAAAACAGGAAAGGACTTATGAGTTACAGATTAAT 360
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 Db 361 ACAGATTTTCCATCTTTTGACCAAGAAATTTGCCAAGCCCAAGATTTACCCAGGAGATTTCT 420
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 QY 706 TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTTCTCAGAAAGTTGGATCTCAGAT 765
 Db 481 TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTTCTCAGAAAGTTGGATCTCAGAT 540
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RESULT 6
LOCUS   AL525390/c
DEFINITION 1057 bp mRNA linear EST 24-MAR-2004
AL525390 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC011YG07 3-PRIME, mRNA sequence.
AL525390
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31063254.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6656.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC011AD04NP1&c=6656.r.

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    digested with Not I and EcoR V sites of the pCMVSPORT 6
    vector. Library was normalized."

ORIGIN
Query Match 40.2%; Score 917.6; DB 1; Length 1057;
Best Local Similarity 96.4%; Pred. No. 4e-137;
Matches 954; Conservative 13; Mismatches 19; Indels 4; Gaps 3;

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DB      987  KGGAKTCTCCACTATGAATAAAMYR-CTTCTCTGGGARG--TAGGAGGCCAGTCCAGGCA 931
QY      1322  GTTCTCTCCAGGCGAGTGTCCAGAAAATCAGTACGCCCTTCCATTTGAAAATAGCTTC 1381
DB      930  GTTCCTCCAGGCGAGTGTCCAGAAAATCAGAACGCCCTCCATTTGAAAATAGCTTC 871
QY      1382  TTATCGGGTCCCTGCTCTTTGGTGTCCTGTCTCTGGTGATAGGCCCTCGCTCTCGGGTA 1441
DB      870  TTATCGGGTCCCTGCTCTTTGGTGTCCTGTCTCTGGTGATAGGCCCTCGCTCTCGGGTA 811
QY      1442  GAATCTCTCGGAATCACTCCGAGGAAGAGTTACTCAAGCTGGATTATTCATCAATG 1501
DB      810  GAATCTCTCGGAATCACTCCGAGGAAGAGTTACTCAAGCTGGATTATTCATCAATG 751
QY      1502  GGATCTATCGGACATCTAAGGATGAACCTCGGTGCTCTTAAATTCATTTAGTAACGAG 1561
DB      750  GGATCTATCGGACATCTAAGGATGAACCTCGGTGCTCTTAAATTCATTTAGTAACGAG 691
QY      1562  AGCCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTGTATTTGAA 1621

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Db      690  AGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTGTATTTTGA 631
QY      1622  GACAGGAAATGCCCCCTCTGCTTTCC-TTTTTTTTTTGGAGACAGAGTCTGCTCTG 1680
DB      630  GACAGGAAATGCCCCCTCTGCTTTCTGCTTTCTTTTGGAGACAGAGTCTGCTCTG 571
QY      1681  TTGCCAGGCTGAGTGCAGTACGACCATCTCGGCTCTCACGCAACCTCGTCTCTGG 1740
DB      570  TTGCCAGGCTGAGTGCAGTACGACCATCTCGGCTCTCACGCAACCTCGTCTCTGG 511
QY      1741  GTTCAAGCGATTCTCTGCTCCTCAGCCTCCTAAAGTATCTGGGATTAACAGGCATG 1800
DB      510  GTTCAAGCGATTCTCTGCTCCTCAGCCTCCTAAAGTATCTGGGATTAACAGGCATG 451
QY      1801  ACACCTGGGCGATTTTGTATTTTATAGTAGAGACGGGTTTACCATGTTGGTCAGG 1860
DB      450  ACACCTGGGCGATTTTGTATTTTATAGTAGAGACGGGTTTACCATGTTGGTCAGG 391
QY      1861  GTCTCAAACTCCTGACCTAGTATGATCCACCTCTCGGCTCCCAAGTCTGGGATTA 1920
DB      390  GTCTCAAACTCCTGACCTAGTATGATCCACCTCTCGGCTCCCAAGTCTGGGATTA 331
QY      1921  GGCATGAGCCACACAGCTGCGCCCTCTCTGTTTATGTTTGTGTTTGTGAGAGGA 1980
DB      330  GGCATGAGCCACACAGCTGCGCCCTCTCTGTTTATGTTTGTGTTTGTGAGAGGA 271
QY      1981  AGTGGGAACCAAAATAGTAAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAA 2040
DB      270  AGTGGGAACCAAAATAGTAAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAA 211
QY      2041  AGCTCTATGTAAAGTAAATAGTAAATTTGCGATATTAATTTCAAAATTTCAAT 2100
DB      210  AGCTCTATGTAAAGTAAATAGTAAATTTGCGATATTAATTTCAAAATTTCAAT 151
QY      2101  TATGCAAGAAACAGGTTAGGACATCTAGTTCCTCAATTCATTTCATCTTTGTT 2160
DB      150  TATGCAAGAAACAGGTTAGGACATCTAGTTCCTCAATTCATTTCATCTTTGTT 91
QY      2161  TAAATCAACTGTTTATCAATTTCTAAATGATTTGCTTTTCTTTTATATGATTC 2220
DB      90  TAAATCAACTGTTTATCAATTTCTAAATGATTTGCTTTTCTTTTATATGATTC 31
QY      2221  TTAATACTTATTCAGATGATTTCTCTTC 2250
DB      30  TTAACACTYATTCAGATGATTTCTCTTC 1

RESULT 7
BX350141/c
LOCUS   BX350141
DEFINITION 884 bp mRNA linear EST 08-APR-2004
BX350141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0DI054YH07 3-PRIME, mRNA sequence.
BX350141
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Carnivora; Insectivora; Marsupialia; Eutheria; Hominidae; Homo.
TITLE 1 (bases 1 to 884)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

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6656.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA1023ZA03_CS02129_1&c=6656.r

FEATURES		Location/Qualifiers	
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0D1054YH07"		
	/tissue_type="PLACENTA COT 25-NORMALIZED"		
		/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
		/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
Query Match		36.2%;	Score 826.6; DB 5; Length 884;
Best Local Similarity		98.5%;	Pred. No. 1.6e-122;
Matches	865; Conservative	0; Mismatches	10; Indels 3; Gaps 3;
QY	596	CATCTTTGACCAAGAAATTTGCCAAGCCAGAGTTACCCAGGAAGATCTCTCTTACATG	655
DB	884	CTTCTTTGGACCAAGAAATTTGGCAAGCCAGAGTTA-CCGAGGAAGATTTCTCTTACATG	826
QY	656	GCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACACAGATTATTCAGAGCCCA	715
DB	825	G-CAATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACACAGATTATTCAGAGCCCA	767
QY	716	CGATATCTCATGGAGAGACACACTTTCAGAAAGTTTGGATCTCTAGATCACTGGAGA	775
DB	766	CCAATATCTCATGGAGAGACACAC-TTCTCAGAAAGTTTGAATCCCTCAGATCACTGGAGA	708
QY	776	AACATTTAAGATGGAATGAAGCAAGTCCCACTCTTGTCTTATAAGGAAAAAGGCCATT	835
DB	707	AACATTTAAGATGGAATGAAGCAAGTCCCACTCTTGTCTTATAGGAAAAAGGCCATT	648
QY	836	CTCAGAGTTTCAAAATTTTCTCTGATCAAGAAATAGTCTCATCTGCTGCCTGAAAAATGTGA	895
DB	647	CTCAGAGTTTCAAAATTTTCTCTGATCAAGAAATAGTCTCATCTGCTGCCTGAAAAATGTGA	588
QY	896	GTGCGCTCCCACTACGGTGGCAGTTGCTTCTCCACATACCACTCCGGTACTCCAAAGC	955
DB	587	GTGCGCTCCCACTACGGTGGCAGTTGCTTCTCCACATACCACTCCGGTACTCCAAAGC	528
QY	956	CGCCACCTTTCTACCCCAATGCTTTCAGTGACACCTTCTGGGAGCTTCCAGCCACAGC	1015
DB	527	CGCCACCTTTCTACCCCAATGCTTTCAGTGACACCTTCTGGGAGCTTCCAGCCACAGC	468
QY	1016	TGGCCACACAGCTCCCACTGTAAACACCTGTCTCAGCTTCCCAAGCCCTCATTT	1075
DB	467	TGGCCACACAGCTCCCACTGTAAACACCTGTCTCAGCTTCCCAAGCCCTCATTT	408
QY	1076	CTACAGTTTTCACAGGGCTGGCGGTACACTCCAAAGCAATGGGTACAAACAGCAGTTCTCTGA	1135
DB	407	CTACAGTTTTCACAGGGCTGGCGGTACACTCCAAAGCAATGGGTACAAACAGCAGTTCTCTGA	348
QY	1136	CTACCACTTTTCAGGCACTTACGGAGCTCGAAAGGAGCTTTAGAAACCATACCGTTTACAG	1195
DB	347	CTACCACTTTTCAGGCACTTACGGAGCTCGAAAGGAGCTTTAGAAACCATACCGTTTACAG	288
QY	1196	AAATCTCCAACTTAACTTTTGAACACAGGGAATGTGTATACCTTCTGCACTTTCATGT	1255
DB	287	AAATCTCCAACTTAACTTTTGAACACAGGGAATGTGTATACCTTCTGCACTTTCATGT	228
QY	1256	CAAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGTAGGAGGCCAGTTC	1315
DB	227	CAAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGTAGGAGGCCAGTTC	168
QY	1316	CAGGCACTTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCTTCCATTTGAAAAAT	1375
DB	167	CAGGCACTTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCTTCCATTTGAAAAAT	108

Qy	1376	GGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGGTGTATAGGCTCTGCTCTCC	1435
Db	107	GGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGGTGTATAGGCTCTGCTCTCC	48
Qy	1436	TGGGTAGAATCCTTTTCGGAATCACTCCGAGGAAACGT	1473
Db	47	TGGGTAGAATCCTCTCGGAATCACTCCGAGGAAACGT	10
RESULT 8			
BQ424639			
LOCUS	BQ424639	853 bp	mRNA linear EST 23-MAY-2002
DEFINITION	AGENCOURT_7896936 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6159709		
ACCESSION	BQ424639		
VERSION	BQ424639.1 GI:21119954		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 853)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13509 row: d column: 14 High quality sequence stop: 735.		
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source	1. .853 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6159709" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_72" /note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."		
ORIGIN	Query Match 34.9%; Score 797.2; DB 4; Length 853; Best Local Similarity 99.4%; Pred. No. 8.3e-118; Matches 821; Conservative 0; Mismatches 3; Indels 2; Gaps 2;		
Qy	441	CATATCAGGGGCAAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTAGACA	500
Db	16	CATTGCAAGGGGCAAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTAGACA	75
Qy	501	ACCCAACTGCTACTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCAAA	560
Db	76	ACCCAACTGCTACTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCAAA	135
Qy	561	AGCACTTATGAGTTACAGGATAATTACAGATTTTCCATTTTGACCAAGAAATTTGCCAAG	620
Db	136	AGCACTTATGAGTTACAGGATAATTACAGATTTTCCATTTTGACCAAGAAATTTGCCAAG	195
Qy	621	CBAAGAGTTACCCCGAGGAAGATTTCTCTTACATGGCCAATTTTCAAGCAGTCACTCC	680
Db	196	CBAAGAGTTACCCCGAGGAAGATTTCTCTTACATGGCCAATTTTCAAGCAGTCACTCC	255

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QY 681 CCTAGCCCATCATCACAGATTATTTCAAAGCCACCGATATCTCATGGAGAGACACACT 740
Db 256 CTAGCCCATCATCACAGATTATTTCAAAGCCACCGATATCTCATGGAGAGACACT 315

QY 741 TTCTCAGAAGTTTGATCCTCAGATCACCTGGAGAAACTATTAAAGATGATGAAGCAAG 800
Db 316 TTCTCAGAAGTTTGATCCTCAGATCACCTGGAGAAACTATTAAAGATGATGAAGCAAG 375

QY 801 TGGCCAGCTCTTGTCTTATAAGGAAAAGGCCATTTCTCAGAGTTCAAAATTTCTCTCTGA 860
Db 376 TGGCCAGCTCTTGTCTTATAAGGAAAAGGCCATTTCTCAGAGTTCAAAATTTCTCTCTGA 435

QY 861 TCAAGAAATAGCTCATCTGCTGCTGAAATGTAGTGGCTCCAGCTACGCTGACGTCAGT 920
Db 436 TCAAGAAATAGCTCATCTGCTGCTGAAATGTAGTGGCTCCAGCTACGCTGACGTCAGT 495

QY 921 TGTCTTCTCACATACACCTCGGCTACTCCAAAGCCCGCACCTCTTACCCACCAATGC 980
Db 496 TGTCTTCTCACATACACCTCGGCTACTCCAAAGCCCGCACCTCTTACCCACCAATGC 555

QY 981 TTCAGTGACACTTCTGGGACTTCCAGCCACAGCTGGCCACACAGCTTCCACCTGTAAAC 1040
Db 556 TTCAGTGACACTTCTGGGACTTCCAGCCACAGCTGGCCACACAGCTTCCACCTGTAAAC 615

QY 1041 CACTGTCACTTCTAGCCTCCACAGACCTCATTTCTACAGTTTTTACAGGGCTGGCG 1100
Db 616 CACTGTCACTTCTAGCCTCCACAGACCTCATTTCTACAGTTTTTACAGGGCTGGCG 675

QY 1101 TACACTCCAAGCAATGGCTTACAAACAGCAGCTCTGACTACACCTTTTCAGGCACTACGGA 1160
Db 676 TACACTCCAAGCAATGGCTTACAAACAGCAGCTCTGACTACACCTTTTCAGGCACTACGGA 735

QY 1161 CTCGAAGGACGCTTAGAAACCATACCGTTTACAGAAATCTCCAACTTAACCTTTGAACAC 1220
Db 736 CTCGAAGGACGCTTAGAAACCATACCGTTTACAGAAATCTCCCACTTAACCTTTGAACAC 795

QY 1221 A-GGGAAATGTATAA-CCCTACTGACCTTTCTATGTCAAAATGTGG 1264
Db 796 AGGGAAATGTATAAACCCCTACTGACCTTTCTATGTCAAAATGTGG 841

RESULT 9
AL549886 1036 bp mRNA linear EST 25-MAR-2004
LOCUS AL549886 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI054YH07 5-PRIME, mRNA sequence.
ACCESSION AL549886
VERSION 1
KEYWORDS Full-length cDNA libraries and normalization
SOURCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1036)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31271704.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6656.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI054CD04QP1&c=6656.r.
location/Qualifiers
1. .1036
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FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DI054YH07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 31.5%; Score 719.8; DB 1; Length 1036;
Best Local Similarity 87.0%; Pred. No. 2e-105;
Matches 853; Conservative 32; Mismatches 75; Indels 21; Gaps 9;

QY 1 GCGGAGCATCCGCTGCGGTCTCTCGCGAGACCCCGCGCGGATTCGCGGTCCTTCCCGC 60
Db 22 GCGGAGATCCGCTGCGGTCTCTCGCGAGACCCCGCGCGGATTCGCGGTCCTTCCCGC 81

QY 61 GCGCGGACAGAGCTGTCTCGCACCTGTGATGGAGCGGGCGCGGGTCTCTCGAC 120
Db 82 GCGCGGACAGAGCTGTCTCGCACCTGTGATGGAGCGGGCGCGGGTCTCTCGAC 141

QY 121 GCCAGAGAGAAATCTCATCATCTGTGCGAGCCTTTTAA-AGCAAACTAAGACAGAGGA 179
Db 142 GCCAGAGAGAAATCTCATCATCTGTGCGAGCCTTTTAAAGCAAACTAAGACAGAGGA 201

QY 180 GGATTATCTTGAACCTTTGAAGACCAAACTAAACTGAAATTTAAATTTTCTTCGGGG 239
Db 202 GGATTATCTTGAACCTTTGAAGACCAAACTAAACTGAAATTTTAAANGNCTTCGGGG 261

QY 240 AGAAGGAGCTTGAACCTTTTGAATTAATTTGCTTCTCTGACACTAAAGGCTGTCTGC 299
Db 262 CGNCGGCGGCTTGAACCTTTTGAATTAATTTGCTTCTCTGACACTAAAGGCTGTCTGC 321

QY 300 ----TAGTCAGAAATGCTCTCAAAAAGAGTCTAGA-----AGATGTTGTCAATGACAT 347
Db 322 SCMCCTCTCCCTTCTCCCTCAACCCACSMCYCMCCCCCCCCCCCCCCCCCCCCCCCC 381

QY 348 CCAGTCATCTCTTTTAAAGGGAATCAGA-GGCAATGAGCCGCTATATACCTCAACTCAAG 406
Db 382 CCCCCCTCTCTTTTAAAGGGAATCAGACGCAATGAGCCGCTATATACCTCAACTCAAG 441

QY 407 AAGACTGCAATTAATTTCTGCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAACT 466
Db 442 AAGACTGCAATTAATTTCTGCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAACT 501

QY 467 TGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACTATTTTCTGTC 526
Db 502 TGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACTATTTTCTGTC 561

QY 527 CCAACGAGGAGCTGTCCATTGAAACCAAGCAAGCAAGTAACTTACAGTACAGGATAATTA 586
Db 562 CCAACGAGGAGCTGTCCATTGAAACCAAGCAAGCAAGTAACTTACAGTACAGGATAATTA 621

QY 587 CAGATTTTCCATCTTTGACCAAGAAATTTGCAAGCAAGTAACTTACAGTACAGGATAATTA 646
Db 622 CAGATTTTCCATCTTTGACCAAGAAATTTGCAAGCAAGTAACTTACAGTACAGGATAATTA 681

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Db 682 TCTTACATGCGCAATTTTCAACAGCAGTCACTCCCTAGCCCAATCATCACAGATTAAT 741

QY 707 CAAAGCCACCGATATCTCATGAGAGACACACTTTTCTCAGAGTTTGGATCCTCAGATC 766
Db 742 CAAAGCCACCGATATCTCATGAGAGACACACTTTTCTCAGAGTTTGGATCCTCAGATC 801

QY 767 ACCTGAGAGAACTATTATTAGATGATGAAGCAAGTCCAGCTCTCTTGTATTAAGGAAA 826
Db 802 ACCTGAGAGAACTATTATTAGATGATGAAGCAAGTCCAGCTCTCTTGTATTAAGG-AA 860

QY 827 AAGGCCAATCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTG 886
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Db      861 AAGGCCATCTCAGAGTTACAAATTTT-CTCTGATCAAG-AATAGCTCATCTGTCGCTG 918
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Db      919 AWAATGTGAGT--CSCTCCAGTACGGTGGCAGTGTCTTTC--ACATACAACTCGGCTA 974
Qy      947 CTCCAAAGCCGCCACCTTC 967
Db      975 CWCAAAGCCGCCACCTCTT 995

RESULT 10
LOCUS   CF593691
DEFINITION AGENCOURT 15623843 NIH_MGC 147 Homo sapiens cDNA clone
IMAGE:30531452 5', mRNA sequence.
ACCESSION CF593691
VERSION   CF593691.1 GI:36347497
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-rcmail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM622. row: d column: 21
High quality sequence stop: 677.

FEATURES
source
1..839
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30531452"
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/clone_lib="NIH_MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamHI; Oligo-dT primed using primer
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insert size 2.3 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN
Query Match 31.4%; Score 718.2; DB 8; Length 839;
Best Local Similarity 98.8%; Pred. No. 3.8e-105;
Matches 734; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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Db 69 GCGAGCATCCGTCGGTCTCGCGAGACCCCGCGGATTCGGTCTCCCGC 128
Qy 61 GCGCGGACAGAGCTCTCTCGCACCTGGATGTCAGCGGGCGCGGGTCTCTCGAC 120

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Db      129 GGCGCGACAGAGCTCTCTCGCACCTGATGCGAGCGGGCGCGGGTCTCTCGAC 188
Qy      121 GCAGAGAGAAATCTCATCATCTGTGCGAGCTTTCTTAAAGCAAATAAGACGAGGAG 180
Db      189 GCAGAGAGAAATCTCATCATCTGTGCGAGCTTTCTTAAAGCAAATAAGACGAGGAG 248
Qy      181 GATTATCTTGTGACCTTTGAAGACCAAACTAAACTGAATTTAAATTTGTTCTTCGGGGA 240
Db      249 GATTATCTTGTGACCTTTGAAGACCAAACTAAACTGAATTTAAATTTGTTCTTCGGGGA 308
Qy      241 GAAGGAGCTTGTGACTTTACACTTTTGGTAAATAATTTGTTCTTCTGACACTAAGGCTCTGTCT 300
Db      309 GAAGGAGCTTGTGACTTTTACACTTTTGGTAAATAATTTGTTCTTCTGACACTAAGGCTCTGTCT 368
Qy      301 AGTCAGAAATTCCTCAAAAAGAGCTCTAGAAGATGTTGTCTTATGACATCCAGTCACTCTT 360
Db      369 AGTCAGAAATTCCTCAAAAAGAGCTCTAGAAGATGTTGTCTTATGACATCCAGTCACTCTT 428
Qy      361 TCTAAGGGAATCAGAGGCAATGAGCCGCTATATATCTTCAACTCAAGAGACTGCAATTAAT 420
Db      429 TCTAAGGGAATCAGAGGCAATGAGCCGCTATATATCTTCAACTCAAGAGACTGCAATTAAT 488
Qy      421 TCTTGTCTGTTCAACAAAACATATCAGGGGACAAAGCATGTAACTTTGATGATCTTCGAC 480
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Qy      481 ACTCGAAAAACAGCTAGACAAACCACTGCTACTATTTTCTGTCCTCCCAAGGAGAGCC 540
Db      549 ACTCGAAAAACAGCTAGACAAACCACTGCTACTATTTTCTGTCCTCCCAAGGAGAGCC 608
Qy      541 TGTCCATTGAAACAGCAAAAGAGCTTATGAGTTACAGGATAATTAAGATTTTCCATCT 600
Db      609 TGTCCATTGAAACAGCAAAAGAGCTTATGAGTTACAGGATAATTAAGATTTTCCATCT 668
Qy      601 TTGACCAAAATTTGCCAAGCCAGAGTTATCCCGAGAGATTTCTCTTACATGGCCAA 660
Db      669 TTGACCAAAATTTGCCAAGCCAGAGTTATCCCGAGAGATTTCTCTTACATGGGCCA 728
Qy      661 TTTTTCACAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATCAAGCCCAACCGAT 720
Db      729 TTTTTCACAGCAGTCACTCCCTTAGCCCATCATCACAGATTAATCAAGCCCAACCGAT 788
Qy      721 ATCTCATGG-AGAGACACACTTT 742
Db      789 ATCTCATGGAAGAGACACACTTT 811

RESULT 11
LOCUS   DA581021
DEFINITION DA581021 HLJUNG1 Homo sapiens cDNA clone HLJUNG1000111 5', mRNA
sequence.
ACCESSION DA581021
VERSION   DA581021.1 GI:80549400
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 785)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagaatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
JOURNAL  PUBMED
16344560

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LOCUS	BM480136		
DEFINITION	AGENCOURT_6468228 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574073	728 bp	mRNA linear EST 05-FEB-2002
ACCESSION	5', mRNA sequence.		
VERSION	BM480136		
KEYWORDS	EST.		
SOURCE	BM480136.1 GI:18529178		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;		
JOURNAL	Cataarrhini; Homnidae; Homo.		
COMMENT	1 (bases 1 to 728)		
	NIH-MGC http://mgs.nci.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: ggapbs-i@mail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM12322 Row: C Column: 02		
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Best Local Similarity	99.9%; Pred. No. 1.6e-102;		
Matches 713; Conservative	0; Mismatches 0; Indels 1; Gaps 1;		
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Qy	1691	TGGAGTCAGTAGCAGATCTCGGCTCTACCGCACTCCGCTCTCTCTGGGTTCAACGGA	1750
Db	121	TGGAGTCAGTAGCAGATCTCGGCTCTACCGCACTCCGCTCTCTCTGGGTTCAACGGA	180
Qy	1751	TTCTCTCGCTCAGCCCTCCCTAAGTATCTGGATTACAGGATGTGCCACACACCTCGGT	1810
Db	181	TTCTCTCGCTCAGCCCTCCCTAAGTATCTGGATTACAGGATGTGCCACACACCTCGGT	240
Qy	1811	GAATTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCAAAC	1870

Db 241 GATTTTGTATTTTAGTAGAGACGGGTTTCCACATGTTGTCAGGCTGGTCTCAAACT 300
QY 1871 CTTGACCTAGTATCCACCTCTCGGCTCCCAAGTGTGGGATTACAGGATGAGCC 1930
Db 301 CTTGACCTAGTATCCACCTCTCGGCTCCCAAGTGTGGGATTACAGGATGAGCC 360
QY 1931 ACCACAGTGGCCCTCTCTGTTTATGTTGTTTGGTTTGGAGAGGAATGAAGTGGGAAC 1990
Db 361 ACCACAGTGGCCCTCTCTGTTTATGTTTGGTTTGGAGAGGAATGAAGTGGGAAC 420
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QY 2051 AAAGTAAATAAGTAAATTTGCCATATAAATTTCAAAATTCAACTGGCTTTTATGCAAGA 2110
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QY 2111 AACAGTTTAGGACATCTAGGTTTCCAAATTCATTCACATCTTGGTTCCAGATAAAATCAAC 2170
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RESULT 13

DR004375

LOCUS

DEFINITION DR004375 717 bp mRNA linear EST 17-MAY-2005
TC105495 Human placenta, large insert, pcMV expression library Homo sapiens cDNA clone TC105495 5', similar to Homo sapiens, hypothetical protein FLJ10298, clone MGC:26021 IMAGE:4824116, complete cds, mRNA sequence.

ACCESSION

DR004375

DR004375.1 GI:66264248

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

Catarrhini; Homnidae; Homo.

1 (bases 1 to 717)

Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,

Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly from

cDNA libraries optimized for large and rare transcripts

Unpublished (2005)

Contact: Kovacs, KF

High Throughput cDNA Cloning

Origene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188

Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length

cloning project at Origene Technologies, Inc.

Please contact Origene for access.

Origene Technologies, Inc.

6 Taft Ct. Suite 100,

Rockville, MD 20850

Tel: (301) 340-3188

http://www.origene.com

Seq primer: pcMV6 5prime forward vector primer, Origene

Technologies Inc.

Location/Qualifiers

1..717

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/note="Vector: pcMV6-XL4; Site 1: EcoRI; Site 2: XhoI/Sall

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transcription optimized for large and GC rich mRNA

transcripts, cDNA size selection, optimized ligation for

large inserts into mammalian expression vector, random

clones selected for end sequence verification of

full-length genes"

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 2.8e-102;
Matches 701; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GGGCGGACAGAGCTGCTCGCACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC 120

Db 75 GGGCGGACAGAGCTGCTCGCACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC 134

QY 121 GCCAGAGAGAAATCTCATCATCTGTGCAGCTTCTTAAAGCAAACTAAGACGAGGGAG 180

Db 135 GCCAGAGAGAAATCTCATCATCTGTGCAGCTTCTTAAAGCAAACTAAGACGAGGGAG 194

QY 181 GATTATCTTGTACCTTTGAAGACCAAACTAAACTTAAATTTTAAATGTTCTTCGGGGGA 240

Db 195 GATTATCTTGTACCTTTGAAGACCAAACTAAACTTAAATTTTAAATGTTCTTCGGGGGA 254

QY 241 GAAGGAGCTGTGACTTACACTTTGGTAATAATTTGCTTCCTGACACCTAAGAGCTGTGCT 300

Db 255 GAAGGAGCTGTGACTTACACTTTGGTAATAATTTGCTTCCTGACACCTAAGAGCTGTGCT 314

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QY 601 TTGACCAAGAAATTTGCCAAGCCAAAGAGTTATCCCGAGGAAGATTTCTTTATACGGCCAA 660

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RESULT 14

BM480099

LOCUS

DEFINITION

BM480099

729 bp mRNA linear

EST 05-FEB-2002

AGENCOUNT_6468229 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574049

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5', mRNA sequence.
ACCESSION BM480099
VERSION BM480099.1 GI:18529141
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12322 row: b column: 02
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            Technologies. Note: this is a NIH_MGC Library."
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Query Match 30.7%; Score 700.4; DB 3; Length 729;
Best Local Similarity 99.7%; Pred. No. 2.8e-102;
Matches 712; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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VERSION BF312571.1 GI:11260389
KEYWORDS EST.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1017 row: m column: 12
High quality sequence stop: 756.
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            California, Berkeley) using ZAP-cDNA synthesis kit
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            Note: this is a NIH_MGC Library."
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4 GCGGAGCATCCGCTCGGTCCTCGCGAGACCCCGCGGATTCGCGGTCCTTCGCCG 63
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Db |||||
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Job time : 25182 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 20, 2007, 00:48:04 ; Search time 18533 Seconds
(without alignments)
1607.449 Million cell updates/sec

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Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15136766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Database : GenEmbl:*
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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2211	100.0	2284	2	BD378361 SECRETED
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7	2211	100.0	2284	2	DD249590
8	2211	100.0	2284	2	AR429104
9	2211	100.0	2284	2	AR534995
10	2211	100.0	2284	2	AR691142
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19	2211	100.0	2284	2	AR809329
20	2211	100.0	2284	2	AR810275
21	2211	100.0	2284	2	AR834082
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35	2210	99.9	2333	5	BC032998
36	2072	93.7	2015	2	BD227259
37	2039	92.2	2345	5	AB060888
38	2022	91.5	2221	2	AX876122
39	2022	91.5	2221	2	BD155963
40	2022	91.5	2221	2	BD447120
41	2022	91.5	2221	2	CQ776818
42	2022	91.5	2221	5	AK001160
43	1573.5	71.2	144000	5	AC007621
44	1573.5	71.2	188344	12	AC131617
45	1239	56.0	1907	14	BC120333
46	1216	55.0	735	2	CQ735543
47	1179.5	53.3	2288	6	BC039930
48	1164.5	52.7	2286	2	BD447563
49	1164.5	52.7	2286	2	CQ777667
50	865	39.1	517	2	BD458602
51	845	38.2	548	2	BD059530
52	791	35.8	855	2	AX867136
53	791	35.8	855	2	BD147198
54	780.5	35.3	805	2	AX869834
55	780.5	35.3	805	2	BD149896
56	707	32.0	196033	12	AC162418
57	707	32.0	209109	12	AC149660
58	688.5	31.1	224870	12	AC129657
59	688.5	31.1	250782	12	AC128093
60	678	30.7	188300	6	AC163198
61	678	30.7	195236	6	AC126692
62	678	30.7	244911	12	AC159128
63	633	28.6	422	2	BD071236
64	522	23.6	1627	11	AJ719946
65	503	22.7	1326	6	BC031372
66	386	17.5	188344	12	AC131617
67	343.5	15.5	242590	12	AC133722
68	271.5	12.3	244911	12	AC159128
69	242	10.9	295	2	AX894034
70	242	10.9	295	2	BD029567
71	242	10.9	295	2	AR729828
72	221	10.0	2165	11	BX929877
73	206.5	9.3	1919	6	BC019471
74	204.5	9.2	2058	5	AF264781
75	203	9.2	171026	11	BX572619
76	197	8.9	112864	12	AC024127

c 77	197	8.9	187516	5	AP002813	AP002813 Homo sapi	c 150	162.5	7.3	214306	12	CR385054	CR385054 Danio rer
c 78	197	8.9	191589	5	AP002992	AP002992 Homo sapi	151	161.5	7.3	11334	12	AC014605	AC014605 Drosophil
c 79	196.5	8.9	1826	2	AR541982	Sequence	152	161	7.3	1275	4	AB181301	AB181301 Triticum
c 80	196.5	8.9	1826	2	AR699144	Sequence	153	161	7.3	2376	10	AY702017	AY702017 Equid her
c 81	196.5	8.9	218688	6	AC132452	Mus muscu	154	160.5	7.3	1431	5	HSMUCIN2	Z34277 H.sapiens (
c 82	195.5	8.8	1389	2	CQ722760	Sequence	155	160.5	7.3	1638	5	AR578236	AR578236 Sequence
c 83	195.5	8.8	1969	5	BC011765	Sequence	156	160.5	7.3	2365	5	BC025688	BC025688 Homo sapi
c 84	194.5	8.8	1642	2	BD223134	98 human	157	160.5	7.3	2753	2	CQ612249	CQ612249 Sequence
c 85	194.5	8.8	1642	2	AR243832	Sequence	158	160.5	7.3	3168	13	AY060815	AY060815 Drosophil
c 86	190	8.6	1742	13	AK112387	Ciona int	159	160.5	7.3	22622	2	CQ612248	CQ612248 Sequence
c 87	188	8.5	1661	2	CS326948	Sequence	160	160.5	7.3	94585	12	AC176204	AC176204 Strongylo
c 88	188	8.5	1661	2	CS366058	Sequence	c 161	160.5	7.3	167366	13	AC104605	AC104605 Drosophil
c 89	188	8.5	1661	2	DD039569	SECRETED	162	160.5	7.3	290042	13	AE003435	AE003435 Drosophil
c 90	188	8.5	1661	2	AR79424	Sequence	163	160	7.2	1115	5	AY344834	AY344834 Anopheles
c 91	188	8.5	1661	2	AR302828	Sequence	164	160	7.2	2148	5	AF253321	AF253321 Homo sapi
c 92	188	8.5	1661	2	AR915566	Sequence	165	160	7.2	8106	5	AF488829	AF488829 Homo sapi
c 93	188	8.5	1661	2	AX464090	Sequence	166	160	7.2	10174	2	CS035313	CS035313 Sequence
c 94	188	8.5	1661	2	AY358754	Homo sapi	167	160	7.2	10174	2	CS044265	CS044265 Sequence
c 95	183.5	8.3	4047	5	HS298318	Homo sapi	168	160	7.2	10174	2	CS350720	CS350720 Sequence
c 96	183.5	8.3	168002	12	CT583679	Homo sapi	169	160	7.2	10174	5	AL096857	Novel hum
c 97	176.5	8.0	2091	6	BC098053	Danio rer	c 170	159.5	7.2	110000	10	CR926130	Continuation (2 of
c 98	176.5	8.0	271704	12	AC111375	AC111375 Rattus no	c 171	159.5	7.2	171875	12	CR926130	CR926130 Danio rer
c 99	175.5	7.9	179075	12	AC150138	AC150138 Gallus ga	172	159	7.2	1115	13	AY344835	AY344835 Anopheles
c 100	175	7.9	131676	5	AC139749	AC139749 Homo sapi	173	159	7.2	37445	13	U51998	U51998 Caenorhabdi
c 101	173.5	7.8	155281	12	AC168594	AC168594 Strongylo	c 174	159	7.2	129565	11	CR848731	CR848731 Zebrafish
c 102	172.5	7.8	1720	5	HUMMUC2A	M74027 Human mucin	c 175	159	7.2	183614	11	CR735107	CR735107 Zebrafish
c 103	172.5	7.8	3811	5	HUMMUC2A	M94131 Human mucin	c 176	159	7.2	196461	6	AL627314	AL627314 Mouse DNA
c 104	172.5	7.8	15720	2	AX926462	Sequence	177	158.5	7.2	984	5	HSU78550	HSU78550 Homo sapien
c 105	172.5	7.8	15720	2	AX951715	Sequence	178	158.5	7.2	1134	2	CQ750558	CQ750558 Sequence
c 106	172.5	7.8	15720	2	AX959992	Sequence	179	158.5	7.2	1604	2	DD058256	DD058256 EXTRACELL
c 107	172.5	7.8	15720	2	AX959993	Sequence	180	158.5	7.2	1604	2	AX704762	AX704762 Sequence
c 108	172.5	7.8	15720	2	BD399825	BREAST CA	181	158.5	7.2	2388	2	CS300768	CS300768 Sequence
c 109	172.5	7.8	15720	2	BD421463	CANCER DI	c 182	158.5	7.2	119883	12	AC181410	AC181410 Strongylo
c 110	172.5	7.8	15720	2	CQ834018	Sequence	183	158.5	7.2	120612	5	AC108518	AC108518 Homo sapi
c 111	172.5	7.8	15720	2	CS114746	Sequence	c 184	158.5	7.2	138320	12	AC181434	AC181434 Strongylo
c 112	172.5	7.8	15720	2	CS273953	Sequence	c 185	158.5	7.2	243533	12	AC096320	AC096320 Rattus no
c 113	172.5	7.8	15720	2	CS353065	Sequence	186	158	7.1	245273	12	AC137407	AC137407 Rattus no
c 114	172.5	7.8	15720	2	DD018353	SELECTION	187	158	7.1	252902	12	AC129164	AC129164 Rattus no
c 115	172.5	7.8	15720	2	DD018354	SELECTION	188	158	7.1	268213	12	AC103285	AC103285 Rattus no
c 116	172.5	7.8	15720	2	AX193491	Sequence	189	157.5	7.1	2065	5	BLXHORDCA	BLXHORDCA
c 117	172.5	7.8	15720	2	AX330186	Sequence	190	157.5	7.1	2350	5	HUMSUBMAND	HUMSUBMAND
c 118	172.5	7.8	15720	2	HUMMUC2X	L21998 Homo sapien	191	157.5	7.1	2429	2	DD139754	DD139754 EXTRACELL
c 119	172	7.8	155358	11	CQ934734	Sequence	192	157.5	7.1	2429	2	AX174734	AX174734 Sequence
c 120	171.5	7.8	10371	2	CQ934734	Sequence	193	157.5	7.1	7382	5	HS298317	HS298317 Homo sapi
c 121	171	7.7	131199	12	AC180826	AC180826 Strongylo	194	157.5	7.1	174597	12	AC183563	AC183563 Canis fam
c 122	169.5	7.7	95933	12	AC178870	AC178870 Strongylo	195	157.5	7.1	232316	12	AC098608	AC098608 Rattus no
c 123	168.5	7.6	82064	12	AC006937	AC006937 Drosophil	196	157.5	7.1	1367	10	AY034640	AY034640 Equine he
c 124	168.5	7.6	158125	12	CT030000	CT030000 Danio rer	197	157	7.1	110000	4	CR382127	CR382127 Yarrowia
c 125	168	7.6	28291	13	CBF56H9	Z74473 Caenorhabdi	198	156.5	7.1	1322	10	AY034644	AY034644 Equine he
c 126	168	7.6	148945	12	CR759744	CR759744 Danio rer	199	156.5	7.1	9964	2	CQ729631	CQ729631 Sequence
c 127	167	7.6	215743	11	CR749741	CR749741 Zebrafish	200	156	7.1	2300	2	CQ611372	CQ611372 Sequence
c 128	166	7.5	1413	4	AB181300	AB181300 Triticum	c 201	156	7.1	3161	2	CQ611375	CQ611375 Sequence
c 129	165.5	7.5	6300	6	MMU511869	AY511869 Mus muscu	c 202	156	7.1	9958	4	SCVJR151C	SCVJR151C
c 130	165.5	7.5	6616	6	AH012557S4	AY184388 Mus muscu	c 203	156	7.1	48628	12	AC013119	AC013119 Drosophil
c 131	165.5	7.5	189095	12	AC167551	AC167551 Mus muscu	c 204	156	7.1	160986	12	AC108481	AC108481 Strongylo
c 132	165.5	7.5	193924	6	AC102524	AC102524 Mus muscu	c 205	156	7.1	252074	12	AC176683	AC176683 Strongylo
c 133	165.5	7.5	200074	6	AC164070	AC164070 Mus muscu	c 206	156	7.1	296227	13	AE003430	AE003430 Drosophil
c 134	165	7.5	1866	5	HSMUC58C	X74955 H.sapiens M	c 207	156	7.1	33321	13	AC116986	AC116986 Dictyoste
c 135	165	7.5	190110	12	CR854881	CR854881 Danio rer	c 208	155.5	7.0	1112	13	AY344832	AY344832 Anopheles
c 136	164.5	7.4	197012	6	AL669823	AL669823 Mouse DNA	c 209	155.5	7.0	2806	4	S66938	S66938 C-hordein l
c 137	164.5	7.4	206201	12	AC164757	AC164757 Bos tauru	c 210	155.5	7.0	5403	13	TRBTCNAA	TRBTCNAA
c 138	164	7.4	1115	13	AY344833	AY344833 Anopheles	c 211	155.5	7.0	110000	4	AP008207	AP008207 205
c 139	164	7.4	14094	2	AR906579	AR906579 Sequence	c 212	155.5	7.0	157563	12	AC176250	AC176250 Strongylo
c 140	164	7.4	14094	5	AJ606308	AJ606308 Homo sapi	c 213	155.5	7.0	159509	4	AP004225	AP004225 Oryza sat
c 141	164	7.4	14246	2	AR906578	AR906578 Sequence	c 214	155.5	7.0	159509	4	AP004258	AP004258 Oryza sat
c 142	164	7.4	14246	5	AJ606307	AJ606307 Homo sapi	c 215	155.5	7.0	172642	4	AP004258	AP004258 Oryza sat
c 143	164	7.4	17847	2	CS143783	CS143783 Sequence	c 216	155	7.0	2194	5	HSM807334	HSM807334
c 144	164	7.4	124104	5	AC061979	AC061979 Homo sapi	c 217	155	7.0	2922	2	CS168201	CS168201 Sequence
c 145	164	7.4	198646	6	AC150683	AC150683 Mus muscu	c 218	155	7.0	2922	2	CS168201	CS168201 Sequence
c 146	163	7.4	153619	12	AC173552	AC173552 Strongylo	c 219	155	7.0	2922	2	AK096699	AK096699 Homo sapi
c 147	163	7.4	172504	5	AP001999	AP001999 Homo sapi	c 220	155	7.0	143605	12	AC171190	AC171190 Bos tauru
c 148	163	7.4	232304	11	BX322616	BX322616 Zebrafish	c 221	155	7.0	146917	12	AC142043	AC142043 Rattus no
c 149	162.5	7.3	152177	11	AL935114	AL935114 Zebrafish	c 222	155	7.0	188084	6	AC124523	AC124523 Mus muscu

c 223	155	7.0	209973	12	AC073755	AC073755 Mus muscu	296	151	6.8	228387	12	CR788237	CR788237 Danio rer
224	154.5	7.0	10713	5	HSNCSBEX	Z72496 H.sapiens M	297	151	6.8	285860	13	AE003551	AE003551 Drosophil
225	154.5	7.0	33359	13	CEFS5B11	Z83318 Caenorhabdi	298	150.5	6.8	1470	13	LS1132603	AJ122603 Litomosoi
226	154.5	7.0	195349	12	AC006705	AC006705 Caenorhab	299	150.5	6.8	1630	5	HSNCSB5A	X74370 H.sapiens M
227	154	7.0	1115	13	AY344830	AY344830 Anopheles	300	150.5	6.8	2057	5	HSNCSB5A	BX648904 Homo sapi
228	154	7.0	2282	4	AK124374	AK124374 Homo sapi	301	150.5	6.8	3097	4	COICTS2CHI	L41662 Coccidioid
229	154	7.0	37777	4	SPBC215	AL033534 S.pombe c	302	150.5	6.8	25080	2	CO737837	CO737837 Sequence
230	154	7.0	99886	5	HS598F2	AL021579 Human DNA	303	150.5	6.8	32797	13	CEW01F37	Z92815 Caenorhabdi
c 231	154	7.0	110000	12	AC127805_1	Continuation (2 of	304	150.5	6.8	75254	11	BX510925	BX510925 Zebrafish
c 232	154	7.0	110000	13	AC116984_3	Continuation (4 of	c 305	150.5	6.8	106121	12	AC179263	AC179263 Strongylo
233	154	7.0	127643	11	BX321877	BX321877 Zebrafish	c 306	150.5	6.8	121936	6	AL691513	AL691513 Mouse DNA
234	154	7.0	317853	12	CB936344	CR936344 Danio rer	307	150.5	6.8	150224	10	AY665713	AY665713 Equine he
c 235	153.5	6.9	4755	2	CQ612725	CQ612725 Sequence	c 308	150.5	6.8	182881	12	CT025755	CT025755 Mus muscu
236	153.5	6.9	65443	12	AC014845	AC014845 Drosophil	309	150.5	6.8	212955	12	AC136676	AC136676 Rattus no
237	153.5	6.9	149430	10	AY464052	AY464052 Equine he	310	150	6.8	1584	14	SSGMUC2	U01281 Sus scrofa
238	153.5	6.9	189694	13	AC009848	AC009848 Drosophil	311	150	6.8	15984	15	AF224509	AF224509 Bacteroid
239	153.5	6.9	192367	12	AC121410	AC121410 Rattus no	c 312	150	6.8	88203	11	AC097628	AC097628 Takifugu
240	153.5	6.9	197156	13	AE003760	AE003760 Drosophil	c 313	150	6.8	132242	12	AC176969	AC176969 Strongylo
241	153.5	6.9	209201	6	AC139244	AC139244 Mus muscu	c 314	150	6.8	190628	12	AC176547	AC176547 Strongylo
242	153.5	6.9	220091	12	AC118835	AC118835 Rattus no	315	150	6.8	198927	6	AC155273	AC155273 Mus muscu
243	153.5	6.9	237055	12	AC095177	AC095177 Rattus no	316	150	6.8	204611	12	AC171208	AC171208 Mus muscu
244	153	6.9	2014	5	AK093828	AK093828 Homo sapi	c 317	150	6.8	252074	12	AC176683	AC176683 Strongylo
245	153	6.9	2490	2	CS113291	CS113291 Sequence	318	149.5	6.8	47026	13	CBRG41B17	AC084584 Caenorhab
246	153	6.9	2861	5	AK130557	AK130557 Homo sapi	319	149.5	6.8	82054	12	AC006937	AC006937 Drosophil
247	153	6.9	3407	11	AY587262	AY587262 Sparus au	320	149.5	6.8	99171	12	AC176529	AC176529 Strongylo
248	153	6.9	61830	4	AP007157_26	Continuation (27 o	321	149.5	6.8	160208	13	AC184651	AC184651 Strongylo
249	153	6.9	111824	5	AL160412	AL160412 Human DNA	322	149.5	6.8	163183	12	AC009842	AC009842 Drosophil
c 250	153	6.9	176147	11	AL929105	AL929105 Zebrafish	c 323	149.5	6.8	178400	11	BX294376	BX294376 Zebrafish
c 251	153	6.9	179429	12	AC120374	AC120374 Mus muscu	c 324	149.5	6.8	178595	12	AC176386	AC176386 Strongylo
c 252	153	6.9	181999	12	AC162853	AC162853 Mus muscu	325	149.5	6.8	180051	6	AC139223	AC139223 Mus muscu
c 253	153	6.9	209579	6	AC124764	AC124764 Mus muscu	c 326	149.5	6.8	221935	12	AC176595	AC176595 Strongylo
254	152.5	6.9	1112	13	AY344831	AY344831 Anopheles	c 327	149.5	6.8	289893	13	AE003576	AE003576 Drosophil
255	152.5	6.9	143605	12	AC171190	AC171190 Bos tauru	328	149	6.7	471	2	CQ516037	CQ516037 Sequence
c 256	152.5	6.9	146636	12	AC176815	AC176815 Strongylo	329	149	6.7	515	2	E11860	E11860 Genomic DNA
c 257	152	6.9	1115	13	AY344829	AY344829 Anopheles	330	149	6.7	2903	2	AE003521	AE003521 Saccharom
258	152	6.9	1297	2	AR448257	AR448257 Sequence	331	149	6.7	2903	4	EB003521	EB003521 Saccharom
259	152	6.9	5795	6	RNNUCASG7	U06752 Rattus norv	332	149	6.7	4830	8	DQ331761	DQ331761 Synthetic
c 260	152	6.9	12573	4	SPAPB15E9	AL691401 S.pombe c	c 333	149	6.7	84902	5	AC021216	AC021216 Homo sapi
c 261	152	6.9	110000	15	CR936257_24	Continuation (25 o	c 334	149	6.7	110000	15	CR936257_17	Continuation (18 o
c 262	152	6.9	110459	5	AC117378	AC117378 Homo sapi	335	149	6.7	110000	15	AE017180_30	Continuation (31 o
263	152	6.9	141699	12	AC184804	AC184804 Strongylo	c 336	149	6.7	151160	12	AC151022	AC151022 Callithri
264	152	6.9	210156	12	AC136829	AC136829 Rattus no	c 337	149	6.7	166000	13	AC104511	AC104511 Drosophil
265	152	6.9	236493	12	AC106220	AC106220 Rattus no	338	149	6.7	316613	4	SCCHRIII	XS9720 S.cerevisia
c 266	152	6.9	269921	12	AC099286	AC099286 Rattus no	339	149	6.7	332030	13	AE003491	AE003491 Drosophil
267	151.5	6.9	1403	5	HS2298319	AJ298319 Homo sapi	340	148.5	6.7	1268	10	AY034643	AY034643 Equine he
268	151.5	6.9	1416	13	AGAO10903	AJ010903 Anopheles	341	148.5	6.7	1515	5	HUMGASMCUB	LO7518 Homo sapien
269	151.5	6.9	4458	13	DMU42402	U42402 Drosophila	342	148.5	6.7	38181	6	AC175742	AC175742 Mus muscu
270	151.5	6.9	4829	2	CQ589581	CQ589581 Sequence	c 343	148.5	6.7	41746	6	AC175658	AC175658 Mus muscu
271	151.5	6.9	5561	6	AK122540	AK122540 Mus muscu	c 344	148.5	6.7	66208	5	AL450284	AL450284 Human DNA
272	151.5	6.9	5754	13	DMU42403	U42403 Drosophila	345	148.5	6.7	110000	4	CR382132_28	Continuation (29 o
c 273	151.5	6.9	110000	4	CR382129_05	Continuation (6 of	346	148.5	6.7	133325	11	AL627423	AL627423 Zebrafish
c 274	151.5	6.9	110000	13	AC116984_0	AC116984 Dictyoste	c 347	148.5	6.7	185817	11	BX296521	BX296521 Zebrafish
c 275	151.5	6.9	110000	13	AC116984_1	Continuation (2 of	348	148.5	6.7	219218	12	AC020817	AC020817 Mus muscu
c 276	151.5	6.9	110000	15	AE009442_11	Continuation (12 o	349	148.5	6.7	221879	12	AC096704	AC096704 Rattus no
c 277	151.5	6.9	110000	15	AE009442_11	Continuation (15 o	350	148.5	6.7	222343	12	AC114531	AC114531 Rattus no
c 278	151.5	6.9	121987	12	AC179766	AC179766 Strongylo	351	148.5	6.7	222603	12	AC125755	AC125755 Rattus no
c 279	151.5	6.9	122334	5	AC092898	AC092898 Homo sapi	352	148.5	6.7	234097	12	AC120493	AC120493 Rattus no
c 280	151.5	6.9	132457	5	AC016584	AC016584 Homo sapi	353	148	6.7	1044	2	AX840040	AX840040 Sequence
281	151.5	6.9	162388	11	BX569794	BX569794 Zebrafish	354	148	6.7	1044	2	AX840626	AX840626 Sequence
282	151.5	6.9	174142	12	CT583645	CT583645 Danio rer	355	148	6.7	1710	13	GCY299721	AJ299721 Geodia cy
283	151.5	6.9	175351	12	AC117900	AC117900 Rattus no	356	148	6.7	2032	2	AR195309	AR195309 Sequence
284	151.5	6.9	177554	12	AC176076	AC176076 Strongylo	357	148	6.7	2032	2	AR222274	AR222274 Sequence
c 285	151.5	6.9	219471	6	CR974473	CR974473 Mouse DNA	358	148	6.7	2032	2	AR907772	AR907772 Sequence
286	151.5	6.9	247341	12	AC099178	AC099178 Rattus no	359	148	6.7	2032	13	DMU17693	U17693 Drosophila
c 287	151.5	6.9	260558	11	BX950188	BX950188 Zebrafish	c 360	148	6.7	2570	2	DD154362	DD154362 NOVEL ANT
288	151	6.8	2161	11	XELFM1C1X	LO2115 Frog integu	c 361	148	6.7	7417	2	CQ594035	CQ594035 Sequence
c 289	151	6.8	5929	2	CQ578280	CQ578280 Sequence	c 362	148	6.7	31095	5	AL391319	AL391319 Human DNA
c 290	151	6.8	11963	2	CQ578279	CQ578279 Sequence	c 363	148	6.7	31497	2	DD174506	DD174506 Repeat Se
c 291	151	6.8	48836	12	AC020151	AC020151 Drosophil	c 364	148	6.7	39746	2	CQ589580	CQ589580 Sequence
c 292	151	6.8	139530	11	BX545917	BX545917 Zebrafish	365	148	6.7	42248	12	AC020375	AC020375 Drosophil
c 293	151	6.8	145071	13	AC115598	AC115598 Dictyoste	366	148	6.7	52158	12	AC013185	AC013185 Drosophil
c 294	151	6.8	181063	13	AC010107	AC010107 Drosophil	367	148	6.7	66765	2	CQ874958	CQ874958 Sequence
295	151	6.8	184657	13	AC010043	AC010043 Drosophil	368	148	6.7	66765	5	AF414442	AF414442 Homo sapi

c 369	148	6.7	110000	4	AE016820.05	Continuation (6 of	442	146	6.6	2431	15	AV298902	AV298902 Pseudomon
c 370	148	6.7	110000	12	CR005268_12	Continuation (13 o	443	146	6.6	2709	2	CQ580851	CQ580851 Sequence
c 371	148	6.7	118947	12	AC006321	AC006321 Homo sapi	444	146	6.6	2965	11	CR855611	CR855611 Xenopus t
c 372	148	6.7	129502	5	HSJ726C3	AL121756 Human DNA	445	146	6.6	3749	13	DROSTUBBLE	L11451 Drosophila
c 373	148	6.7	151609	13	AC009462	AC009462 Drosophila	446	146	6.6	3787	13	AY865070	AY865070 Drosophila
c 374	148	6.7	154429	12	AC177039	AC177039 Strongylo	447	146	6.6	28247	12	AC139180	AC139180 Clona sav
c 375	148	6.7	156998	12	AL136099	AL136099 Homo sapi	c 448	146	6.6	103681	4	SCU12980	U12980 Saccharomyc
c 376	148	6.7	157141	13	AC016445	AC016445 Drosophila	449	146	6.6	109780	12	AC178206	AC178206 Strongylo
c 377	148	6.7	177855	13	AC010211	AC010211 Drosophila	450	146	6.6	110000	15	CR382139_15	Continuation (16 o
c 378	148	6.7	183137	5	AC008734	AC008734 Homo sapi	451	146	6.6	110000	45	BA000012_40	Continuation (41 o
c 379	148	6.7	187397	12	AC180120	AC180120 Strongylo	452	146	6.6	148325	11	CR005124	CR005124 Zebrafish
c 380	148	6.7	201064	12	AC187748	AC187748 Pan trogl	453	146	6.6	150331	12	CR749749	CR749749 Danio rer
c 381	148	6.7	210832	12	AC175267	AC175267 Bos tauru	454	146	6.6	159874	12	CT573061	CT573061 Danio rer
c 382	148	6.7	213005	5	AP005059	AP005059 Homo sapi	455	146	6.6	166865	12	AC178932	AC178932 Strongylo
c 383	148	6.7	228842	13	AE003720	AE003720 Drosophila	c 456	146	6.6	167612	12	CT868729	CT868729 Mus muscu
c 384	148	6.7	292632	13	AE003600	AE003600 Drosophila	457	146	6.6	190846	5	AC006372	AC006372 Homo sapi
c 385	147.5	6.7	1236	2	DD104401	DD104401 YEAST SCR	c 458	146	6.6	321250	15	SC093911	AL939111 Streptomy
c 386	147.5	6.7	1236	2	AR878401	AR878401 Sequence	459	145.5	6.6	1986	13	AY864359	AY864359 Drosophila
c 387	147.5	6.7	1236	2	AX662312	AX662312 Sequence	460	145.5	6.6	2026	13	AY864357	AY864357 Drosophila
c 388	147.5	6.7	1316	10	AY034637	AY034637 Equine he	461	145.5	6.6	2114	2	BD237106	BD237106 Compounds
c 389	147.5	6.7	2594	13	AY119618	AY119618 Drosophila	c 462	145.5	6.6	2114	2	AR225506	AR225506 Sequence
c 390	147.5	6.7	3736	2	CQ612939	CQ612939 Sequence	c 463	145.5	6.6	2114	2	DD064076	DD064076 COMPOSITI
c 391	147.5	6.7	4971	4	AF201084	AF201084 Secale ce	c 464	145.5	6.6	2114	2	AR562929	AR562929 Sequence
c 392	147.5	6.7	6108	13	CFTR3381	U12516 Caenorhabdi	c 465	145.5	6.6	2114	2	AX321627	AX321627 Sequence
c 393	147.5	6.7	9435	13	AF269242	AF269242 Plasmodi	466	145.5	6.6	3173	10	D88734	D88734 Equine herp
c 394	147.5	6.7	35920	13	CELLC1	Z82277 Caenorhabdi	467	145.5	6.6	110000	4	CR382130_02	Continuation (3 of
c 395	147.5	6.7	106111	4	NCB23G1	BX284754 Neurospor	468	145.5	6.6	110000	4	AE017345_01	Continuation (2 of
c 396	147.5	6.7	148285	12	AC178037	AC178037 Strongylo	c 469	145.5	6.6	110000	15	AE004965_01	Continuation (2 of
c 397	147.5	6.7	168211	5	AP006309	AP006309 Homo sapi	470	145.5	6.6	146413	12	AC0051652	AC0051652 Homo sapi
c 398	147.5	6.7	175953	12	AC180648	AC180648 Strongylo	c 471	145.5	6.6	178372	12	AX569797	AX569797 Danio rer
c 399	147.5	6.7	188483	12	AC176780	AC176780 Strongylo	472	145.5	6.6	181047	11	AX139110	AX139110 Danio rer
c 400	147.5	6.7	205076	6	AC154392	AC154392 Mus muscu	c 473	145.5	6.6	191401	11	AX470130	AX470130 Zebrafish
c 401	147.5	6.7	215678	10	DQ120516	DQ120516 Cercopith	c 474	145.5	6.6	200799	12	AC158244	AC158244 Pongo pyg
c 402	147.5	6.7	235050	12	AC106979	AC106979 Rattus no	c 475	145.5	6.6	200922	12	AC173162	AC173162 Bos tauru
c 403	147.5	6.7	241531	12	AC122959	AC122959 Rattus no	c 476	145.5	6.6	233284	12	AC133678	AC133678 Rattus no
c 404	147.5	6.7	241765	12	AC132557	AC132557 Rattus no	c 477	145.5	6.6	246911	11	AX085193	AX085193 Zebrafish
c 405	147.5	6.7	249301	12	AC109524	AC109524 Rattus no	c 478	145.5	6.6	254733	13	AC117075	AC117075 Dictyoste
c 406	147.5	6.7	255326	12	AC136556	AC136556 Rattus no	c 479	145.5	6.6	283225	12	AC181180	AC181180 Strongylo
c 407	147.5	6.7	278876	12	AC120936	AC120936 Rattus no	c 480	145.5	6.6	282656	10	AX626556	AX626556 Human her
c 408	147.5	6.7	284274	12	AC117062	AC117062 Rattus no	481	145	6.6	1342	4	SCSBC1A	X60294 S.cereale S
c 409	147	6.6	2025	13	AY864360	AY864360 Drosophila	482	145	6.6	1368	2	AL0377	AL0377 Artificial
c 410	147	6.6	2025	13	AY864362	AY864362 Drosophila	483	145	6.6	1378	11	XELSPAA	M19971 X.laavis sp
c 411	147	6.6	2856	5	AX225376	AX225376 Homo sapi	484	145	6.6	1399	4	AJ937839	AJ937839 Triticum
c 412	147	6.6	4408	11	BC045339	BC045339 Danio rer	485	145	6.6	1480	13	AK116673	AK116673 Clona int
c 413	147	6.6	20467	13	AF190751	AF190751 Drosophila	486	145	6.6	1909	5	HSM809054	BC468903 Homo sapi
c 414	147	6.6	71774	4	NCB9K17	BX294016 Neurospor	487	145	6.6	2173	6	BC005769	BC005769 Mus muscu
c 415	147	6.6	84474	5	AL662854	AL662854 Human DNA	488	145	6.6	2291	2	CQ612726	CQ612726 Sequence
c 416	147	6.6	96019	12	AC178912	AC178912 Strongylo	489	145	6.6	2374	13	AY118372	AY118372 Drosophila
c 417	147	6.6	128441	12	AC168510	AC168510 Strongylo	490	145	6.6	2534	6	BC053341	BC053341 Mus muscu
c 418	147	6.6	224129	6	AC115640	AC115640 Rattus no	491	145	6.6	3030	4	VCA429230	AJ429230 Volvox ca
c 419	147	6.6	228492	6	AC132058	AC132058 Rattus no	492	145	6.6	3170	10	D88733	D88733 Equine herp
c 420	146.5	6.6	1329	4	AF234646	AF234646 Triticum	493	145	6.6	3789	4	AF280605	AF280605 Triticum
c 421	146.5	6.6	2016	13	AY864355	AY864355 Drosophila	494	145	6.6	4808	13	AY075323	AY075323 Drosophila
c 422	146.5	6.6	2016	13	AY864358	AY864358 Drosophila	495	145	6.6	5371	6	MM091967	U91967 Mus muscu
c 423	146.5	6.6	2675	13	AY864363	AY864363 Drosophila	c 496	145	6.6	9636	2	AR178096	AR178096 Sequence
c 424	146.5	6.6	2675	13	AY864370	AY864370 Drosophila	c 497	145	6.6	9636	2	I95887	I95887 Sequence 1
c 425	146.5	6.6	3743	13	DI1314911	AJ114911 Dictyoste	c 498	145	6.6	9636	13	PFAP230X	L08135 Plasmodium
c 426	146.5	6.6	3789	13	AY865068	AY865068 Drosophila	c 499	145	6.6	9654	13	PFAP230A	L04162 Plasmodium
c 427	146.5	6.6	4182	2	CQ737825	CQ737825 Sequence	500	145	6.6	13631	2	CQ600014	CQ600014 Sequence
c 428	146.5	6.6	31685	13	U67956	U67956 Sequence 3	c 501	145	6.6	15148	13	AE001393	AE001393 Plasmodium
c 429	146.5	6.6	40892	2	A59672	A59672 Caenorhabdi	c 502	145	6.6	153440	13	AC105263	AC105263 Drosophila
c 430	146.5	6.6	134568	12	AC122758	AC122758 Mus muscu	c 503	145	6.6	154562	12	AC126897	AC126897 Rattus no
c 431	146.5	6.6	138342	12	AC179738	AC179738 Strongylo	c 504	145	6.6	157180	4	NCB18D24	AL513466 Neurospor
c 432	146.5	6.6	178293	12	AC179689	AC179689 Strongylo	c 505	145	6.6	157628	12	AC179112	AC179112 Strongylo
c 433	146.5	6.6	202215	6	AC158657	AC158657 Mus muscu	506	145	6.6	189307	12	AC148580	AC148580 Gasterost
c 434	146.5	6.6	203546	6	AC162465	AC162465 Mus muscu	c 507	145	6.6	172904	13	AC007414	AC007414 Drosophila
c 435	146.5	6.6	214146	12	AC096822	AC096822 Rattus no	c 508	145	6.6	182499	12	AC157191	AC157191 Bos tauru
c 436	146.5	6.6	216609	12	AC142133	AC142133 Rattus no	c 509	145	6.6	194230	6	CR933736	CR933736 Mouse DNA
c 437	146.5	6.6	243951	12	AC095143	AC095143 Rattus no	510	145	6.6	194609	12	AC013775	AC013775 Mus muscu
c 438	146.5	6.6	264754	12	AC128542	AC128542 Rattus no	511	145	6.6	196424	6	AC108321	AC108321 Rattus no
c 439	146.5	6.6	277621	12	AC095191	AC095191 Rattus no	512	145	6.6	207086	6	AL596117	AL596117 Mouse DNA
c 440	146.5	6.6	303774	12	AC105878	AC105878 Rattus no	c 513	145	6.6	249354	12	AC131193	AC131193 Rattus no
c 441	146	6.6	1148	10	AY034636	AY034636 Equine he	c 514	145	6.6	275390	13	AE003831	AE003831 Drosophila

661	142	6.4	110000	12	LMFLCHR16_01	Continuation (2 of	c 734	140.5	6.4	13152	2	CS270981	Sequence
662	142	6.4	165677	12	AC172459	CR172459 Bos tauru	c 735	140.5	6.4	13152	2	AX570447	Sequence
663	142	6.4	168311	11	CR792425	CR792425 Zebrafish	736	140.5	6.4	14328	2	CX897514	Sequence
664	142	6.4	196537	12	AC123389	AC123389 Rattus no	737	140.5	6.4	14328	2	CS270985	Sequence
665	142	6.4	198056	12	AC106280	AC106280 Rattus no	738	140.5	6.4	14328	2	AX570451	Sequence
666	142	6.4	282355	12	AC104401	AC104401 Rattus no	739	140.5	6.4	78917	12	AC018146	Drosophil
667	141.5	6.4	2293	2	CS047820	CS047820 Sequence	740	140.5	6.4	87124	13	AC004371	Drosophil
668	141.5	6.4	2960	13	AY057052	AY057052 Mamestra	741	140.5	6.4	107069	15	DQ116941	Streptomy
669	141.5	6.4	3263	2	CQ585087	CQ585087 Sequence	742	140.5	6.4	110000	4	AP008214_180	Continuation (181
670	141.5	6.4	3296	13	BT003186	BT003186 Drosophil	743	140.5	6.4	110000	4	CR382124_05	Continuation (6 of
671	141.5	6.4	3486	2	AR527989	AR527989 Sequence	744	140.5	6.4	110000	15	BA0005672_16	Continuation (17 o
672	141.5	6.4	3689	13	AY128472	AY128472 Drosophil	745	140.5	6.4	110000	15	BA000030_00	Streptomy
673	141.5	6.4	3794	13	AY865063	AY865063 Drosophil	746	140.5	6.4	123466	11	CR974440	Zebrafish
674	141.5	6.4	39215	13	CE01054	ZY4030 Caenorhabdi	747	140.5	6.4	125021	6	AC007504	Arabidops
675	141.5	6.4	52505	4	AY448010S7	AY448010 Ipomoea t	748	140.5	6.4	135403	12	AP005423	Oryza sat
676	141.5	6.4	117199	12	CT005251_4	Continuation (5 of	749	140.5	6.4	146735	12	AC178122	Strongylo
677	141.5	6.4	146938	11	CR407704	CR407704 Zebrafish	750	140.5	6.4	171686	12	AC186522	Zea mays
678	141.5	6.4	150195	12	AC184114	AC184114 Zea mays	751	140.5	6.4	172081	6	AC137124	Mus muscu
679	141.5	6.4	158696	6	AC133581	AC133581 Mus muscu	752	140.5	6.4	181288	13	AC008003	Drosophil
680	141.5	6.4	169614	11	BX511115	BX511115 Zebrafish	753	140.5	6.4	192484	6	AC122767	Mus muscu
681	141.5	6.4	184690	6	AC164304	AC164304 Mus muscu	754	140.5	6.4	200542	5	CNS01RG3	Human chr
682	141.5	6.4	192548	12	AC129738	AC129738 Rattus no	755	140.5	6.4	200720	4	AP005795	Oryza sat
683	141.5	6.4	209551	6	AC162454	AC162454 Mus muscu	756	140.5	6.4	234684	6	AC133618	Rattus no
684	141.5	6.4	241373	12	AC126747	AC126747 Rattus no	757	140.5	6.4	251269	12	AC119030	Rattus no
685	141.5	6.4	251872	12	AC125998	AC125998 Rattus no	758	140.5	6.4	290034	13	AE003577	Drosophil
686	141	6.4	1736	15	AB102689	AB102689 Streptoco	759	140.5	6.4	349980	2	CS272299	Sequence
687	141	6.4	1912	6	AH003203S2	U33442 Rattus norv	761	140	6.3	852	6	RRINPMR	Z11875 R.rattus mR
688	141	6.4	2039	6	BC082555	BC082555 Mus muscu	762	140	6.3	1196	10	AY034641	Equine he
689	141	6.4	2130	6	AK103679	AK103679 Oryza sat	763	140	6.3	1653	4	TAE276509	Triticum
690	141	6.4	2282	6	AF099018	AF099018 Mus muscu	764	140	6.3	2475	6	AJ715791	Spalax ju
691	141	6.4	2628	4	CAU64206	U64206 Candida alb	765	140	6.3	4500	4	AB182389	Oryza sat
692	141	6.4	3255	2	AF280606	AF280606 Triticum	766	140	6.3	6353	2	CQ580242	Sequence
693	141	6.4	3925	2	QF056448	QF056448 Sequence	767	140	6.3	8429	2	CQ580241	Sequence
694	141	6.4	3953	2	CQ145348	CQ145348 Sequence	768	140	6.3	13443	12	AC013070	Drosophil
695	141	6.4	3953	2	CQ303653	CQ303653 Sequence	769	140	6.3	74699	12	AC178623	Strongylo
696	141	6.4	3953	2	CQ340982	AC096997 Takifugu	770	140	6.3	110000	13	CR382131_34	Continuation (35 o
700	141	6.4	74841	11	AC096997	Continuation (2 of	771	140	6.3	113285	6	AL732606	Mouse DNA
701	141	6.4	110000	4	CR380947_00	CR382139 Debaryomy	772	140	6.3	113285	6	AL732606	Mouse DNA
702	141	6.4	110000	4	CR382139_01	Continuation (2 of	773	140	6.3	116782	12	AC178680	Strongylo
703	141	6.4	110000	4	AP008207_426	Continuation (427	774	140	6.3	126115	12	AC168606	Strongylo
704	141	6.4	147210	12	AC179711	AC179711 Strongylo	775	140	6.3	148394	12	AC178771	Strongylo
705	141	6.4	148887	7	AP003448	AP003448 Oryza sat	776	140	6.3	148945	12	CR759944	Danio rer
706	141	6.4	160802	5	AC148477	AC148477 Homo sapi	777	140	6.3	158257	6	AC158128	Mus muscu
707	141	6.4	173961	12	AC180594	AC180594 Strongylo	778	140	6.3	158478	12	AC181882	Strongylo
708	141	6.4	192670	12	CR456627	CR456627 Danio rer	779	140	6.3	163364	12	AC184404	Strongylo
709	141	6.4	228089	10	AF453898	AF453898 Heliothis	780	140	6.3	167743	12	BX322580	Danio rer
710	141	6.4	248871	12	AC094352	AC094352 Rattus no	781	140	6.3	172674	13	AC007807	Drosophil
711	141	6.4	252215	12	AC095632	AC095632 Rattus no	782	140	6.3	186051	6	AC112957	Mus muscu
712	141	6.4	267692	12	AC135138	AC135138 Rattus no	783	140	6.3	188558	12	AC184574	Strongylo
713	141	6.4	294212	12	AC129056	AC129056 Rattus no	784	140	6.3	190866	13	AC007824	Drosophil
714	141	6.4	1133	6	BC111528	BC111528 Mus muscu	785	140	6.3	197507	12	AC140087	Pongo pyg
715	141	6.4	1539	5	AF007190	AF007190 Homo sapi	786	140	6.3	215018	12	AC139113	Pongo pyg
716	140.5	6.4	1593	13	BT023236	BT023236 Drosophil	787	140	6.3	220035	13	AE003716	Drosophil
717	140.5	6.4	1594	13	BT023208	BT023208 Drosophil	788	140	6.3	224098	12	AC111386	Rattus no
718	140.5	6.4	2016	13	AY864361	AY864361 Drosophil	789	140	6.3	327666	12	AC094474	Rattus no
719	140.5	6.4	2032	2	CQ577554	CQ577554 Sequence	790	139.5	6.3	1795	2	BD062750	Modulator
720	140.5	6.4	2124	13	LDU78523	U78523 Leishmania	791	139.5	6.3	1795	2	CS288452	Sequence
721	140.5	6.4	2675	13	AY864364	AY864364 Drosophil	792	139.5	6.3	1795	2	AX439671	Sequence
722	140.5	6.4	2675	13	AY864365	AY864365 Drosophil	793	139.5	6.3	3463	2	CQ585035	Sequence
723	140.5	6.4	2675	13	AY864366	AY864366 Drosophil	794	139.5	6.3	29865	12	AC020047	Drosophil
724	140.5	6.4	2780	13	AK112792	AK112792 Ciona int	795	139.5	6.3	72769	15	CP000255_28	Continuation (29 o
725	140.5	6.4	3428	13	BT024279	BT024279 Drosophil	796	139.5	6.3	80272	11	AL591180	Zebrafish
726	140.5	6.4	3794	13	AY865069	AY865069 Drosophil	797	139.5	6.3	110000	4	AP008213_147	Continuation (148
727	140.5	6.4	3801	13	AY865071	AY865071 Drosophil	798	139.5	6.3	110000	4	AP008213_147	Continuation (19 o
728	140.5	6.4	3873	13	AY428796	AY428796 Dictyoste	799	139.5	6.3	110000	4	AP007164_18	Continuation (10 o
729	140.5	6.4	4282	2	CQ577553	CQ577553 Sequence	800	139.5	6.3	110000	12	AC156266_05	Continuation (6 of
730	140.5	6.4	4921	13	AF221506	AF221506 Drosophil	801	139.5	6.3	11882	13	AC115612	Dictyoste
731	140.5	6.4	4921	13	AF221506	AF221506 Drosophil	802	139.5	6.3	122559	12	AC179825	Strongylo
732	140.5	6.4	4921	13	AF221506	AF221506 Drosophil	803	139.5	6.3	127955	12	AC139907	Rattus no
733	140.5	6.4	4921	13	AF221506	AF221506 Drosophil	804	139.5	6.3	131676	5	AC139749	Homo sapi
							805	139.5	6.3	132624	12	AC179088	Strongylo
							806	139.5	6.3	138203	2	DD159574	Genes for

c 807	139.5	6.3	138203	15	AY310323	AY310323 Streptomy	c 880	138.5	6.3	15768	12	AC017147	AC017147 Drosophi
c 808	139.5	6.3	144695	4	AP005451	AP005451 Oryza sat	c 881	138.5	6.3	42793	4	SC9168	238061 S.cerevisia
c 809	139.5	6.3	150893	12	AC152035	AC152035 Dasytus n	c 882	138.5	6.3	110000	15	CP000088	Continuation (19 o
810	139.5	6.3	154000	12	AC152045	AC152045 Dasytus n	883	138.5	6.3	110000	15	CP000379	Continuation (12 o
811	139.5	6.3	159802	4	AP005447	AP005447 Oryza sat	884	138.5	6.3	110000	15	CP000379	Continuation (13 o
c 812	139.5	6.3	162356	12	AC181958	AC181958 Strongylo	885	138.5	6.3	120676	12	AC180589	AC180589 Strongylo
c 813	139.5	6.3	165619	12	CR847893	CR847893 Danio rer	c 886	138.5	6.3	122447	12	AC168795	AC168795 Strongylo
814	139.5	6.3	166468	11	AC186558	AC186558 Gasterost	c 887	138.5	6.3	128546	12	AC168472	AC168472 Strongylo
c 815	139.5	6.3	177787	12	AC180451	AC180451 Strongylo	c 888	138.5	6.3	138354	6	AC182453	AC182453 Mus muscu
c 816	139.5	6.3	194300	12	AC166196	AC166196 Aotus nan	c 889	138.5	6.3	166954	12	AC150676	AC150676 Bos tauru
c 817	139.5	6.3	223311	12	AC094165	AC094165 Rattus no	c 890	138.5	6.3	167390	5	AC007263	AC007263 Homo sapi
c 818	139.5	6.3	243793	12	AC111708	AC111708 Rattus no	c 891	138.5	6.3	175679	13	AC010025	AC010025 Drosophill
c 819	139.5	6.3	276852	12	AC095438	AC095438 Rattus no	892	138.5	6.3	177590	12	AC006563	AC006563 Drosophill
c 820	139.5	6.3	283601	12	AC123500	AC123500 Rattus no	893	138.5	6.3	179821	12	AC147950	AC147950 Papio anu
c 821	139.5	6.3	286771	12	AC134154	AC134154 Rattus no	894	138.5	6.3	181388	12	AC130062	AC130062 Rattus no
c 822	139.5	6.3	290777	12	AC169364	AC169364 Bos tauru	895	138.5	6.3	188864	12	AC135951	AC135951 Macaca mu
c 823	139.5	6.3	328402	12	AC112887	AC112887 Rattus no	c 896	138.5	6.3	190979	12	AC184331	AC184331 Strongylo
824	139	6.3	867	2	AR279196	AR279196 Sequence	c 897	138.5	6.3	200039	12	AC133765	AC133765 Rattus no
825	139	6.3	867	2	AR279197	AR279197 Sequence	c 898	138.5	6.3	208406	12	AC133405	AC133405 Rattus no
826	139	6.3	867	2	AR884071	AR884071 Sequence	c 899	138.5	6.3	212955	12	AC136676	AC136676 Rattus no
827	139	6.3	867	2	AR884072	AR884072 Sequence	c 900	138.5	6.3	235976	12	AC119627	AC119627 Rattus no
828	139	6.3	1014	2	CQ611376	CQ611376 Sequence	c 901	138.5	6.3	245942	12	AC121374	AC121374 Rattus no
829	139	6.3	1215	6	AB003311	AB003311 Cavia por	902	138.5	6.3	272016	13	AE003539	AE003539 Drosophill
830	139	6.3	1226	10	AY034642	AY034642 Equine he	903	138	6.2	1211	10	AY034639	AY034639 Equine he
831	139	6.3	1352	4	AK122054	AK122054 Oryza sat	904	138	6.2	2024	15	AF010469	AF010469 Haloferax
832	139	6.3	1397	2	AR279198	AR279198 Sequence	905	138	6.2	5985	2	CQ858277	CQ858277 Sequence
c 833	139	6.3	1397	2	AR279199	AR279199 Sequence	906	138	6.2	9308	6	AB093227	AB093227 Mus muscu
834	139	6.3	1397	2	AR884073	AR884073 Sequence	907	138	6.2	13134	6	AY929611	AY929611 Mus muscu
c 835	139	6.3	1397	2	AR884074	AR884074 Sequence	908	138	6.2	14032	6	AY772010	AY772010 Mus muscu
836	139	6.3	3168	5	AB202102	AB202102 Homo sapi	909	138	6.2	14049	6	DO097265	DO097265 Mus muscu
837	139	6.3	9248	4	SCAF000227	SCAF000227 Secale ce	c 910	138	6.2	33554	4	AC167920	AC167920 Mycosphae
838	139	6.3	10652	6	AF441786	AF441786 Mus muscu	911	138	6.2	48612	12	AC167552	AC167552 Mus muscu
c 839	139	6.3	21598	4	SPBP19A11	SPBP19A11 Mus muscu	c 912	138	6.2	49265	1	AB201308	AB201308 unculture
840	139	6.3	32367	6	AF520421S2	AF520422 Mus muscu	913	138	6.2	59720	4	AP004629	AP004629 Lotus jap
841	139	6.3	35265	5	CT009610	CT009610 Human DNA	c 914	138	6.2	71479	6	BX005170	BX005170 Mouse DNA
842	139	6.3	38011	12	AC174159	AC174159 Homo sapi	c 915	138	6.2	110000	4	CR382131	Continuation (27 o
c 843	139	6.3	70175	4	NC13E11	AL353820 Neurospor	c 916	138	6.2	110000	12	AC120236	AC120236 Rattus no
c 844	139	6.3	92091	11	BX649491	BX649491 Zebrafish	917	138	6.2	117149	5	AC083984	AC083984 Homo sapi
c 845	139	6.3	110000	15	CP000384	Continuation (29 o	918	138	6.2	126932	12	AC174739	AC174739 Strongylo
c 846	139	6.3	139861	12	AC180376	AC180376 Strongylo	c 919	138	6.2	160766	12	AC137686	AC137686 Homo sapi
c 847	139	6.3	140822	12	AC179647	AC179647 Strongylo	c 920	138	6.2	165849	12	AC114251	AC114251 Rattus no
c 848	139	6.3	174808	12	AC184623	AC184623 Strongylo	921	138	6.2	170425	12	AC024490	AC024490 Homo sapi
c 849	139	6.3	191616	12	AC148723	AC148723 Salmo sal	c 922	138	6.2	171096	10	AY037858	AY037858 Cercopith
c 850	139	6.3	197473	12	AC109740	AC109740 Rattus no	c 923	138	6.2	186782	12	AC172425	AC172425 Bos tauru
c 851	139	6.3	221972	12	CR388218	CR388218 Danio rer	c 924	138	6.2	195337	12	AC180126	AC180126 Strongylo
852	139	6.3	227127	6	AC090437	AC090437 Mus muscu	c 925	138	6.2	196582	12	AC178518	AC178518 Strongylo
c 853	139	6.3	227677	12	CR388157	CR388157 Danio rer	c 926	138	6.2	200439	6	AC160032	AC160032 Mus muscu
c 854	139	6.3	232936	12	AC094153	AC094153 Rattus no	927	138	6.2	211149	12	AC133832	AC133832 Rattus no
c 855	139	6.3	237455	12	AC096815	AC096815 Rattus no	c 928	138	6.2	215717	12	AC134484	AC134484 Rattus no
856	139	6.3	240931	12	AC107097	AC107097 Rattus no	c 929	138	6.2	218838	6	AC153828	AC153828 Mus muscu
857	139	6.3	248614	12	BX548029	BX548029 Danio rer	c 930	138	6.2	221029	12	AC140292	AC140292 Mus muscu
c 858	139	6.3	248793	12	AC103080	AC103080 Rattus no	c 931	138	6.2	231716	6	AC135409	AC135409 Rattus no
c 859	139	6.3	251411	12	AC110407	AC110407 Rattus no	c 932	138	6.2	253094	12	AC113774	AC113774 Rattus no
c 860	139	6.3	274903	12	AC095233	AC095233 Rattus no	c 933	138	6.2	253362	12	AC095732	AC095732 Rattus no
861	139	6.3	294769	12	AC098907	AC098907 Rattus no	c 934	138	6.2	260662	12	AC180829	AC180829 Strongylo
862	138.5	6.3	1016	5	AF007192	AF007192 Homo sapi	c 935	138	6.2	268447	12	AC132359	AC132359 Mus muscu
863	138.5	6.3	1612	6	MMU70652	U70652 Mus musculu	936	137.5	6.2	1216	4	AY667097	AY667097 Aegilops
864	138.5	6.3	1710	4	YSCS22	M16165 Yeast (S.ce	937	137.5	6.2	2352	11	AY648768	AY648768 Danio rer
865	138.5	6.3	2086	4	WHTGGLN	M36999 Wheat gamma	938	137.5	6.2	2551	4	YSCAER2	M5861 S.cerevisia
866	138.5	6.3	2202	13	AK114835	AK114835 Ciona int	939	137.5	6.2	3150	2	CQ583125	CQ583125 Sequence
867	138.5	6.3	2601	14	BC105310	BC105310 Bos tauru	940	137.5	6.2	3794	13	AY865073	AY865073 Drosophill
868	138.5	6.3	3183	2	AR261979	AR261979 Sequence	941	137.5	6.2	4452	11	AY507659	AY507659 Danio rer
869	138.5	6.3	3183	2	AR487471	AR487471 Sequence	942	137.5	6.2	4490	11	AY507658	AY507658 Danio rer
870	138.5	6.3	3183	13	D50685	D50685 Trypanosoma	943	137.5	6.2	4518	2	DD062470	DD062470 Methods f
871	138.5	6.3	4104	2	AR527741	AR527741 Sequence	944	137.5	6.2	4519	2	DD062469	DD062469 Methods f
872	138.5	6.3	4104	2	AR778359	AR778359 Sequence	945	137.5	6.2	4578	11	AY507660	AY507660 Danio rer
873	138.5	6.3	4116	2	CQ606066	CQ606066 Sequence	946	137.5	6.2	5718	4	AF234647	AF234647 Triticum
874	138.5	6.3	5163	2	AR097042	AR097042 Sequence	947	137.5	6.2	32986	13	U13646	U13646 Caenorhabdi
875	138.5	6.3	5163	2	AR279261	AR279261 Sequence	948	137.5	6.2	34852	13	AF106582	AF106582 Caenorhab
876	138.5	6.3	5318	2	AR097041	AR097041 Sequence	949	137.5	6.2	37902	4	AC149378	AC149378 Phakoposr
877	138.5	6.3	5318	2	AR279260	AR279260 Sequence	950	137.5	6.2	94341	4	CT954251	CT954251 M.truncat
c 878	138.5	6.3	6116	2	CQ606065	CQ606065 Sequence	951	137.5	6.2	99360	4	NCB112	AL513444 Neurospor
c 879	138.5	6.3	7295	4	SCU30626	U30626 Saccharomyc	c 952	137.5	6.2	99802	15	BX571857	Continuation (28 o

c 953	137.5	6.2	110000	4	AP008214_278	Continuation (279	c1026	137	6.2	274091	12	CT574544	CT574544	Danio rer
c 954	137.5	6.2	110000	4	CR380958_12	Continuation (13 o	1027	137	6.2	314743	13	AE003495	AE003495	Drosophil
c 955	137.5	6.2	110000	4	AE016816_6	Continuation (7 of	1028	136.5	6.2	734	11	DQ120982	DQ120982	Huho tai
c 956	137.5	6.2	110000	4	AP007151_36	Continuation (37 o	1029	136.5	6.2	900	4	DQ146396	DQ146396	Triticum
c 957	137.5	6.2	110000	15	BA000033_27	Continuation (28 o	1030	136.5	6.2	1512	2	AR778517	AR778517	Sequence
c 958	137.5	6.2	110000	15	BA000035_13	Continuation (14 o	1031	136.5	6.2	1512	8	DQ332622	DQ332622	Synthetic
c 959	137.5	6.2	111150	5	CR759772_13	Continuation (14 o	1032	136.5	6.2	1592	6	BC094915	BC094915	Mus muscu
c 960	137.5	6.2	111122	12	AC186577	CR759772 Human DNA	1033	136.5	6.2	1611	6	MMU70651	MMU70651	Mus muscu
c 961	137.5	6.2	142010	4	AP003928	AC186577 Zee may	1034	136.5	6.2	1795	5	GIEMUCIA	GIEMUCIA	Sequence
c 962	137.5	6.2	142952	5	AL391495	AP003928 Oryza sat	1035	136.5	6.2	1923	2	AX952986	AX952986	Sequence
c 963	137.5	6.2	150330	6	AL331186	AL391495 Human DNA	1036	136.5	6.2	1923	2	DD240139	DD240139	NOVEL PHO
c 964	137.5	6.2	153108	5	AL355273	AL331186 Mus muscu	1037	136.5	6.2	2163	4	AC109569	AC109569	Oryza sat
c 965	137.5	6.2	160618	12	AC181688	AL355273 Human DNA	1038	136.5	6.2	3584	4	SCYNL283C	SCYNL283C	Sequence
c 966	137.5	6.2	165997	12	AC167506	AC181688 Strongylo	1039	136.5	6.2	3637	2	AC952985	AC952985	Sequence
c 967	137.5	6.2	166052	12	AC117008	AC167506 Samiri b	1040	136.5	6.2	3637	2	DD240138	DD240138	NOVEL PHO
c 968	137.5	6.2	170885	6	AC126933	AC117008 Rattus no	1041	136.5	6.2	3803	13	AY865075	AY865075	Drosophil
c 969	137.5	6.2	171307	5	AC104020	AC126933 Mus muscu	1042	136.5	6.2	12412	13	AC006669	AC006669	Caenorhab
c 970	137.5	6.2	177685	12	AC149985	AC104020 Homo sapi	1043	136.5	6.2	42596	13	U41263	U41263	Caenorhabdi
c 971	137.5	6.2	194709	12	AC132640	AC149985 Strongylo	1044	136.5	6.2	61052	12	AC123513	AC123513	Dictyoste
c 972	137.5	6.2	207210	6	AC162937	AC132640 Rattus no	1045	136.5	6.2	61187	5	HS8316	HS8316	Human DNA
c 973	137.5	6.2	212528	6	AC182761	AC162937 Mus muscu	1046	136.5	6.2	79554	4	NCB11B23	NCB11B23	Neurospor
c 974	137.5	6.2	231190	12	AC107096	AC182761 Mus muscu	1047	136.5	6.2	84519	12	AC180269	AC180269	Strongylo
c 975	137.5	6.2	232334	12	AC108634	AC107096 Rattus no	1048	136.5	6.2	94549	12	AC149512	AC149512	Xenopus t
c 976	137.5	6.2	235471	6	AC124662	AC108634 Rattus no	1049	136.5	6.2	96558	5	HS598A24	HS598A24	Human DNA
c 977	137.5	6.2	242309	12	AC098167	AC124662 Mus muscu	1050	136.5	6.2	104708	12	AC139336	AC139336	Rattus no
c 978	137.5	6.2	242516	12	AC106523	AC098167 Rattus no	1051	136.5	6.2	109794	14	AP004042	AP004042	Oryza sat
c 979	137.5	6.2	248568	12	AC115184	AC106523 Rattus no	1052	136.5	6.2	110000	4	AP008214_257	AP008214_257	Continuation (258
c 980	137.5	6.2	261414	12	AC122960	AC115184 Rattus no	1053	136.5	6.2	110000	4	AP008217_280	AP008217_280	Continuation (281
c 981	137.5	6.2	316613	4	SCCHR111	X59720 S cerevisia	1054	136.5	6.2	110952	12	AP004042	AP004042	Oryza sat
c 982	137.5	6.2	319857	12	AC006782	AC006782 Caenorhab	1055	136.5	6.2	117199	12	AC176437	AC176437	Strongylo
c 983	137.5	6.2	329976	12	AC127764	AC127764 Rattus no	1056	136.5	6.2	117224	12	AC1010712	AC1010712	Drosophil
c 984	137	6.2	1124	6	AB003320	AB003320 Mus muscu	1057	136.5	6.2	121440	12	AC178928	AC178928	Strongylo
c 985	137	6.2	1969	13	AY864508	AY864508 Drosophil	1058	136.5	6.2	135541	6	AC138108	AC138108	Mus muscu
c 986	137	6.2	2129	13	AY552257	AY552257 Drosophil	1059	136.5	6.2	136240	13	AC117070	AC117070	Dictyoste
c 987	137	6.2	4616	14	DQ497629	DQ497629 Bos tauru	1060	136.5	6.2	142275	12	AC141996	AC141996	Rattus no
c 988	137	6.2	5943	12	CQ363124	CQ363124 Sequence	1061	136.5	6.2	145177	4	AP004708	AP004708	Oryza sat
c 989	137	6.2	26356	13	AF077538	AF077538 Caenorhab	1062	136.5	6.2	147516	4	AP004622	AP004622	Oryza sat
c 990	137	6.2	30255	4	AF077538	AF077538 Nectria h	1063	136.5	6.2	152955	6	AC145575	AC145575	Mus muscu
c 991	137	6.2	34828	13	U41994	U41994 Caenorhabdi	1064	136.5	6.2	157564	11	BX537304	BX537304	Zebrafish
c 992	137	6.2	35793	11	AY016024	AY016024 Takifugu	1065	136.5	6.2	165025	12	AC133393	AC133393	Pan trogl
c 993	137	6.2	35793	13	U80846	U80846 Caenorhabdi	1066	136.5	6.2	170275	12	AC090446	AC090446	Baboon cy
c 994	137	6.2	42909	13	U53341	U53341 Caenorhabdi	1067	136.5	6.2	171820	6	AC151281	AC151281	Mus muscu
c 995	137	6.2	86196	5	AL592046	AL592046 Human DNA	1068	136.5	6.2	174097	5	AC069513	AC069513	Homo sapi
c 996	137	6.2	89216	4	CT867975	CT867975 M.truncat	1069	136.5	6.2	174254	6	AC165443	AC165443	Mus muscu
c 997	137	6.2	95978	13	AV449461	AV449461 Oikopleur	1070	136.5	6.2	177677	12	AC173371	AC173371	Strongylo
c 998	137	6.2	96573	12	AC136672	AC136672 Rattus no	1071	136.5	6.2	177935	6	AC129209	AC129209	Mus muscu
c 999	137	6.2	110000	2	AR863642_04	Continuation (5 of	1072	136.5	6.2	179668	4	AC134045	AC134045	Oryza sat
c1000	137	6.2	110000	15	AS016822_10	Continuation (11 o	1073	136.5	6.2	183319	6	AC154502	AC154502	Mus muscu
c1001	137	6.2	122007	12	AP007900	AP007900 Lotus jap	1074	136.5	6.2	185781	12	AC133071	AC133071	Pan trogl
c1002	137	6.2	123784	12	AC180386	AC180386 Strongylo	1075	136.5	6.2	187080	6	AC154808	AC154808	Mus muscu
c1003	137	6.2	130269	6	AC111067	AC111067 Mus muscu	1076	136.5	6.2	187883	6	AC165141	AC165141	Mus muscu
c1004	137	6.2	130913	12	AC096869	AC096869 Rattus no	1077	136.5	6.2	198599	5	AC108448	AC108448	Homo sapi
c1005	137	6.2	140216	12	AC177159	AC177159 Strongylo	1078	136.5	6.2	204455	6	AC117232	AC117232	Mus muscu
c1006	137	6.2	142870	6	AL607025	AL607025 Mouse DNA	1079	136.5	6.2	206120	12	AC163879	AC163879	Bos tauru
c1007	137	6.2	147935	6	AC175744	AC175744 Mus muscu	1080	136.5	6.2	208625	12	AC164605	AC164605	Mus muscu
c1008	137	6.2	159448	11	AC147905	AC147905 Xenopus t	1081	136.5	6.2	214060	6	AC131081	AC131081	Mus muscu
c1009	137	6.2	161030	12	AC148042	AC148042 Chloroceb	1082	136.5	6.2	218605	12	AC133816	AC133816	Rattus no
c1010	137	6.2	165127	12	AC148043	AC148043 Chloroceb	1083	136.5	6.2	232885	12	AC106163	AC106163	Rattus no
c1011	137	6.2	166564	11	CR376845	CR376845 Zebrafish	1084	136.5	6.2	237588	12	AC025581	AC025581	Mus muscu
c1012	137	6.2	169913	12	AC031980	AC031980 Homo sapi	1085	136.5	6.2	244434	12	AC111461	AC111461	Rattus no
c1013	137	6.2	169994	11	BX321875	BX321875 Zebrafish	1086	136.5	6.2	258319	12	AC127770	AC127770	Rattus no
c1014	137	6.2	172884	6	AC140084	AC140084 Chloroceb	1087	136.5	6.2	271870	12	AC162814	AC162814	Bos tauru
c1015	137	6.2	174097	5	AC069513	AC069513 Homo sapi	1088	136.5	6.2	298050	15	AL935260	AL935260	Lactobaci
c1016	137	6.2	194815	6	AC121793	AC121793 Mus muscu	1089	136	6.2	989	4	AB027423	AB027423	Oryza sat
c1017	137	6.2	196835	12	AC142538	AC142538 Homo sapi	1090	136	6.2	996	4	AB027422	AB027422	Oryza sat
c1018	137	6.2	197530	6	AC099174	AC099174 Rattus no	1091	136	6.2	1167	4	D55714	D55714	Oryza sativ
c1019	137	6.2	200412	13	AC115666	AC115666 Rattus no	1092	136	6.2	1185	6	AB221697	AB221697	Mus muscu
c1020	137	6.2	203498	13	AC011697	AC011697 Drosophil	1093	136	6.2	1281	4	AK073757	AK073757	Oryza sat
c1021	137	6.2	207685	6	AC132404	AC132404 Mus muscu	1094	136	6.2	1416	4	AB027421	AB027421	Oryza sat
c1022	137	6.2	213347	6	AL831741	AL831741 Mouse DNA	1095	136	6.2	1549	6	MMU70657	MMU70657	Mus muscu
c1023	137	6.2	233270	12	AC129038	AC129038 Rattus no	1096	136	6.2	2097	2	CQ733408	CQ733408	Sequence
c1024	137	6.2	242082	12	AC121699	AC121699 Rattus no	1097	136	6.2	2150	2	AR146449	AR146449	Sequence
c1025	137	6.2	268930	12	AC119562	AC119562 Rattus no	1098	136	6.2	2150	2	AR579955	AR579955	Sequence

1099	136	6.2	2161	4	AK122053	AK122053 Oryza sat	1172	135.5	6.1	117983	12	AC178646	AC178646 Strongylo
1100	136	6.2	2165	2	CQ733483	CQ733483 Sequence	1173	135.5	6.1	126592	6	AC183374	AC183374 Mus muscu
1101	136	6.2	2188	4	AF001978	AF001978 Candida a	CI174	135.5	6.1	150259	12	AC177577	AC177577 Strongylo
1102	136	6.2	2684	5	BC059356	BC059356 Homo sapi	CI175	135.5	6.1	152206	12	AC174251	AC174251 Strongylo
1103	136	6.2	3015	2	BD129573	BD129573 Polynucle	CI176	135.5	6.1	153206	12	AC178242	AC178242 Strongylo
1104	136	6.2	3015	2	BD277873	BD277873 Methi and	CI177	135.5	6.1	155683	12	AC180041	AC180041 Strongylo
1105	136	6.2	3015	13	LMSAP2GN	Z46970 L.mexicana	CI178	135.5	6.1	161996	13	AC008284	AC008284 Drosophil
1106	136	6.2	6783	2	CS252723	CS252723 Sequence	CI179	135.5	6.1	167254	5	CNS05TDS	AL357093 Human chr
1107	136	6.2	6783	2	CS274060	CS274060 Sequence	CI180	135.5	6.1	168122	12	AC146997	AC146997 Arabacia p
1108	136	6.2	6783	2	DD088837	DD088837 A method	CI181	135.5	6.1	171849	5	AC010616	AC010616 Homo sapi
1109	136	6.2	6783	2	AC583631	AC583631 Sequence	CI182	135.5	6.1	172527	12	AC181183	AC181183 Strongylo
1110	136	6.2	10792	13	LSU54556	US4556 Litomosoid	CI183	135.5	6.1	175506	13	AC008004	AC008004 Drosophil
1111	136	6.2	26142	4	SC8277	Z46833 S.cerevisia	CI184	135.5	6.1	176231	13	AC008367	AC008367 Drosophil
1112	136	6.2	37487	2	DD158931	DD158931 NOVEL COM	CI185	135.5	6.1	177816	12	AC017643	AC017643 Drosophil
1113	136	6.2	37487	2	DD158931	DD158931 Sequence	CI186	135.5	6.1	183915	12	AC141939	AC141939 Rattus no
1114	136	6.2	74014	4	NCB73A16	AX695389 Sequence	CI187	135.5	6.1	188464	6	AC101660	AC101660 Mus muscu
1115	136	6.2	104629	11	BX323045	BX323045 Zebrafish	CI188	135.5	6.1	195729	12	AC178061	AC178061 Strongylo
1116	136	6.2	104737	11	CR848045	CR848045 Zebrafish	CI189	135.5	6.1	198421	6	AC163279	AC163279 Mus muscu
1117	136	6.2	106286	4	AC157758	AC157758 Medicago	CI190	135.5	6.1	200011	6	AC153573	AC153573 Mus muscu
1118	136	6.2	109422	15	CP000046_27	Continuation (28 o	CI191	135.5	6.1	204850	12	AC184603	AC184603 Strongylo
1119	136	6.2	110000	4	CR382127_20	Continuation (21 o	CI192	135.5	6.1	210061	12	AC181870	AC181870 Strongylo
1120	136	6.2	110000	15	CP000384_04	Continuation (5 of	CI193	135.5	6.1	214204	12	AC133776	AC133776 Rattus no
1121	136	6.2	114052	12	AC176959	AC176959 Strongylo	CI194	135.5	6.1	220242	11	BX664631	BX664631 Zebrafish
1122	136	6.2	117577	4	AC152752	AC152752 Medicago	CI195	135.5	6.1	227897	12	AC111962	AC111962 Rattus no
1123	136	6.2	122884	5	HS1158812	AL034396 Human DNA	CI196	135.5	6.1	229480	11	AL929150	AL929150 Zebrafish
1124	136	6.2	127576	12	AC178144	AC178144 Strongylo	CI197	135.5	6.1	231008	12	AC129166	AC129166 Rattus no
1125	136	6.2	166640	12	AC176417	AC176417 Strongylo	CI198	135.5	6.1	234469	12	AC119697	AC119697 Rattus no
1126	136	6.2	169584	12	AC144463	AC144463 Gorilla g	CI199	135.5	6.1	237997	12	AC093989	AC093989 Rattus no
1127	136	6.2	171495	12	CT030188	CT030188 Danilo rer	CI200	135.5	6.1	240410	6	AC158617	AC158617 Mus muscu
1128	136	6.2	172764	10	DO279927	DO279927 Human her	CI201	135.5	6.1	246913	6	AC109542	AC109542 Rattus no
1129	136	6.2	172765	11	BX842701	BX842701 Zebrafish	CI202	135.5	6.1	264977	12	AC097564	AC097564 Rattus no
1130	136	6.2	172887	12	BX323011	BX323011 Danilo rer	CI203	135.5	6.1	279242	12	AC114079	AC114079 Rattus no
1131	136	6.2	174097	12	AC184616	AC184616 Strongylo	CI204	135.5	6.1	290783	13	AE003803	AE003803 Drosophil
1132	136	6.2	179836	5	AL590822	AL590822 Human DNA	CI205	135.5	6.1	307443	13	AE003751	AE003751 Drosophil
1133	136	6.2	196879	12	AC173077	AC173077 Bos tauru	CI206	135.5	6.1	349980	2	AX492783	AX492783 Sequence
1134	136	6.2	202214	12	CR848809	CR848809 Danilo rer	CI207	135.5	6.1	349980	2	AX553950	AX553950 Sequence
1135	136	6.2	213432	12	AC068198	AC068198 Homo sapi	CI208	135	6.1	7730	4	ASQ389679	AJ389679 Aegilops
1136	136	6.2	217735	6	AL596116	AL596116 Mouse DNA	CI209	135	6.1	777	4	TAE389668	AJ389668 Triticum
1137	136	6.2	227026	12	AC136659	AC136659 Rattus no	CI210	135	6.1	778	4	TSP389674	AJ389674 Triticum
1138	136	6.2	229259	12	AC096212	AC096212 Rattus no	CI211	135	6.1	792	4	TSP389669	AJ389669 Triticum
1139	136	6.2	235407	12	AC094280	AC094280 Rattus no	CI212	135	6.1	798	4	WHTGLIGP	M16060 Wheat (T.ae
1140	136	6.2	245967	12	AC112091	AC112091 Rattus no	CI213	135	6.1	800	4	TMA389671	AJ389671 Triticum
1141	136	6.2	254650	12	AC128790	AC128790 Rattus no	CI214	135	6.1	801	4	TSP389676	AJ389676 Triticum
1142	136	6.2	261608	12	AC097158	AC097158 Rattus no	CI215	135	6.1	801	4	TMA389672	AJ389672 Triticum
1143	136	6.2	349391	15	BX572095	BX572095 Prochloro	CI216	135	6.1	850	4	TCO389670	AJ389670 Triticum
1144	135.5	6.1	1350	4	AJ781266	AJ781266 Monascus	CI217	135	6.1	947	4	AF120267	AF120267 Triticum
1145	135.5	6.1	1718	4	AK058540	AK058540 Oryza sat	CI218	135	6.1	956	4	AF144104	AF144104 Triticum
1146	135.5	6.1	1836	4	AB066561	AB066561 Oryza sat	CI219	135	6.1	956	4	BD057194	BD057194 Productio
1147	135.5	6.1	1949	13	AY864511	AY864511 Drosophil	CI220	135	6.1	1140	2	BD057194	BD057194 Productio
1148	135.5	6.1	2891	4	YSCUTP1A	M31733 S.cerevisia	CI221	135	6.1	1232	11	AY852250	AY852250 Meleagris
1149	135.5	6.1	3045	4	AB236168	AB236168 Pichia mi	CI222	135	6.1	1475	4	AK058368	AK058368 Oryza sat
1150	135.5	6.1	3089	2	CQ845920	CQ845920 Sequence	CI223	135	6.1	1507	5	BC013325	BC013325 Homo sapi
1151	135.5	6.1	3089	5	AK131434	AK131434 Homo sapi	CI224	135	6.1	1701	14	AF411243	AF411243 Bos tauru
1152	135.5	6.1	3794	13	AY865060	AY865060 Drosophil	CI225	135	6.1	2127	5	AF043446	AF043446 Cercopit
1153	135.5	6.1	3949	2	BD160924	BD160924 Galactose	CI226	135	6.1	2179	5	AF043447	AF043447 Cercopit
1154	135.5	6.1	4386	13	DME294538	AJ294538 Drosophil	CI227	135	6.1	2385	4	TDU437000	AJ437000 Triticum
1155	135.5	6.1	5396	2	CQ600026	CQ600026 Sequence	CI228	135	6.1	2391	4	DQ073548	DQ073548 Leymus mu
1156	135.5	6.1	12664	15	AB005029	AB005029 Halobacte	CI229	135	6.1	2425	2	CS047824	CS047824 Sequence
1157	135.5	6.1	22398	11	FR0271723	AJ271723 Fugu rubr	CI230	135	6.1	2426	12	AC020448	AC020448 Drosophil
1158	135.5	6.1	77410	12	AC183198	AC183198 Bos tauru	CI231	135	6.1	2481	2	AR548073	AR548073 Sequence
1159	135.5	6.1	78529	15	BA000017_28	Continuation (29 o	CI232	135	6.1	3435	4	AK10185	AK10185 Oryza sat
1160	135.5	6.1	82649	11	CR762486	CR762486 Zebrafish	CI233	135	6.1	3832	13	AY865089	AY865089 Drosophil
1161	135.5	6.1	85918	12	DNBR33H2	AL121812 Drosophil	CI234	135	6.1	4138	8	DQ659099	DQ659099 Synthetic
1162	135.5	6.1	93554	12	AC181412	AC181412 Strongylo	CI235	135	6.1	4186	13	AY061106	AY061106 Drosophil
1163	135.5	6.1	95882	5	AC104667	AC104667 Homo sapi	CI236	135	6.1	8259	14	AY158087	AY158087 Bos tauru
1164	135.5	6.1	98521	6	AC094507	AC094507 Rattus no	CI237	135	6.1	9402	2	CQ574607	CQ574607 Sequence
1165	135.5	6.1	110000	2	DD086466_07	Continuation (18 of	CI238	135	6.1	10789	12	AC017895	AC017895 Drosophil
1166	135.5	6.1	110000	4	CR382123_09	Continuation (10 o	CI239	135	6.1	28709	12	AC160844	AC160844 Homo sapi
1167	135.5	6.1	110000	4	AE016817_10	Continuation (11 o	CI240	135	6.1	55963	6	AL663069	AL663069 Mouse DNA
1168	135.5	6.1	110000	4	AP007150_07	Continuation (18 of	CI241	135	6.1	79554	4	NCB11B23	AL669991 Neurosp
1169	135.5	6.1	110000	15	CP0000431_01	Continuation (2 of	CI242	135	6.1	90373	13	AC115680	AC115680 Dictyoste
1170	135.5	6.1	110000	15	AE014295_15	Continuation (16 o	CI243	135	6.1	117327	5	AL663093	AL663093 Human DNA
1171	135.5	6.1	110000	15	BA000018_27	Continuation (28 o	CI244	135	6.1	124457	5	AC115115	AC115115 Homo sapi

1245	135	6.1 141134	12	AC176729	Strongylo	cl1318	134.5	6.1 165277	12	CR628321	CR628321	Danio rer
1246	135	6.1 144082	12	AC181046	Strongylo	cl1319	134.5	6.1 167889	6	AC175667	AC175667	Mus muscu
1247	135	6.1 157052	11	AL929459	Zebrafish	cl1320	134.5	6.1 168354	4	AP005185	AP005185	Oryza sat
1248	135	6.1 169895	12	AC178023	Strongylo	cl1321	134.5	6.1 168991	12	AC090411	AC090411	Homo sapi
1249	135	6.1 171657	10	AY961628	Human her	cl1322	134.5	6.1 169461	6	AC182486	AC182486	Mus muscu
1250	135	6.1 175302	12	AC020587	Homo sapi	cl1323	134.5	6.1 174673	4	AP005196	AP005196	Oryza sat
1251	135	6.1 187701	6	AC102341	Mus muscu	cl1324	134.5	6.1 179023	12	AC164924	AC164924	Callithri
1252	135	6.1 188872	13	AC099009	Drosophi	cl1325	134.5	6.1 181047	12	AC016765	AC016765	Homo sapi
1253	135	6.1 193341	12	AC134500	Rattus no	cl1326	134.5	6.1 181861	12	AC180715	AC180715	Strongylo
1254	135	6.1 196337	13	AC005894	Drosophi	cl1327	134.5	6.1 183783	11	BX539325	BX539325	Zebrafish
1255	135	6.1 196558	6	AC073946	Mus muscu	cl1328	134.5	6.1 186708	11	BX323873	BX323873	Zebrafish
1256	135	6.1 203127	11	BX322566	Zebrafish	cl1329	134.5	6.1 187303	12	CR318651	CR318651	Danio rer
1257	135	6.1 211585	6	AL626784	Mouse DNA	cl1330	134.5	6.1 190628	12	AC024700	AC024700	Homo sapi
1258	135	6.1 212357	12	AC127133	Rattus no	cl1331	134.5	6.1 192936	6	AC148320	AC148320	Mus muscu
1259	135	6.1 232382	12	AC098991	Rattus no	cl1332	134.5	6.1 205871	12	AC171150	AC171150	Callithri
1260	135	6.1 233760	11	BX681417	Zebrafish	cl1333	134.5	6.1 206116	6	AC132949	AC132949	Mus muscu
1261	135	6.1 234778	12	AC097097	Rattus no	cl1334	134.5	6.1 207267	6	AC145346	AC145346	Mus muscu
1262	135	6.1 238340	12	AC130161	Rattus no	cl1335	134.5	6.1 218334	12	AC162697	AC162697	Bos tauru
1263	135	6.1 239972	12	AC095835	Rattus no	cl1336	134.5	6.1 219754	6	AC175461	AC175461	Mus muscu
1264	135	6.1 242171	13	AB003832	Drosophi	cl1337	134.5	6.1 223662	6	AC170597	AC170597	Mus muscu
1265	135	6.1 245628	12	AC156406	Bos tauru	cl1338	134.5	6.1 227458	12	AC110137	AC110137	Rattus no
1266	135	6.1 250902	12	AC131965	Rattus no	cl1339	134.5	6.1 229615	12	AC095673	AC095673	Rattus no
1267	135	6.1 266726	12	AC112860	Rattus no	cl1340	134.5	6.1 248378	12	AC128989	AC128989	Rattus no
1268	135	6.1 273619	12	AC112862	Rattus no	cl1341	134.5	6.1 349575	15	BX927154	BX927154	Corynebact
1269	135	6.1 278499	12	AC178901	Strongylo	cl1342	134.5	6.1 349980	2	AX127150	AX127150	Sequence
1270	134.5	6.1 1923	2	AR562235	Sequence	cl1343	134.5	6.1 349980	2	AX127151	AX127151	Sequence
1271	134.5	6.1 1923	2	AX112078	Sequence	cl1344	134	6.1 492	5	HUMMTR	L46721	Homo sapien
1272	134.5	6.1 1949	13	AY864510	Drosophi	cl1345	134	6.1 1261	4	DQ267479	DQ267479	Hordeum v
1273	134.5	6.1 2047	4	AK107645	Oryza sat	cl1346	134	6.1 2075	4	AK111479	AK111479	Oryza sat
1274	134.5	6.1 2058	2	CQ751984	Sequence	cl1347	134	6.1 2490	2	CS113399	CS113399	Sequence
1275	134.5	6.1 2080	11	AB006322	Danio rer	cl1348	134	6.1 2663	10	EBVELLFL1	AX9106	Epstein-Bar
1276	134.5	6.1 2428	11	BC053239	Danio rer	cl1349	134	6.1 3783	2	AX358421	AX358421	Sequence
1277	134.5	6.1 3169	4	AB182388	Oryza sat	cl1350	134	6.1 4287	2	CQ610164	CQ610164	Sequence
1278	134.5	6.1 3170	4	AK111824	Oryza sat	cl1351	134	6.1 5658	2	AX358423	AX358423	Sequence
1279	134.5	6.1 3184	11	CR942683	Xenopus t	cl1352	134	6.1 9113	8	CVP0G1408	U1228	Promoter-pr
1280	134.5	6.1 3220	11	BC117640	Danio rer	cl1353	134	6.1 32768	2	BD003751	BD003751	Polynucle
1281	134.5	6.1 3426	4	AY553933	Triticum	cl1354	134	6.1 32768	2	CQ788980	CQ788980	Sequence
1282	134.5	6.1 5337	2	AX345341	Sequence	cl1355	134	6.1 32768	2	AR218839	AR218839	Sequence
1283	134.5	6.1 9931	2	CS360445	Sequence	cl1356	134	6.1 33706	13	C6C255G4	Z70680	Caenorhabdi
1284	134.5	6.1 13123	4	DQ419514	Aspergill	cl1357	134	6.1 38773	3	CET06E4	Z70756	Caenorhabdi
1285	134.5	6.1 33998	12	AC145651	Homo sapi	cl1358	134	6.1 79426	6	AL807830	AL807830	Mouse DNA
1286	134.5	6.1 38311	5	AP007215	Homo sapi	cl1359	134	6.1 80060	11	CR936846	CR936846	Zebrafish
1287	134.5	6.1 76995	12	AC168706	Strongylo	cl1360	134	6.1 82895	4	AL732348	AL732348	Oryza sat
1288	134.5	6.1 87093	15	AP006620	Nocardia	cl1361	134	6.1 89019	4	BX842624	BX842624	Neurospor
1289	134.5	6.1 88400	2	CQ924550	Sequence	cl1362	134	6.1 110000	12	CR382130	CR382130	Continuation (14 o
1290	134.5	6.1 88400	2	DD090936	CLONING G	cl1363	134	6.1 110000	12	AC095248	Continuation (4 of	
1291	134.5	6.1 110000	4	AP008213_194	Continuation (195	cl1364	134	6.1 110000	15	CR91197_09	Continuation (10 o	
1292	134.5	6.1 110000	4	CR382130_08	Continuation (9 of	cl1365	134	6.1 124321	4	OSA245900	Continuation (10 o	
1293	134.5	6.1 110000	4	CR382132_10	Continuation (11 o	cl1366	134	6.1 149052	12	AC179275	Continuation (10 o	
1294	134.5	6.1 110000	15	BA000036_23	Continuation (24 o	cl1367	134	6.1 160432	11	AL929072	Continuation (14 o	
1295	134.5	6.1 110000	15	BA000036_24	Continuation (25 o	cl1368	134	6.1 172918	11	BX323457	Zebrafish	
1296	134.5	6.1 110254	11	CR759879	Zebrafish	cl1369	134	6.1 173714	12	AC147748	Continuation (14 o	
1297	134.5	6.1 125354	6	AC175818	Mus muscu	cl1370	134	6.1 179355	6	AC115631	Mus muscu	
1298	134.5	6.1 129213	12	AC181800	Strongylo	cl1371	134	6.1 180695	12	AC140661	Pan trogl	
1299	134.5	6.1 133853	12	AC179271	Strongylo	cl1372	134	6.1 185587	6	AC140346	Mus muscu	
1300	134.5	6.1 137955	12	AC182791	Sorex ara	cl1373	134	6.1 188130	6	AC105976	Mus muscu	
1301	134.5	6.1 144283	6	AC175385	Mus muscu	cl1374	134	6.1 196783	6	AC137855	Mus muscu	
1302	134.5	6.1 146080	11	AL953855	Zebrafish	cl1375	134	6.1 203669	12	AC113929	Homo sapi	
1303	134.5	6.1 149530	12	AC181461	Strongylo	cl1376	134	6.1 210658	5	AC138775	Homo sapi	
1304	134.5	6.1 150110	12	AC097722	Homo sapi	cl1377	134	6.1 220811	6	AC087795	Genomic S	
1305	134.5	6.1 150214	5	AP006345	Homo sapi	cl1378	134	6.1 241943	12	AC107476	Rattus no	
1306	134.5	6.1 151241	6	AC179922	Mus muscu	cl1379	134	6.1 242302	12	AC095431	Rattus no	
1307	134.5	6.1 153364	12	AC173965	Mus muscu	cl1380	134	6.1 242302	12	AC095431	Rattus no	
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1391	133.5	6.0	1397	4	WHTGLIGY	M16064 Wheat (T.ae	1464	133	6.0	2125	5	AB220498	AB220498 Macaca fa
1392	133.5	6.0	1858	4	AB059812	AB059812 Triticum	1465	133	6.0	2139	5	AF043448	AF043448 Cercopith
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1404	133.5	6.0	120646	12	AC176957	AC176957 Strongylo	1477	133	6.0	3228	8	DQ331924	DQ331924 Synthetic
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1421	133.5	6.0	185195	6	AC134565	AC134565 Mus muscu	1494	133	6.0	110000	4	CR382128	CR382128 13
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ALIGNMENTS

RESULT 1
BD140585
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD140585 2284 bp DNA linear PAT 18-SEP-2002
Polypeptides and nucleic acids encoding the same.
BD140585
BD140585.1 GI:23235530
JP 2002505850-A/68.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 2284)
Wood, W.I., Goddard, A., Gurney, A.L., Yuan, J., Baker, K.P. and
Zheng, J.
Patent: JP 2002505850-A 68 26-FEB-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002505850-A/68
PD 26-FEB-2002
PR 01-DEC-1998 JP 2000523338
PR 03-DEC-1997 US 60/067411, 11-DEC-1997 US 60/069334 PR
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12-DEC-1997 US 60/069425, 16-DEC-1997 US 60/069696 PR
16-DEC-1997 US 60/069694, 16-DEC-1997 US 60/069702 PR
17-DEC-1997 US 60/069870, 17-DEC-1997 US 60/069873 PR
18-DEC-1997 US 60/068017, 05-JAN-1998 US 60/070440 PR
09-FEB-1998 US 60/074086, 09-FEB-1998 US 60/074092 PR
25-FEB-1998 US 60/075945
PI WILLIAM I WOOD, AUDREY GODDARD, AUSTIN L GURNEY, JEAN YUAN, KEVIN
PI P BAKER,

PI JIAN ZHENG
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12P21/02,
PC C12P21/08, C12Q1/68, C12N15/00, C12N5/00
CC Polypeptides and nucleic acids encoding the same FH Key
Location/Qualifiers
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Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-944-929-83 (1-431) x BD140585 (1-2284)

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RESULT 2
BD378361 2284 bp DNA linear PAT 04-NOV-2005
LOCUS SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
DEFINITION THE SAME.
ACCESSION BD378361
VERSION BD378361.1 GI:92277455
KEYWORDS JP 2003524387-A/68.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Roy, M.A., Napier, M.A., Tumas, D., Kljavin, I. J., Hillan, K.J.,
Gurney, A.L., Grimaldi, C.J., Godowski, P.J., Goddard, A.,
Gerritsen, M.E., Filvaroff, E., Dan, Eaton, L., Botstein, D.,
Baker, K.P., Ferrata, N. and Wood, W.I.
TITLE SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
JOURNAL THE SAME
Patent: JP 2003524387-A 68 19-AUG-2003;
Genentech Inc, Kevin P Baker, David Botstein, Dan L Eaton, Napoleone
Ferrara, Ellen Filvaroff, Mary E Gerritsen, Audrey Goddard, Paul J
Godowski, Christopher J Grimaldi, Austin L Gurney, Kenneth J Hillan,
Ivar J Kljavin, Mary A Napier, Margaret Ann Roy, Daniel Tumas, William
I Wood
COMMENT OS Homo Sapien
PN JP 2003524387-A/68
PD 19-AUG-2003
PF 01-DEC-1999 JP 2000585407
PR 01-DEC-1998 US US9825108, 16-DEC-1998 US 60/112850, PR
22-DEC-1998 US 60/113296
PI margaret ann roy, mary a napier, daniel tumas, ivar j kljavin, PI
kenneth j hillan, austin l gurney, christopher
PI j grimaldi, paul j

PI godowski,
PI audrey goddard,mary e gerritsen,ellen filvaroff,dan PI 1
eaton,david botstein,
PI kevin p baker,napoleone ferrara,william i wood CC
FH Key Location/Qualifiers.
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
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DB 1246 CTTTCTATGTCAANTGTGGAGTCTTCCACTATGATAAACTGCTTCTGGGAAGGTAGG 1305
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB 1306 GAGGCCAGTCCAGGAGTCTCTCCAGGCGAGTGTCCAGAAATCAGTACGGCTTCCA 1365
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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AR252736 2284 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 514 from patent US 6478825.
DEFINITION AR252736
ACCESSION AR252736
VERSION AR252736.1 GI:27300644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 514 12-NOV-2002;
Osteotech, Inc.; Batontown, NJ
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Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-09-944-929-83 (1-431) x AR252736 (1-2284)
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21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLeuLysSerLeuLysValValIleAsp 40
286 CTAAGCCTGCTGCTAGTCAAGATTCCTCAAAAGAGCTAGAGATGTGTGATGAC 345
41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
346 ATCCAGTCATCTCTTCTAAGGGAATCAGAGCAATGAGCCGTATATACTTCAACTCA 405
61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
406 GAAGACTGCATTAATCTTCTGCTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465
81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
706 TCAAGCCCAACCATATCTCATGGAGACACACTTCTCAGAAGTTTGGATCCTCAGAT 765
181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
766 CACCTGGAGAACTATTAAAGTGGATGAAGCAAGTGCCAGCTCCTTGCTTATAGGAA 825
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826 AAAGGCCAATCTCAGAGTTTCAACAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
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241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
946 ACTCCAAAGCCGCCACCTTCTACCCACCAAGTCTCATGTCAGTACACCTCTGGGACTTC 1005
261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
1006 CAGCCACAGCTGGCCACCAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCCAAG 1065
281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
1126 GCAGTTCTGACTACCACTTTCAGGCACCTCAGGACCTCAGGACTCGAAGGACGCTTAGAACCAT 1185
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1306 GAGGCCAGTCAGGAGATTCCTCCAGGCGAGTGTCCAGAAATATAGTACGGCTTCCA 1365
381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400

1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTCTCTGGTAGAGC 1425
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1426 CTCGTCTCTCGGTAGAACTCTTTCGGAATCACTCCGAGAAACGTTTACTCAAGACTG 1485
421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431
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RESULT 4
DD028540 2284 bp DNA linear PAT 04-NOV-2005
LOCUS Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
DEFINITION the Same.
ACCESSION DD028540
VERSION DD028540.1 GI:92561177
KEYWORDS JP 2004203742-A/369.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2284)
AUTHORS Grimaldi, C.J., Ashkenazi, A.J., Desnoyers, L., Baker, K.P.,
Godowski, P.J., Goddard, A., Gerritsen, M.E., Gerber, H., Fong, S.,
Ferrara, N., Eaton, D.L., Botstein, D., Gurney, A.L., Kljavin, I.J.,
Napier, M.A., Zhang, Z., Wood, W.I., Williams, M.P., Tumas, D.,
Watanabe, C.K., Stewart, T.A., Roy, M.A., Paoni, N.F. and Pan, J.
TITLE Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
the Same
JOURNAL Patent: JP 2004203742-A 369 22-JUL-2004;
Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney,
Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan
OS Homo Sapien
PN JP 2004203742-A/369
PD 22-JUL-2004
PF 25-SEP-2002 JP 2002341509
PR 02-JUN-1999 US US9912252, 23-JUN-1999 US 60/141037, PR
26-JUL-1999 US 60/145698, 20-JUL-1999 US 60/144758, PR
06-JAN-2000 US US000376, 11-FEB-2000 US US0003565, PR
18-FEB-2000 US US0004341, 22-FEB-2000 US US0004414, PR
24-FEB-2000 US US0004914, 24-FEB-2000 US US0005004, PR
02-MAR-2000 US US0005841, 15-MAR-2000 US US0006884, PR
05-JAN-2000 US US0000219, 20-DEC-1999 US US990911, PR
16-DEC-1999 US US930095, 28-JUL-1999 US 60/146222, PR
17-AUG-1999 US 60/149396, 15-SEP-1999 US US9921090, PR
15-SEP-1999 US US9921547, 08-OCT-1999 US 60/158663, PR
30-NOV-1999 US US9928313, 01-DEC-1999 US US9928301, PR
20-MAR-2000 US US0007377, 07-JUL-1999 US 60/143048, PR
christopher j grimaldi, avi j ashkenazi, luc desnoyers, kevin p baker,
PI paul j godowski, audrey goddard, mary e gerritsen, hanspeter pi
gerber, PI sherman fong, napoleone ferrara, dan l eaton, david botstein, PI
austin l gurney, PI ivar j kljavin, mary a napier, zemin zhang, william PI i
wood, mickey PI p williams,
PI daniel tumas, colin k watanabe, timothy a stewart, margaret ann
PI roy, PI nicholas f paoni, james pan
CC PI
FH Key Location/Qualifiers.
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1. 2284
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source
ORIGIN
Alignment Scores: 2.72e-139 Length: 2284
Pred. No.: 2211.00 Matches: 431
Score:

Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
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QY	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
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QY	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200
DB	766	CACCTGGAGAACTATTAAAGATGATGAAGCAAGTCCCGAGCTCTTCTGTATAAGGAA	825
QY	201	LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
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QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
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LOCUS	DD031661	2284 bp	DNA linear PAT 04-NOV-2005
DEFINITION	COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES.		
ACCESSION	DD031661		
VERSION	DD031661.1	GI:92605001	
KEYWORDS	JP 2004516227-A/57.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2284) Watanabe,C.K., Yan,M., Shelton,D.L., Smith,V., Stewart,T.A., Wood,W.I., Tumas,D., Gurney,A.L., Pennica,D., Ashkenazi,A.J., Baker,K.P., Lu,Y., Pan,J., Kabakoff,R.C., Henzel,W., Hebert,C. and Goddard,A.		
TITLE	COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED		
JOURNAL	Patent: JP 2004516227-A 57 03-JUN-2004;		
COMMENT	Genentech Inc et al OS Homo sapiens PN JP 2004516227-A/57 PD 03-JUN-2004 PF 02-MAR-2000 JP 2000603379 PR 30-NOV-1999 US US9928313,02-DEC-1999 US US9928564, PR 18-FEB-2000 US US0004341,22-FEB-2000 US US0004414, PR 30-NOV-1999 US US9928409,01-DEC-1999 US US9928301, PR 01-DEC-1999 US US9928634,02-DEC-1999 US US9928551, PR 18-FEB-2000 US US0004342,02-DEC-1999 US US9928565, PR 16-DEC-1999 US US9930095,20-DEC-1999 US US9930999, PR 30-DEC-1999 US US9931274,05-JAN-2000 US US0000219, PR 06-JAN-2000 US US000377,05-JAN-2000 US US0000376, PR 11-FEB-2000 US US0003565,29-NOV-1999 US US9928214, PR 15-SEP-1999 US US9921090,05-OCT-1999 US US9923089, PR 04-MAY-1999 US 60/132371,14-MAY-1999 US 60/134287, PR 02-JUN-1999 US US9912252,23-JUN-1999 US 60/141037, PR 20-JUL-1999 US 60/144758,26-JUL-1999 US 60/145698, PR 28-JUL-1999 US 60/146222,20-APR-1999 US US9908615, PR 23-MAR-1999 US 60/125775,12-MAR-1999 US 60/123957, PR 23-MAR-1999 US 60/123618,08-MAR-1999 US US9905028, PR 28-APR-1999 US 60/131445,12-APR-1999 US 60/128849, PR 01-SEP-1999 US US9920111,08-SEP-1999 US US9920594, PR 13-SEP-1999 US US9920944,15-SEP-1999 US US9921547, PR 29-OCT-1999 US 60/162506 PI colin k watanabe,minhong yan,david l shelton,victoria smith, PI timothy a stewart,william i wood,daniel tumas,austin l gurney, PI diane pennica,avi j ashkenazi,kevin p baker,yammi lu,james pan, PI rhona c kabakoff,william henzel,carolyn hebert,audrey goddard CC		

FEATURES FH Key Location/Qualifiers.

source

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ORIGIN

Alignment Scores:

Pred. No.: 2,72e-139 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
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US-09-944-929-83 (1-431) x DD031661 (1-2284)

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DB 706 TCAAGCCCAACCGATATCTCATGGAGACACACTTTCTCAGAAGTTTGGATCTCAGAT 765
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DB 1186 CCGTTTACAGAAATCTCCAACTTTAACTTTGAACACACAGGAATGTATTAACCTTACTCA 1245
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RESULT 6
DD039442 2284 bp DNA linear PAT 04-NOV-2005
LOCUS Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
DEFINITION the Same.
ACCESSION DD039442
VERSION DD039442.1 GI:92629391
KEYWORDS JP 2004522402-A/369.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Zhang, Z., Wood, W.I., Ashkenazi, A.J., Botstein, D., Napier, M.A.,
Klavin, I.J., Gurney, A.L., Grimaldi, C.J., Godowski, P.J.,
Goddard, A., Paoni, N.F., Stewart, T.A., Tamas, D., Watanabe, C.K.,
Williams, M.P., Baker, K.P., Pan, J., Roy, M.A., Gerritsen, M.E.,
Gerber, H., Fong, S., Ferrara, N., Eaton, D.L. and Desnoyers, L.
Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
the Same
Patent: JP 2004522402-A 369 29-JUL-2004;
Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney,
Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan
OS Homo Sapien
PN JP 2004522402-A/369
PD 29-JUL-2004
PF 30-MAR-2000 JP 2001500766
PR 06-JAN-2000 US US0000376,11-FEB-2000 US US00003565, PR
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08-OCT-1999 US 60/158663,02-MAR-2000 US US0005841, PR
20-MAR-2000 US US0007377,02-JUN-1999 US US9912552 PI zemin
zhang,william i wood,avi j ashkenazi,david pi botstein,mary
PI a napier,

PI ivar j kljavin,austin l gurney,christopher j grimaldi,paul j
 PI godowski,
 PI audrey goddard,nicholas f paoni,timothy
 PI a steward,daniel tumas,
 PI colin k watanabe,mickey p williams,kevin p baker,james pan, PI
 margaret ann roy,mary e gerritsen,hanspeter gerber, sherman PI
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 PI napoleone ferrara,dan l eaton,luc desnoyers
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Location/Qualifiers.

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US-09-944-929-83 (1-431) x DD039442 (1-2284)

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 DEFINITION the Same.
 ACCESSION DD249590
 VERSION DD249590.1 GI:99025485
 KEYWORDS JP 2005304500-A/369.
 SOURCE unidentified
 ORGANISM unclassified
 unclassified sequences.
 REFERENCE 1 (bases 1 to 2284)
 AUTHORS Napiier,M.A., Kljavin,I.J., Gurney,A.L., Grimaldi,C.J.,
 Watanabe,C.K., Stewart,T.A., Zhang,Z., Wood,W.I., Williams,P.M.,
 Tumas,D., Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H.,
 Fong,S., Paoni,N.P., Pan,J., Roy,M.A., Ferrara,N., Baton,D.I.,
 Desnoyers,L., Botstein,D., Baker,K.P. and Ashkenazi,A.J.
 TITLE Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding
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 Patent: JP 2005304500-A 369 04-NOV-2005;
 Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney,
 Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan
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 PP 14-MAR-2005 JP 2005117472
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Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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DB: 2 Gaps: 0

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ACCESSION AR534995
VERSION AR534995.1 GI:53925785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.
and Wood,W.I.
TITLE Antibodies against a secreted polypeptide that stimulates release
of proteoglycans from cartilage
JOURNAL Patent: US 6734288-A 82 11-MAY-2004;
Genentech, Inc.; San Francisco, CA
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DEFINITION Sequence 82 from patent US 6908993.
ACCESSION AR691142
VERSION AR691142.1 GI:74478541
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6908993-A 82 21-JUN-2005;
Genentech, Inc.; South San Francisco, CA
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 ACCESSION AR693626
 VERSION AR693626.1 GI:75184121
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 ORGANISM Unknown.
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 AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: US 6913919-A 514 05-JUL-2005;
 Genetech, Inc.; South San Francisco, CA
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 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
 Db 646 CTTTACATGGCCAAATTTTACAAAGCAGTCACTCCCTAGCCCATCATCATCAGATATAT 705
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 Db 706 TCAAAGCCCAACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
 Db 766 CACTCGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCTTGTCTTATAGGAA 825
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 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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 Db 1066 ACCCTCATTTCTACAGTTTTTACGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
 QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrfile 320
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 DB 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATCAATAAAAGTCTTCTCGGAAGGTAGG 1305
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 LOCUS 2284 bp DNA linear PAT 20-SEP-2005
 DEFINITION Sequence 82 from patent US 6929947.
 ACCESSION AR705580
 VERSION AR705580.1 GI:75924126
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 2284)
 AUTHORS Botstein, D., Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L.,
 Roy, M. A. and Wood, W. I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: US 6929947-A 82 16-AUG-2005;
 Genentech, Inc.; South San Francisco, CA
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 /organism="unknown"
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 Alignment Scores:
 Pred. No.: 2,72e-139 Length: 2284
 Score: 2211.00 Matches: 431
 Percent Similarity: 100.0% Conservative: 0
 Best local Similarity: 100.0% Mismatches: 0
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 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40
 DB 286 CTAAGGCTGTCTAGTACAGATTGCCTCAAAAGAGTCTAGAAGATGTTGTCAITGAC 345
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 DB 346 ATCCAGTCATCTCTTTCTAAGGAAATCAGAGCAATGAGCCCGGTATATATCTCAACTCAA 405
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
 DB 406 GAAGATCGCATTAATTCCTGCTGTTTCACAAAAACATATCAGGGGCAAGAGCATGTAC 465
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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RESULT 13

AR706178

LOCUS

DEFINITION

 Sequence 514 from patent US 6930170.
 2284 bp DNA linear PAT 20-SEP-2005

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 DB 646 CTCTTACATGGCCCAATTTTTCACAAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
 QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
 DB 706 TCAAAGCCCAACCATATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCTCTCAGAT 765
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla 240
 DB 886 GAAAAATGTGAGTGGCTCCAGCTACGGTGGCAGTGTCTTCCACATACCACCTCGGCT 945
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
 DB 946 ACTCCAAAGCCGCGCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
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 QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
 DB 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATGAATAAAAGTCTTCTCGGAAGGTAGG 1305
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 DB 1426 CTGCTCTCTCGGTAGATCTCTTCGGAATCACTCCGCAAGAAAGTGTACTCAAGACTG 1485
 QY 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431
 DB 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

ACCESSION AR706178
VERSION AR706178.1 GI:75924899
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.
TITLE PRO1184 polypeptides
JOURNAL Patent: US 6930170-A 514 16-AUG-2005;
Genentech, Inc.; South San Francisco, CA;
WOX;

FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN
Alignment Scores: 2,72e-139 Length: 2284
Pred. No.: 2211.00 Matches: 431
Score: 2211.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-944-929-83 (1-431) x AR706178 (1-2284)

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QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40
DB 286 CTAAAGGCTCTGCTAGTCAAGATTCCCTCAAAAGAGCTAGAGAGTGTGCTTAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerGln 60
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QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisIleThrAspTyr 160
DB 646 CTCCTACATGGCCCAATTTTACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGTCTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATTCTCAGAGTTCACAAAATTTCTCTGATCAAGAAATAGCTCATCTGCGCCT 895
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RESULT 14
LOCUS AR708652 2284 bp DNA linear PAT 21-SEP-2005
DEFINITION Sequence 82 from patent US 6936254.
ACCESSION AR708652
VERSION AR708652.1 GI:75998546
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Baker, K.P., Botstein, D., Eaton, D.L., Ferrara, N., Filvaroff, E.,
Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C.,
Gurney, A.L., Hillan, K.J., Kljavin, I.J., Napier, M.A., Roy, M.A.,
Tumas, D. and Wood, W.I.
TITLE Method of inducing fetal hemoglobin synthesis
JOURNAL Patent: US 6936254-A 82 30-AUG-2005;
Genentech, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Alignment Scores: 2,72e-139 Length: 2284
Pred. No.: 2211.00 Matches: 431
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
DB 286 CTAAGGCTCTGCTAGTAGTCAGAAATGCCTCAAAAGAGCTAGAGAGATGTTGCA 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrGln 60
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QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCATTAATTTCTTGCTGTTCAACAAAAAATATATCAGGGGACAAAGCATGTAAC 465
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RESULT 15
AR757551 2284 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 514 from patent US 6953836.
DEFINITION AR757551
ACCESSION AR757551
VERSION AR757551.1 GI:83322728
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Desnoyers, L., Goddard, A., Godowski, P. J., Gurney, A. L. and Wood, W. I.
TITLE PRO844 polypeptides
JOURNAL Patent: US 6953836-A 514 11-OCT-2005;
Genentech, Inc.: South San Francisco, CA
FEATURES
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Pred. No.: 2211.00 Matches: 431
Score: 2211.00 Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0% Gaps: 0
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DB 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCCACTGCTACCTATTTTCTGT 525
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Db 1066 ACCCTCATTTCTACAGTTTTCACGGGTGCGGCTACACTCCAGCAATGGCTACAACA 1125
QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db 1126 GCAGTTCTCAGTACCACCTTTCAGGCACCTACGGACTCGAAGGCAGCTTAGAACCATA 1185
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTGGGAAGGTAGG 1305
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1306 GAGGCCAGTCCAGGCAGTTCTCCAGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA 1365
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1366 TTTGAAAAATGGCTTCTTATCGGTCCTCTCTTTGGTGTCTCTGTTCTCTGGTGATAGGC 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
Db 1426 CTCGTCCTCTCGGTAGAAATCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GATTTATGATCAATGGGATCTATGTGGACATC 1518
```

Search completed: September 20, 2007, 06:28:00
Job time : 20395 secs

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: September 20, 2007, 01:26:41; Search time 725 Seconds
        (without alignments)
        4405.455 Million cell updates/sec

Title: US-09-944-929-83
Perfect score: 2211
Sequence: 1 MFFGGESLTVLVIICFLT.....LRRKRYSLDYLINGIYVDI 431
Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Total number of hits satisfying chosen parameters: 11240424
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-THR=4 -MODEL=frame+ p2n.model -DEV=SOFT
-O=/abss/ABSSWEB spo1/US09944929/runat_19092007_174926_26375/app query.fasta_1
-DE=N Geneseq -QFMT=fastap -SUFFIX=ing -SIMRANGE=0.0005 -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=1500 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=1500 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=0 -MINLEN=0
-USER=US09944929 @CGN.1.1.265 @runat_19092007_174926_26375 -NCPU=6 -NO_MMAP
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database: N Geneseq 200701.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*
15: geneseqn2006s.*
16: geneseqn2007s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
No. Score Match Length DB ID Description
RESULT 1
ID AAX80059 standard; cDNA; 2284 BP.
DE Human PRO361 nucleotide sequence.
PN WO928462-A2.
PD 10-JUN-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 2
ID AAA49567 standard; cDNA; 2284 BP.
DE Human PRO361 cDNA.
PN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 3
ID AAF44268 standard; cDNA; 2284 BP.
DE Human PRO361 nucleotide sequence SEQ ID NO:514.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 4
ID ACA64519 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 5
ID ABX96832 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 6
ID ABX78486 standard; DNA; 2284 BP.
DE DNA encoding Novel human secreted protein PRO361.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 7
ID ABX77120 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 8
ID ABX80978 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein cDNA, #182.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 9
ID ACD44487 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 10
ID ABX75951 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO361.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 11
ID ABX89662 standard; cDNA; 2284 BP.
DE cDNA encoding novel secreted and transmembrane protein PRO361.
PN US2002168715-A1.
PD 14-NOV-2002.
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PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 12
ID ABX79658 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein cDNA, #182.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 13
ID ACA93679 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 14
ID ABX81361 standard; DNA; 2284 BP.
DE Novel human secreted or transmembrane protein PRO846 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 15
ID ACA93177 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 16
ID ABX17261 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 17
ID ABX34148 standard; cDNA; 2284 BP.
DE cDNA encoding human pro361 protein.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 18
ID ACA04368 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #15.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 19
ID ACA68116 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US200217164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 20
ID ACA88565 standard; cDNA; 2284 BP.
DE Human secreted and transmembrane polypeptide PRO361 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 21
ID ACD82072 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 22
ID ADA38025 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 23
ID ADA21711 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 24
ID ADA10498 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO361.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 25
ID ADA18042 standard; cDNA; 2284 BP.
DE cDNA encoding human PRO361 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 26
ID ADA28150 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 27
ID ADA94730 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 28
ID ADA38955 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

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Query Match: 100.0% Indels: 0
RESULT 29
ID ADA93076 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003060407-A1.
PD 27-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 30
ID ACH65633 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003044806-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 31
ID ADA22637 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.
PN US2003040473-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 32
ID ACD39623 standard; cDNA; 2284 BP.
DE Human cDNA encoding PRO846.
PN US2003017982-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 33
ID ADA06803 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #146.
PN US2003049638-A1.
PD 13-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 34
ID ADA39496 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003059782-A1.
PD 27-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 35
ID ADB96522 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003054403-A1.
PD 20-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 36
ID ADC57994 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003027754-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 37
ID ADC25838 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0%
RESULT 38
ID ADC25596 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 39
ID ADC55358 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003045463-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 40
ID ADC12225 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003049681-A1.
PD 13-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 41
ID ADC56647 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003064375-A1.
PD 03-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 42
ID ADC11692 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003069403-A1.
PD 10-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 43
ID ADC25717 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 44
ID ADC14814 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 45
ID ADD08346 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 46
ID ADC82171 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003083461-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 47
ID ADD07813 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 48
ID ADC82704 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 49
ID ADD08884 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 50
ID ADD07133 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 51
ID ADC83380 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 52
ID ADD55487 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 53
ID ADD56445 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 54
ID ADD54883 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 55
ID ADE31902 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO361.
PN US2003068647-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 56
ID ADE27037 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 57
ID ADE26504 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 58
ID ADF67441 standard; cDNA; 2284 BP.
DE Human PRO361 nucleotide sequence SEQ ID NO:514.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 59
ID ADH27502 standard; cDNA; 2284 BP.
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 60
ID ADI35695 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 61
ID ADI00188 standard; cDNA; 2284 BP.
DE Novel human secreted and transmembrane protein PRO361 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 62
ID ABX75504 standard; cDNA; 2284 BP.
DE Human secreted/transmembrane protein PRO361 cDNA.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 63
ID ABX78062 standard; cDNA; 2284 BP.
DE Human PRO polynucleotide #146.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 64
ID ABX80474 standard; DNA; 2284 BP.
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DE Novel human secreted or transmembrane protein PRO846 DNA.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 65
 ID ACAG9380 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO361.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 66
 ID ABX90451 standard; cDNA; 2284 BP.
 DE Human secreted/transmembrane protein cDNA, #182.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 67
 ID ABX64297 standard; cDNA; 2284 BP.
 DE cDNA encoding human PRO361 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 68
 ID ABX89495 standard; cDNA; 2284 BP.
 DE Human PRO polynucleotide #15.
 PN US2002132768-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 69
 ID ADE71551 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
 PN US2003096742-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 70
 ID ADF35640 standard; cDNA; 2284 BP.
 DE cDNA encoding human PRO361 polypeptide.
 PN US2003194760-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 71
 ID ADG11890 standard; cDNA; 2284 BP.
 DE cDNA encoding human PRO361 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 72
 ID ADG63494 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
 PN US2003211570-A1.
 PD 13-NOV-2003.

PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 73
 ID ADH19760 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO361.
 PN US2003228656-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 74
 ID ADH21253 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO361.
 PN US2003224358-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 75
 ID ADH20293 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO361.
 PN US2003219856-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 76
 ID ADH43223 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
 PN US2003207401-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 77
 ID ADN00461 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
 PN US2004091972-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 78
 ID ADU25385 standard; cDNA; 2284 BP.
 DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.
 PN US2004220385-A1.
 PD 04-NOV-2004.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 79
 ID ADY39548 standard; cDNA; 2284 BP.
 DE Human mucin/chitinase homolog PRO361 precursor cDNA.
 PN US2005048613-A1.
 PD 03-MAR-2005.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 RESULT 80
 ID ADY73829 standard; cDNA; 2284 BP.
 DE Human PRO361 cDNA, SEQ ID NO: 82.
 PN US2005059115-A1.
 PD 17-MAR-2005.
 PA (GETH) GENENTECH INC..
 Percent Similarity: 100.0% Conservative: 0

RESULT 97
 ID AAH05206 standard; cDNA; 855 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:2041.
 PN EPI074617-A2.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 73.9%
 Best Local Similarity: 72.2%
 Query Match: 35.8%
 Indels: 40
 Conservative: 4
 Mismatches: 24
 RESULT 98
 ID AAH07904 standard; cDNA; 805 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:4739.
 PN EPI074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 94.1%
 Best Local Similarity: 92.9%
 Query Match: 35.3%
 Indels: 5
 Conservative: 2
 Mismatches: 5
 RESULT 99
 ID AAV89087 standard; cDNA; 422 BP.
 DE EST clone CC335.
 PN WO9845436-A2.
 PD 15-OCT-1998.
 PA (GENY-) GENETICS INST INC.
 Percent Similarity: 100.0%
 Best Local Similarity: 98.5%
 Query Match: 28.6%
 Indels: 0
 Conservative: 2
 Mismatches: 0
 RESULT 100
 ID ABX53012 standard; cDNA; 402 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2941.
 PN US2002137160-A1.
 PD 26-SEP-2002.
 PA (BYATT/) BYATT J C.
 PA (MATH/) MATHALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Percent Similarity: 82.6%
 Best Local Similarity: 72.0%
 Query Match: 22.5%
 Indels: 1
 Conservative: 14
 Mismatches: 22
 RESULT 101
 ID ADP28197 standard; DNA; 141 BP.
 DE Human secreted protein encoding sequence SEQ ID #195.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 11.8%
 Indels: 0
 Conservative: 0
 Mismatches: 0
 RESULT 102
 ID AAC05822 standard; cDNA; 295 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 9897.
 PN EPI033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Percent Similarity: 91.5%
 Best Local Similarity: 91.5%
 Query Match: 10.9%
 Indels: 2
 Conservative: 0
 Mismatches: 3
 RESULT 103
 ID AAA45200 standard; cDNA; 242 BP.
 DE Human secreted expressed sequence tag SEQ ID NO:1775.
 PN WO200021991-A1.
 PD 20-APR-2000.
 PA (GENY-) GENETICS INST INC.
 Percent Similarity: 95.9%
 Best Local Similarity: 93.9%
 Query Match: 10.3%
 Indels: 0
 Conservative: 1
 Mismatches: 2
 RESULT 104
 ID AAD33828 standard; cDNA; 1766 BP.
 DE Human secreted protein-encoding gene 17 cDNA clone HLDQ272, SEQ ID NO:27.
 PN WO200224719-A1.
 PD 28-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 40.6%
 Indels: 66
 Conservative: 66
 Mismatches: 171
 Query Match: 8.8%
 Best Local Similarity: 23.2%
 Percent Similarity: 34.3%
 (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
 PN 19-MAR-2003.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 34.5%
 Best Local Similarity: 23.2%
 Query Match: 8.9%
 Indels: 187
 Conservative: 61
 Mismatches: 170
 RESULT 110
 ID ABX71003 standard; cDNA; 1826 BP.
 DE Novel human cDNA sequence #228.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (GOOD/) GOODRICH R W.
 Percent Similarity: 32.6%
 Best Local Similarity: 22.2%
 Query Match: 8.9%
 Indels: 215
 Conservative: 55
 Mismatches: 143
 RESULT 111
 ID ADL25760 standard; cDNA; 1987 BP.
 DE Human cancer suppressing protein cDNA #13.
 PN CN1403478-A.
 PD 19-MAR-2003.
 PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
 Percent Similarity: 34.3%
 Best Local Similarity: 23.2%
 Query Match: 8.8%
 Indels: 187
 Conservative: 60
 Mismatches: 171
 RESULT 112
 ID ADL25762 standard; cDNA; 1987 BP.
 DE Human cancer suppressing protein cDNA #14.

Best Local Similarity: 25.9%
 Query Match: 9.3%
 Indels: 106
 Mismatches: 162
 RESULT 105
 ID ADQ86436 standard; cDNA; 2050 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3308.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 34.5%
 Best Local Similarity: 23.4%
 Query Match: 9.2%
 Indels: 187
 Conservative: 60
 Mismatches: 170
 RESULT 106
 ID ADQ83349 standard; cDNA; 2050 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #163.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 34.5%
 Best Local Similarity: 23.4%
 Query Match: 9.2%
 Indels: 187
 Conservative: 60
 Mismatches: 170
 RESULT 107
 ID ADL91882 standard; cDNA; 2058 BP.
 DE Human PRO60929 encoding cDNA SEQ ID NO:103.
 PN WO2004024076-A2.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.5%
 Best Local Similarity: 23.4%
 Query Match: 9.2%
 Indels: 187
 Conservative: 60
 Mismatches: 170
 RESULT 108
 ID ADQ22215 standard; DNA; 2535 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5035.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 34.5%
 Best Local Similarity: 23.4%
 Query Match: 9.2%
 Indels: 187
 Conservative: 60
 Mismatches: 170
 RESULT 109
 ID AAA96478 standard; cDNA; 1716 BP.
 DE cDNA encoding a human transmembrane protein.
 PN WO200056891-A2.
 PD 28-SEP-2000.
 PA (INCY-) INCYTE PHARM INC.
 Percent Similarity: 32.6%
 Best Local Similarity: 22.2%
 Query Match: 8.9%
 Indels: 215
 Conservative: 55
 Mismatches: 143
 RESULT 110
 ID ABX71003 standard; cDNA; 1826 BP.
 DE Novel human cDNA sequence #228.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 32.6%
 Best Local Similarity: 22.2%
 Query Match: 8.9%
 Indels: 215
 Conservative: 55
 Mismatches: 143
 RESULT 111
 ID ADL25760 standard; cDNA; 1987 BP.
 DE Human cancer suppressing protein cDNA #13.
 PN CN1403478-A.
 PD 19-MAR-2003.
 PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
 Percent Similarity: 34.3%
 Best Local Similarity: 23.2%
 Query Match: 8.8%
 Indels: 187
 Conservative: 60
 Mismatches: 171
 RESULT 112
 ID ADL25762 standard; cDNA; 1987 BP.
 DE Human cancer suppressing protein cDNA #14.

PN CN1403478-A.
 PD 19-MAR-2003.
 PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
 Percent Similarity: 34.3%
 Best Local Similarity: 23.2%
 Query Match: 8.8%
 Indels: 187
 RESULT 113
 ID ABA08275 standard; cDNA; 2095 BP.
 DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:51.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 34.3%
 Best Local Similarity: 23.2%
 Query Match: 8.8%
 Indels: 187
 RESULT 114
 ID AAA26405 standard; cDNA; 1642 BP.
 DE Human secreted protein gene 60 SEQ ID NO:70.
 PN WO200006698-A1.
 PD 10-FEB-2000.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Percent Similarity: 37.1%
 Best Local Similarity: 23.0%
 Query Match: 8.8%
 Indels: 121
 RESULT 115
 ID ADA56613 standard; DNA; 1642 BP.
 DE Gene encoding human secreted protein #424.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Percent Similarity: 37.1%
 Best Local Similarity: 23.0%
 Query Match: 8.8%
 Indels: 121
 RESULT 116
 ID ADL71466 standard; cDNA; 1642 BP.
 DE Novel human secreted protein cDNA seqid 70.
 PN US2004034196-A1.
 PD 19-FEB-2004.
 PA (KOMA/) KOMATSOULIS G A.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (DUAN/) DUAN D R.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAF/) LAFLEUR D W.
 PA (WEIY/) WEI Y.
 Percent Similarity: 37.1%
 Best Local Similarity: 23.0%
 Query Match: 8.8%
 Indels: 121
 RESULT 117
 ID AEL28822 standard; cDNA; 1642 BP.
 DE Human secreted protein coding sequence, SEQ ID 802.
 PN US2006223088-A1.
 PD 05-OCT-2006.
 PA (KOMA/) KOMATSOULIS G A.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (DUAN/) DUAN D R.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAF/) LAFLEUR D W.
 PA (WEIY/) WEI Y.
 Percent Similarity: 37.1%
 Best Local Similarity: 23.0%
 Query Match: 8.8%
 Indels: 121
 RESULT 118
 ID ADA56245 standard; DNA; 1895 BP.
 DE Gene encoding human secreted protein #424.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.4%
 Best Local Similarity: 23.6%
 Query Match: 8.8%
 Indels: 189
 RESULT 119
 ID AEL28454 standard; cDNA; 1895 BP.
 DE Human secreted protein coding sequence, SEQ ID 434.
 PN US2006223088-A1.
 PD 05-OCT-2006.
 PA (KOMA/) KOMATSOULIS G A.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (DUAN/) DUAN D R.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAF/) LAFLEUR D W.
 PA (WEIY/) WEI Y.
 Percent Similarity: 37.1%
 Best Local Similarity: 23.0%
 Query Match: 8.8%
 Indels: 121
 RESULT 120
 ID ACH44978 standard; cDNA; 478 BP.
 DE Human foetal brain cDNA #5703.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Percent Similarity: 51.2%
 Best Local Similarity: 51.2%
 Query Match: 8.5%
 Indels: 35
 RESULT 121
 ID AAS21355 standard; cDNA; 1661 BP.
 DE Human cDNA sequence encoding for PRO4315 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 122
 ID ACA03714 standard; cDNA; 1661 BP.
 DE cDNA encoding human PRO polypeptide #112.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 123
 ID ABX89252 standard; cDNA; 1661 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO4315.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 124
 ID ACD41906 standard; cDNA; 1661 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #112.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 125
 ID ACA04135 standard; cDNA; 1661 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 223.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 126
 ID ADA45742 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 127
 ID ADA76173 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003073212-A1.
 PD 17-APR-2003.

Query Match: 8.8%
 Indels: 189
 RESULT 120
 ID ACH44978 standard; cDNA; 478 BP.
 DE Human foetal brain cDNA #5703.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Percent Similarity: 51.2%
 Best Local Similarity: 51.2%
 Query Match: 8.5%
 Indels: 35
 RESULT 121
 ID AAS21355 standard; cDNA; 1661 BP.
 DE Human cDNA sequence encoding for PRO4315 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 122
 ID ACA03714 standard; cDNA; 1661 BP.
 DE cDNA encoding human PRO polypeptide #112.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 123
 ID ABX89252 standard; cDNA; 1661 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO4315.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 124
 ID ACD41906 standard; cDNA; 1661 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #112.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 125
 ID ACA04135 standard; cDNA; 1661 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 223.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 126
 ID ADA45742 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Indels: 196
 RESULT 127
 ID ADA76173 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003073212-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 128
 ID ADA18823 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 129
 ID ADA61446 standard; cDNA; 1661 BP.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 130
 ID ADB19231 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 131
 ID ADB27772 standard; cDNA; 1661 BP.
 DE cDNA encoding human PRO polypeptide #112.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 132
 ID ADA86251 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 133
 ID ADB15815 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 134
 ID ADA47601 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 135
 ID ADA67396 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 136
 ID ADB30403 standard; cDNA; 1661 BP.
 DE cDNA encoding human PRO polypeptide #112.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 137
 ID ADA85699 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 138
 ID ADA96911 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 139
 ID ADA79215 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 140
 ID ADA87354 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003087345-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 141
 ID ADB16556 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 142
 ID ADA91648 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082694-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 143
 ID ADB14711 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003087351-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Mismatches: 49
 Indels: 167
 Query Match: 196
 RESULT 144
 ID ADA67396 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

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Best Local Similarity: 22.0%      Mismatches: 167
Query Match: 8.5%                Indels: 196
RESULT 14
ID ADB18672 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 145
ID ADA93887 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 146
ID ADB19783 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082891-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 147
ID ADB13095 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 148
ID ACD98535 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 149
ID ADA74349 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 150
ID ADB24582 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide SEQ ID NO 223.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 151
ID ADA82106 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 152
ID ADA75069 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 153
ID ADA85147 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 154
ID ADA84595 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 155
ID ADB29851 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 156
ID ADA80379 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 157
ID ADA75621 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 158
ID ADA46846 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 159
ID ADB25142 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide SEQ ID NO 223.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
RESULT 160
ID ADA82106 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%      Mismatches: 49
Query Match: 8.5%                Mismatches: 167
Indels: 196
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RESULT 160
ID ADA93318 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003077721-AL.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 161
ID ADB26668 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003092147-AL.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 162
ID ADB30955 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003096386-AL.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 163
ID ADA60883 standard; cDNA; 1661 BP.
DE Homo sapiens.
PN US2003049817-AL.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 164
ID ADB24030 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide SEQ ID NO 223.
PN US2003077714-AL.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 165
ID ADA96359 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082690-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 166
ID ADA80931 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082702-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 167
ID ADA95807 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082759-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 168
ID ADA93318 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003077721-AL.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 169
ID ADB21601 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082765-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 170
ID ADA77380 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003068797-AL.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 171
ID ADB18120 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003077710-AL.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 172
ID ADA86803 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082709-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 173
ID ADA87906 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082700-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 174
ID ADA46294 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003054516-AL.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 175
ID ADB28324 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003082699-AL.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 176
ID ADB28876 standard; cDNA; 1661 BP.
```


DE cDNA encoding human PRO polypeptide #112.
PN US2003082706-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 177
ID ADA76828 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 178
ID ADA8458 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 179
ID ADA97463 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 180
ID ADB27220 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 181
ID ADB22153 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 182
ID ADA66844 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 183
ID ADB22705 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 184
ID ADB3478 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide SEQ ID NO 223.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 185
ID ADA92200 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 186
ID ADB15263 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 187
ID ADB38515 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 188
ID ADB37963 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 189
ID ADB66435 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 190
ID ADB89515 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 191
ID ADB90247 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 192
ID ADB93348 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196

Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 193
 ID ADB46971 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082687-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 194
 ID ADB86578 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003082697-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 195
 ID ADB7183 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082696-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 196
 ID ADB34340 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide SEQ ID NO 223.
 PN US200307717-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 197
 ID ADB35444 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide SEQ ID NO 223.
 PN US200307719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 198
 ID ADB33788 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide SEQ ID NO 223.
 PN US200307716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 199
 ID ADB34892 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide SEQ ID NO 223.
 PN US200307718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 200
 ID ADB35996 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide SEQ ID NO 223.
 PN US200307720-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49

Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 201
 ID ADB46391 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003082692-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 202
 ID ADC50264 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003092106-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 203
 ID ADC71811 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003092107-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 204
 ID ADC59790 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003092105-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 205
 ID ADC52797 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID223.
 PN US2003087365-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 206
 ID ADC57151 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID223.
 PN US2003087366-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 207
 ID ADC60342 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 208
 ID ADC50817 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 209
 ID ADC50817 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49

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Query Match: 8.5% Indels: 196
RESULT 209
ID ADC65344 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 210
ID ADC54442 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 211
ID ADC53403 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 212
ID ADC58926 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 213
ID ADC55804 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 214
ID ADC58374 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 215
ID ADD03048 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 216
ID ADC90040 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 217
ID ADC69459 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 218
ID ADC48348 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 219
ID ADD09877 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 220
ID ADD04452 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 221
ID ADC80408 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 222
ID ADD10915 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 223
ID ADC47796 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 224
ID ADC79856 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatch: 167
Indels: 196
RESULT 225
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ID ADD09325 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 226
ID ADD41038 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 227
ID ADD52177 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 228
ID ADD52917 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 229
ID ADD53469 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 230
ID ADD51625 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 231
ID ADD02424 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 232
ID ADD01858 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 233
ID ADD54040 standard; cDNA; 1661 BP.

DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 234
ID ADD92357 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 235
ID ADD91253 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 236
ID ADE03867 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 237
ID ADE32164 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 238
ID ADE22096 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 239
ID ADD79320 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 240
ID ADE41856 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 241
ID ADE17673 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.

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PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 242
ID ADD91805 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 243
ID ADE33268 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 244
ID ADE33820 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 245
ID ADD79872 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 246
ID ADD92909 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 247
ID ADE19329 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 248
ID ADE18777 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 249
ID ADE42973 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 250
ID ADD95762 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 251
ID ADE22648 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 252
ID ADD78766 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 253
ID ADE32716 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 254
ID ADE42408 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 255
ID ADD80424 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 256
ID ADD89452 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 257
ID ADE40736 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003199031-A1.
PD 23-OCT-2003.
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PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 258
 ID ADE04535 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003199034-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 259
 ID ADE92664 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003194777-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 260
 ID ADG21373 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207355-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 261
 ID ADG23014 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207384-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 262
 ID ADF97349 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207370-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 263
 ID ADG80413 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207373-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 264
 ID ADG79861 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207372-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 265
 ID ADH55153 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207381-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 266
 ID ADH55705 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207379-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 267
 ID ADI63924 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207385-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 268
 ID ADI64873 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207386-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 269
 ID ADI63372 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207387-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 270
 ID ADH81786 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207388-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 271
 ID ADH81234 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207377-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 272
 ID ACD3964 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49
 Best Local Similarity: 22.0% Mismatches: 167
 Query Match: 8.5% Indels: 196
 RESULT 273
 ID ACA67105 standard; cDNA; 1661 BP.
 DE cDNA encoding human PRO polypeptide #112.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2% Conservative: 49

RESULT 290
 ID ADE88534 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003199054-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 291
 ID ADE94554 standard; cDNA; 1661 BP.
 DE CDNA encoding human PRO polypeptide #112.
 PN US2003199027-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 292
 ID ADE90965 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003199061-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 293
 ID ADE95106 standard; cDNA; 1661 BP.
 DE CDNA encoding human PRO polypeptide #112.
 PN US2003199052-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 294
 ID ADE93216 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003199060-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 295
 ID ADF34797 standard; cDNA; 1661 BP.
 DE CDNA encoding human PRO polypeptide #112.
 PN US2003199029-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 296
 ID ADE92112 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003199051-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 297
 ID ADE90413 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003199063-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 298
 ID ADF99024 standard; cDNA; 1661 BP.

ID ADE91560 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003199058-Al.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 299
 ID ADG02139 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207352-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 300
 ID ADG21925 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207360-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 301
 ID ADG19995 standard; cDNA; 1661 BP.
 DE CDNA encoding human PRO polypeptide #112.
 PN US2003207376-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 302
 ID ADF97901 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207422-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 303
 ID ADG24118 standard; cDNA; 1661 BP.
 DE Novel human secreted and transmembrane protein PRO4315 cDNA.
 PN US2003207426-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 304
 ID ADF98472 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003208055-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 305
 ID ADG03303 standard; cDNA; 1661 BP.
 DE Human PRO polynucleotide #112.
 PN US2003207351-Al.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 31.2%
 Best Local Similarity: 22.0%
 Query Match: 8.5%
 Conservative: 49
 Mismatches: 167
 Indels: 196

RESULT 306
 ID ADF99024 standard; cDNA; 1661 BP.


```
DE Human PRO polynucleotide #112.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 307
ID ADG16609 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 308
ID ADG05068 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 309
ID ADG19335 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 310
ID ADG13172 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 311
ID ADG08229 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 312
ID ADG15399 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 313
ID ADP96797 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 314
ID ADG05982 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 315
ID ADG23566 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 316
ID ADG03855 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 317
ID ADG24756 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 318
ID ADG07053 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 319
ID ADG07605 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 320
ID ADG55100 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 321
ID ADG60764 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Conservative: 49
Mismatches: 167
Indels: 196
Query Match: 8.5%
RESULT 322
ID ADG61968 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207428-A1.
```


Best Local Similarity: 22.0% Mismatches: 167
Query Match: 8.5% Indels: 196
RESULT 339
ID ADH12470 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 340
ID ADG61316 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 341
ID ADH28403 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 342
ID ADG54548 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 343
ID ADG59588 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 344
ID ADI81012 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 345
ID ADG9755 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 346
ID ADI15226 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196

Query Match: 8.5% Indels: 196
RESULT 347
ID ADG9103 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 348
ID ADI14558 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 349
ID ADI18153 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 350
ID ADG63434 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 351
ID ADJ77329 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 352
ID ADJ65451 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 353
ID ADM27587 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196
RESULT 354
ID ADM42311 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0% Mismatches: 49
Query Match: 8.5% Indels: 196

PA (WATA//) WATANABE C K.			
PA (WOOD//) WOOD W I.			
PA (ZHAN//) ZHANG Z.			
Percent Similarity:	31.2%	Conservative:	49
Best Local Similarity:	22.0%	Mismatches:	167
Query Match:	8.5%	Indels:	196
RESULT 362			
ID AED86138 standard; cDNA; 1661 BP.			
DE Human PRO cDNA, seq id 223.			
PN US2005245730-A1.			
PD 03-NOV-2005.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	31.2%	Conservative:	49
Best Local Similarity:	22.0%	Mismatches:	167
Query Match:	8.5%	Indels:	196
RESULT 363			
ID AEG58085 standard; cDNA; 1661 BP.			
DE Human PRO4315 cDNA SEQ ID NO: 223.			
PN US2006073568-A1.			
PD 06-APR-2006.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	31.2%	Conservative:	49
Best Local Similarity:	22.0%	Mismatches:	167
Query Match:	8.5%	Indels:	196
RESULT 364			
ID AEI43730 standard; cDNA; 1661 BP.			
DE Human cancer-related PRO protein coding sequence - SEQ ID 223.			
PN US2006040351-A1.			
PD 23-FEB-2006.			
PA (BAKE//) BAKER K P.			
PA (BERE//) BERESINI M.			
PA (DEFO//) DEFOGE L.			
PA (DESN//) DESNOYERS L.			
PA (FILV//) FILVAROFF E.			
PA (GAOW//) GAO W.			
PA (GERR//) GERRITSEN M E.			
PA (GODD//) GODDARD A.			
PA (GODO//) GODOWSKI P J.			
PA (GURN//) GURNEY A L.			
PA (SHER//) SHERWOOD S.			
PA (SMIT//) SMITH V.			
PA (STEW//) STEWART T A.			
PA (TUNA//) TUNAS D.			
PA (WATA//) WATANABE C K.			
PA (WOOD//) WOOD W I.			
PA (ZHAN//) ZHANG Z.			
Percent Similarity:	31.2%	Conservative:	49
Best Local Similarity:	22.0%	Mismatches:	167
Query Match:	8.5%	Indels:	196
RESULT 365			
ID AEI23813 standard; cDNA; 1661 BP.			
DE Human secreted/transmembrane protein PRO4315 cDNA, SEQ ID NO:223.			
PN EP1672070-A2.			
PD 21-JUN-2006.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	31.2%	Conservative:	49
Best Local Similarity:	22.0%	Mismatches:	167
Query Match:	8.5%	Indels:	196
RESULT 366			
ID AEA61164 standard; DNA; 30542 BP.			
DE Human MUC2 gene genomic sequence SEQ ID NO:74.			
PN US2005130172-A1.			
PD 16-JUN-2005.			
PA (FARB) BAYER CORP.			
Percent Similarity:	34.1%	Conservative:	35
Best Local Similarity:	25.5%	Mismatches:	176
Query Match:	7.9%	Indels:	95
RESULT 367			
ID RAI29504 standard; cDNA; 15720 BP.			
DE C899P determined cDNA sequence.			
PN WO200149716-A2.			
PD 12-JUL-2001.			
PA (CORI-) CORIXA CORP.			

Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 368
 ID AB162358 standard; DNA; 15720 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:695.
 PN WO2000194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 369
 ID AB233690 standard; cDNA; 15720 BP.
 DE Human colon tumour cDNA for clone C899P SEQ ID NO:1058.
 PN WO200283070-A2.
 PD 24-OCT-2002.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 370
 ID ACD13431 standard; cDNA; 15720 BP.
 DE Human DNA encoding a p53 modifier, SEQ ID 103.
 PN WO200299122-A1.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 371
 ID AAD63141 standard; DNA; 15720 BP.
 DE Human mucin 2 (MUC2) DNA.
 PN US2003190656-A1.
 PD 09-OCT-2003.
 PA (WANG/) WANG Y.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 372
 ID AAD62742 standard; DNA; 15720 BP.
 DE Human mucin 2 (MUC2) DNA.
 PN US2003194733-A1.
 PD 16-OCT-2003.
 PA (WANG/) WANG Y.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 373
 ID ADP88237 standard; cDNA; 15720 BP.
 DE Colon cancer marker gene MUC2, SEQ ID NO:14.
 PN EP1349104-A2.
 PD 01-OCT-2003.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 374
 ID ADP88236 standard; cDNA; 15720 BP.
 DE Colon cancer marker gene NOX1, SEQ ID NO:13.
 PN EP1349104-A2.
 PD 01-OCT-2003.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 375
 ID AD029628 standard; DNA; 15720 BP.
 DE Human colorectal cancer-associated protein coding sequence #50.
 PN EP1439393-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 376
 ID ADQ80264 standard; cDNA; 15720 BP.
 DE Intestinal/tracheal mucin 2 cDNA.
 PN WO2004063709-A2.
 PD 29-JUL-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 377
 ID ADZ49011 standard; DNA; 15720 BP.
 DE Insulin signaling pathway related gene, SEQ ID 340.
 PN US2005085436-A1.
 PD 21-APR-2005.
 PA (LIHH/) LI H.
 PA (MAJU/) MA J.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 378
 ID AEA04440 standard; cDNA; 15720 BP.
 DE Human cDNA from gene under-expressed in cancer, MUC2.
 PN WO2005044990-A2.
 PD 19-MAY-2005.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 379
 ID AEA27625 standard; cDNA; 15720 BP.
 DE Human intestinal mucin cDNA.
 PN WO2005047321-A2.
 PD 26-MAY-2005.
 PA (UYCR-) UNIV CREIGHTON.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 380
 ID ABF69940 standard; DNA; 15720 BP.
 DE Colorectal cancer-associated marker DNA SEQ ID NO:118.
 PN WO2006015047-A2.
 PD 09-FEB-2006.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 381
 ID ABF66654 standard; DNA; 15720 BP.
 DE Colorectal carcinoma (CRC) detection method-related human gene SeqID82.
 PN WO2006015742-A2.
 PD 16-FEB-2006.
 PA (UYER-) UNIV ERLANGEN-NUERNBERG.
 Percent Similarity: 35.0% Conservative: 31
 Best Local Similarity: 24.8% Mismatches: 102
 Query Match: 7.8% Indels: 98
 RESULT 382
 ID ADX97496 standard; DNA; 10371 BP.
 DE Pancreatic cancer associated human protein encoding DNA, SEQ ID 44.
 PN EP1471075-A2.
 PD 27-OCT-2004.
 PA (HINZ/) HINZMANN B.
 PA (ROSE/) ROSENTHAL A.
 PA (PILA/) PILARSKY C.
 PA (DAHL/) DAHL E.
 PA (SPEC/) SPECHT T.
 PA (LICH/) LICHNER R.
 Percent Similarity: 35.9% Conservative: 55
 Best Local Similarity: 22.4% Mismatches: 172

Query Match: 7.8% Indels: 91
 RESULT 383
 ID AEA08147 standard; DNA; 14094 BP.
 DE Human mucin 17 (MUC17SEC) coding sequence - SEQ ID 2.
 PN US2005100925-A1.
 PD 12-MAY-2005.
 PA (BATR/) BATRA S.
 PA (MONI/) MONIAUX N.
 Percent Similarity: 39.0%
 Best Local Similarity: 22.9%
 Query Match: 7.4%
 Indels: 95
 RESULT 384
 ID AEA08146 standard; DNA; 14246 BP.
 DE Human mucin 17 coding sequence - SEQ ID 1.
 PN US2005100925-A1.
 PD 12-MAY-2005.
 PA (BATR/) BATRA S.
 PA (MONI/) MONIAUX N.
 Percent Similarity: 39.0%
 Best Local Similarity: 22.9%
 Query Match: 7.4%
 Indels: 95
 RESULT 385
 ID AEB56450 standard; cDNA; 17847 BP.
 DE Radiochemotherapy response detection associated cDNA SEQ ID NO 25.
 PN WO2005073411-A1.
 PD 11-AUG-2005.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Percent Similarity: 37.0%
 Best Local Similarity: 27.6%
 Query Match: 7.4%
 Indels: 107
 RESULT 386
 ID ABZ11530 standard; cDNA; 1638 BP.
 DE Human polynucleotide SEQ ID NO 412.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 39.9%
 Best Local Similarity: 24.4%
 Query Match: 7.3%
 Indels: 49
 RESULT 387
 ID ADM44048 standard; cDNA; 1638 BP.
 DE Novel human arginine-rich protein cDNA #412.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRNA/) DRMANAC R T.
 Percent Similarity: 39.9%
 Best Local Similarity: 24.4%
 Query Match: 7.3%
 Indels: 49
 RESULT 388
 ID ABL28511 standard; DNA; 2753 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37006.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.5%
 Best Local Similarity: 22.9%
 Query Match: 7.3%
 Indels: 110
 RESULT 389
 ID ABL28510 standard; DNA; 22622 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37003.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.5%
 Best Local Similarity: 22.9%
 Query Match: 7.3%
 Indels: 110
 RESULT 390
 ID ADQ22365 standard; DNA; 6564 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5185.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 391
 ID AEL84674 standard; cDNA; 8106 BP.
 DE Tumor marker gene BAT2D1 cDNA SEQ ID NO 41.
 PN WO2006110593-A2.
 PD 19-OCT-2006.
 PA (MACR-) MACROGENICS INC.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 392
 ID ACF12869 standard; cDNA; 10174 BP.
 DE Human cervical cancer cell marker protein SEQ ID NO:82.
 PN WO2002101075-A2.
 PD 19-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 393
 ID ADQ59188 standard; cDNA; 10174 BP.
 DE MSI-H carcinoma cDNA sequence SEQ ID NO:25.
 PN KR2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G.
 PA (KIMN/) KIM N G.
 PA (LEEJ/) LEE J S.
 PA (RHEE/) RHEE H S.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 394
 ID ADX05906 standard; DNA; 10174 BP.
 DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 471.
 PN WO2005012875-A2.
 PD 10-FEB-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 395
 ID ADY19013 standard; DNA; 10174 BP.
 DE DNA encoding a PRO polypeptide, SEQ ID NO 4819.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 396
 ID AEF74590 standard; DNA; 10174 BP.
 DE Human polynucleotide #104.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (VISS) VISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 397
 ID AAF28060 standard; cDNA; 10347 BP.
 DE Human 07CG27 gene cDNA.
 PN WO200116291-A2.
 PD 08-MAR-2001.
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 Percent Similarity: 39.5%
 Best Local Similarity: 26.8%
 Query Match: 7.2%
 Indels: 59
 RESULT 398
 ID ADQ22365 standard; DNA; 6564 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5185.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

ID ADQ97652 standard; DNA; 10361 BP.
DE Human cancer associated sequence HR10-021, SEQ ID 629.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 39.5%
Best Local Similarity: 23.8%
Query Match: 7.2%
Conservative: 39
Mismatch: 127
Indels: 59
RESULT 399
ID AEL84675 standard; DNA; 10383 BP.
DE Tumor marker gene BAT2D1 DNA SEQ ID NO 42.
PN WO2006110593-A2.
PD 19-OCT-2006.
PA (MACR-) MACROGENICS INC.
Percent Similarity: 39.5%
Best Local Similarity: 26.8%
Query Match: 7.2%
Conservative: 39
Mismatch: 127
Indels: 59
RESULT 400
ID ADT07432 standard; DNA; 7140 BP.
DE Human colon specific nucleic acid (CSNA) #19.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 33.2%
Best Local Similarity: 23.8%
Query Match: 7.2%
Conservative: 37
Mismatch: 125
Indels: 139
RESULT 401
ID ADT07433 standard; DNA; 7925 BP.
DE Human colon specific nucleic acid (CSNA) #20.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 33.2%
Best Local Similarity: 23.8%
Query Match: 7.2%
Conservative: 37
Mismatch: 125
Indels: 139
RESULT 402
ID ADI28074 standard; cDNA; 1604 BP.
DE ECMAD gene clone 1825473CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 34.0%
Best Local Similarity: 24.4%
Query Match: 7.2%
Conservative: 36
Mismatch: 153
Indels: 98
RESULT 403
ID AEO99543 standard; cDNA; 2388 BP.
DE Human coding sequence SEQ ID 276.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 34.0%
Best Local Similarity: 24.4%
Query Match: 7.2%
Conservative: 36
Mismatch: 153
Indels: 98
RESULT 404
ID ADP81023 standard; DNA; 1779 BP.
DE Human ovarian specific gene, SEQ ID No 57.
PN WO2004053079-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 33.1%
Best Local Similarity: 22.1%
Query Match: 7.1%
Conservative: 60
Mismatch: 162
Indels: 203
RESULT 405
ID AAD08051 standard; cDNA; 2429 BP.
DE Human extracellular matrix and cell adhesion molecule-7 (XNAD-7) cDNA.
PN WO200142285-A2.
PD 14-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 34.0%
Best Local Similarity: 24.4%
Query Match: 7.1%
Conservative: 36
Mismatch: 153
Indels: 98
RESULT 406
ID AEB29656 standard; cDNA; 7382 BP.
DE Human mucin 5 (subtypes A and C), cDNA SEQ ID 7.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Percent Similarity: 33.2%
Best Local Similarity: 23.1%
Query Match: 7.1%
Conservative: 38
Mismatch: 142
Indels: 109
RESULT 407
ID ABL27926 standard; DNA; 2300 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35251.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 34.6%
Best Local Similarity: 24.8%
Query Match: 7.1%
Conservative: 34
Mismatch: 160
Indels: 68
RESULT 408
ID ABL27928 standard; DNA; 3161 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35257.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 34.6%
Best Local Similarity: 24.8%
Query Match: 7.1%
Conservative: 34
Mismatch: 160
Indels: 68
RESULT 409
ID AAT80043 standard; DNA; 40875 BP.
DE Insert from cosmid 109.
PN WO9704106-A2.
PD 06-FEB-1997.
PA (INNO-) INNOGENETICS NV.
Percent Similarity: 35.9%
Best Local Similarity: 23.3%
Query Match: 7.1%
Conservative: 53
Mismatch: 151
Indels: 120
RESULT 410
ID ADC21532 standard; DNA; 5403 BP.
DE T. cruzi trans-sialidase gene, TS, clone 7F.
PN US2002137667-A1.
PD 26-SEP-2002.
PA (TUFT-) UNIV TUFTS.
Percent Similarity: 36.1%
Best Local Similarity: 26.9%
Query Match: 7.0%
Conservative: 30
Mismatch: 137
Indels: 74
RESULT 411
ID AEL43167 standard; DNA; 5403 BP.
DE T. cruzi neuraminidase (TCNA) gene.
PN US2006229247-A1.
PD 12-OCT-2006.
PA (CHUE/) CHUENKOVA M.
Percent Similarity: 36.1%
Best Local Similarity: 26.9%
Query Match: 7.0%
Conservative: 30
Mismatch: 137
Indels: 74
RESULT 412
ID AEF22095 standard; DNA; 2380 BP.
DE Human non-basal transcription modulator splice variant DNA #237.
PN WO2006005042-A2.
PD 12-JAN-2006.
PA (CEMI-) CEMINES INC.
Percent Similarity: 34.0%
Best Local Similarity: 22.2%
Query Match: 7.0%
Conservative: 56
Mismatch: 176
Indels: 137
RESULT 413
ID ADM02761 standard; cDNA; 2922 BP.
DE Human cDNA of the invention SEQ ID NO:1446.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 34.0%
Best Local Similarity: 22.2%
Query Match: 7.0%
Conservative: 56
Mismatch: 176
Indels: 137
RESULT 414
ID AEC85691 standard; cDNA; 2922 BP.

DE Human cDNA clone PERIC20003870, SEQ ID 1446.
 PN EP1580263-A1. Mismatches: 129
 PD 28-SEP-2005. Indels: 73
 PA (REAS-) RES ASSOC BIOTECHNOLOGY. Conservative: 56
 Percent Similarity: 34.0% Mismatches: 176
 Best Local Similarity: 22.2% Indels: 137
 Query Match: 7.0%
 RESULT 415
 ID ABQ61152 standard; cDNA; 13715 BP.
 DE MUC5B partial gene protein encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC. Conservative: 37
 Percent Similarity: 35.9% Mismatches: 133
 Best Local Similarity: 25.4% Indels: 94
 Query Match: 7.0%
 RESULT 416
 ID ACH89790 standard; DNA; 904 BP.
 DE Human genome derived single exon probe #22985.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G. Conservative: 29
 PD (RANK/) RANK D R. Mismatches: 87
 PA (HANZ/) HANZEL D K. Indels: 18
 Percent Similarity: 45.3%
 Best Local Similarity: 30.0%
 Query Match: 7.0%
 RESULT 417
 ID ADQ59189 standard; DNA; 81679 BP.
 DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:26.
 PN KR2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G. Conservative: 29
 PD (KIMN/) KIM N G. Mismatches: 87
 PA (LEEJ/) LEE J S. Indels: 18
 PA (RHEE/) RHEE H S.
 Percent Similarity: 45.3%
 Best Local Similarity: 30.0%
 Query Match: 7.0%
 RESULT 418
 ID ADQ97651 standard; DNA; 127943 BP.
 DE Human cancer associated sequence HD10-021, SEQ ID 628.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Conservative: 29
 Percent Similarity: 45.3% Mismatches: 87
 Best Local Similarity: 30.0% Indels: 18
 Query Match: 7.0%
 RESULT 419
 ID ABL28828 standard; DNA; 4755 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37957.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY. Conservative: 55
 Percent Similarity: 36.9% Mismatches: 160
 Best Local Similarity: 24.0% Indels: 108
 Query Match: 6.9%
 RESULT 420
 ID ADU01598 standard; cDNA; 3711 BP.
 DE Novel human polynucleotide seqid 65.
 PN WO2004093804-A2.
 PD 04-NOV-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC. Conservative: 57
 Percent Similarity: 38.7% Mismatches: 154
 Best Local Similarity: 22.9% Indels: 70
 Query Match: 6.9%
 RESULT 421
 ID ADL13221 standard; cDNA; 1297 BP.
 DE Human steroid-induced C3A liver cell cDNA #950.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP. Conservative: 25
 Percent Similarity: 35.9% Mismatches: 100

Best Local Similarity: 23.8% Mismatches: 129
 Query Match: 6.9% Indels: 73
 RESULT 422
 ID AAL04593 standard; DNA; 13555 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7281.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Conservative: 54
 Percent Similarity: 33.3% Mismatches: 179
 Best Local Similarity: 21.9% Indels: 137
 Query Match: 6.9%
 RESULT 423
 ID ABL97516 standard; DNA; 13555 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2168.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.. Conservative: 54
 Percent Similarity: 33.3% Mismatches: 179
 Best Local Similarity: 21.9% Indels: 137
 Query Match: 6.9%
 RESULT 424
 ID AAS34526 standard; DNA; 13555 BP.
 DE Human DNA for a novel foetal antigen, SEQ ID NO 1950.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Conservative: 54
 Percent Similarity: 33.3% Mismatches: 179
 Best Local Similarity: 21.9% Indels: 137
 Query Match: 6.9%
 RESULT 425
 ID ABL13399 standard; cDNA; 4829 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34679.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY. Conservative: 64
 Percent Similarity: 38.2% Mismatches: 155
 Best Local Similarity: 23.1% Indels: 109
 Query Match: 6.9%
 RESULT 426
 ID AEL00856 standard; DNA; 6526 BP.
 DE Mucin-like protein associated polynucleotide SEQ ID NO 172.
 PN WO2006082851-A1.
 PD 10-AUG-2006.
 PA (UYTY-) UNIV TOKYO. Conservative: 28
 Percent Similarity: 33.1% Mismatches: 129
 Best Local Similarity: 25.1% Indels: 105
 Query Match: 6.9%
 RESULT 427
 ID ADP84151 standard; DNA; 57082 BP.
 DE Human CA125 genomic DNA amino terminal sequence Segid 1.
 PN WO2004045553-A2.
 PD 03-JUN-2004.
 PA (UYAR-) UNIV ARKANSAS. Conservative: 53
 Percent Similarity: 33.5% Mismatches: 145
 Best Local Similarity: 21.8% Indels: 157
 Query Match: 6.9%
 RESULT 428
 ID ABL05865 standard; cDNA; 5929 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12077.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY. Conservative: 25
 Percent Similarity: 40.2% Mismatches: 100
 Best Local Similarity: 29.7% Indels: 43
 Query Match: 6.8%
 RESULT 429
 ID ABL05864 standard; cDNA; 11963 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12074.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY. Conservative: 25
 Percent Similarity: 40.2% Mismatches: 100
 Best Local Similarity: 29.7% Indels: 43


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Query Match: 6.8% Indels: 43
RESULT 430
ID AEI04880 standard; DNA; 2583 BP.
DE Coccidioides posadasii strain C735 chitinase 2 open reading frame.
PN US2006121061-A1.
PD 08-JUN-2006.
PA (UYOH-) UNIV OHIO MEDICAL.
Percent Similarity: 38.8% Conservative: 49
Best Local Similarity: 23.9% Mismatches: 141
Query Match: 6.8% Indels: 59
RESULT 431
ID AEI04879 standard; DNA; 3090 BP.
DE Coccidioides posadasii strain C735 chitinase 2 (CTS2) gene.
PN US2006121061-A1.
PD 08-JUN-2006.
PA (UYOH-) UNIV OHIO MEDICAL.
Percent Similarity: 38.8% Conservative: 49
Best Local Similarity: 23.9% Mismatches: 141
Query Match: 6.8% Indels: 59
RESULT 432
ID ADP74211 standard; DNA; 149158 BP.
DE Equine herpesvirus 1 genome gm deletion mutant #2.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Percent Similarity: 34.7% Conservative: 25
Best Local Similarity: 24.3% Mismatches: 131
Query Match: 6.8% Indels: 25
RESULT 433
ID ADP74212 standard; DNA; 149261 BP.
DE Equine herpesvirus 1 genome gm deletion mutant #3.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Percent Similarity: 34.7% Conservative: 25
Best Local Similarity: 24.3% Mismatches: 131
Query Match: 6.8% Indels: 25
RESULT 434
ID ADP74216 standard; DNA; 150071 BP.
DE Equine herpesvirus 1 genome gm deletion mutant #1.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Percent Similarity: 34.7% Conservative: 25
Best Local Similarity: 24.3% Mismatches: 131
Query Match: 6.8% Indels: 25
RESULT 435
ID ADP74201 standard; DNA; 150223 BP.
DE Equine herpesvirus 1 genome seqid 1.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Percent Similarity: 34.7% Conservative: 25
Best Local Similarity: 24.3% Mismatches: 131
Query Match: 6.8% Indels: 25
RESULT 436
ID ABV88065 standard; cDNA; 513 BP.
DE Human colon cancer related cDNA SEQ ID NO 1376.
PN WO200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.8% Indels: 0
RESULT 437
ID ABV87510 standard; cDNA; 513 BP.
DE Human colon cancer related cDNA SEQ ID NO 821.
PN WO200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.8% Indels: 0
RESULT 438
ID ABV18096 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 18087.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.7% Indels: 0
RESULT 439
ID ABV47885 standard; cDNA; 515 BP.
DE Human prostate expression marker cDNA 47876.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.7% Indels: 0
RESULT 440
ID AAT45666 standard; DNA; 2903 BP.
DE Partial yeast gene, Lg-FLO1, involved in flocculation.
PN JP08205900-A.
PD 13-AUG-1996.
PA (KIRI) KIRIN BREWERY KK.
Percent Similarity: 38.4% Conservative: 68
Best Local Similarity: 23.0% Mismatches: 198
Query Match: 6.7% Indels: 76
RESULT 441
ID ADS46792 standard; cDNA; 4830 BP.
DE Bacterial polynucleotide #1535.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 39.2% Conservative: 59
Best Local Similarity: 22.2% Mismatches: 142
Query Match: 6.7% Indels: 69
RESULT 442
ID ADH89334 standard; DNA; 1044 BP.
DE H. vulgare C-hordein DNA.
PN WO2003078629-A1.
PD 25-SEP-2003.
PA (BADI) BASF PLANT SCI GMBH.
Percent Similarity: 44.8% Conservative: 24
Best Local Similarity: 30.1% Mismatches: 76
Query Match: 6.7% Indels: 14
RESULT 443
ID ADG44130 standard; DNA; 1044 BP.
DE H. vulgare C-hordein DNA.
PN WO2003077643-A2.
PD 25-SEP-2003.
PA (BADI) BASF PLANT SCI GMBH.
Percent Similarity: 44.8% Conservative: 24
Best Local Similarity: 30.1% Mismatches: 76
Query Match: 6.7% Indels: 14
RESULT 444
ID AAT10117 standard; cDNA; 2032 BP.
DE Drosophila scavenger receptor class CI cDNA.
PN WO9600288-A2.
PD 04-JAN-1996.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Percent Similarity: 36.1% Conservative: 37
Best Local Similarity: 23.5% Mismatches: 108
Query Match: 6.7% Indels: 80
RESULT 445
ID ABS3745 standard; cDNA; 2032 BP.
DE cDNA encoding fruit fly scavenger receptor type CI (dsr-CI).
PN US6429289-B1.
PD 06-AUG-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

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Percent Similarity: 36.1% Conservative: 37
 Best Local Similarity: 23.5% Mismatches: 108
 Query Match: 6.7% Indels: 80
 RESULT 446
 ID AAD33916 standard; cDNA; 2032 BP.
 DE Drosophila melanogaster scavenger receptor class CI (dSR-CI) cDNA.
 PN US6350859-B1.
 PD 26-FEB-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Percent Similarity: 36.1% Conservative: 37
 Best Local Similarity: 23.5% Mismatches: 108
 Query Match: 6.7% Indels: 80
 RESULT 447
 ID ACA10147 standard; cDNA; 2570 BP.
 DE Human NOVX polynucleotide #37.
 PN WO200290504-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 33.8% Conservative: 32
 Best Local Similarity: 25.6% Mismatches: 172
 Query Match: 6.7% Indels: 88
 RESULT 448
 ID ABL16368 standard; DNA; 7417 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 577.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.5% Conservative: 50
 Best Local Similarity: 24.1% Mismatches: 171
 Query Match: 6.7% Indels: 65
 RESULT 449
 ID ABX72626 standard; cDNA; 31497 BP.
 DE Human cDNA encoding CA125 amino terminal extension.
 PN WO200283866-A2.
 PD 24-OCT-2002.
 PA (UYAR-) UNIV ARKANSAS.
 Percent Similarity: 39.4% Conservative: 47
 Best Local Similarity: 23.6% Mismatches: 120
 Query Match: 6.7% Indels: 61
 RESULT 450
 ID ABL13398 standard; cDNA; 39746 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34676.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 36.9% Conservative: 58
 Best Local Similarity: 23.1% Mismatches: 137
 Query Match: 6.7% Indels: 130
 RESULT 451
 ID ADP84154 standard; cDNA; 66765 BP.
 DE Human CA125 cDNA SeqID 4.
 PN WO200404553-A2.
 PD 03-JUN-2004.
 PA (UYAR-) UNIV ARKANSAS.
 Percent Similarity: 39.4% Conservative: 47
 Best Local Similarity: 23.6% Mismatches: 120
 Query Match: 6.7% Indels: 61
 RESULT 452
 ID ADR72872 standard; DNA; 66765 BP.
 DE Human ovarian cancer-related tumour marker CA125 DNA.
 PN WO200407513-A2.
 PD 10-SEP-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Percent Similarity: 39.4% Conservative: 47
 Best Local Similarity: 23.6% Mismatches: 120
 Query Match: 6.7% Indels: 61
 RESULT 453
 ID AAD44410 standard; DNA; 1236 BP.
 DE Human huntington (htql03) protein encoding DNA.
 PN WO200265136-A2.
 PD 22-AUG-2002.
 PA (UYCH-) UNIV CHICAGO.
 Percent Similarity: 41.4% Conservative: 22

Best Local Similarity: 30.5% Mismatches: 82
 Query Match: 6.7% Indels: 38
 RESULT 454
 ID AEI77176 standard; DNA; 2529 BP.
 DE Caenorhabditis elegans heavy metal response gene DNA sequence SeqID 199.
 PN JP2006174802-A.
 PD 06-JUL-2006.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN KOKURITSU KENKO.
 PA (INTE-) INTER-UNIV RES INST CORP RES ORG.
 Percent Similarity: 40.2% Conservative: 34
 Best Local Similarity: 25.6% Mismatches: 107
 Query Match: 6.7% Indels: 33
 RESULT 455
 ID ABL28971 standard; DNA; 3736 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38386.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 35.8% Conservative: 46
 Best Local Similarity: 22.8% Mismatches: 156
 Query Match: 6.7% Indels: 73
 RESULT 456
 ID ABL07579 standard; cDNA; 2709 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17219.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 36.5% Conservative: 42
 Best Local Similarity: 24.5% Mismatches: 136
 Query Match: 6.6% Indels: 87
 RESULT 457
 ID AAZ07198 standard; cDNA; 2113 BP.
 DE Human lung tumour protein SAL-104 5' cDNA sequence.
 PN WO9938973-A2.
 PD 05-AUG-1999.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 40.7% Conservative: 25
 Best Local Similarity: 29.2% Mismatches: 66
 Query Match: 6.6% Indels: 62
 RESULT 458
 ID AAC79152 standard; cDNA; 2114 BP.
 DE Human lung tumour-specific cDNA #105.
 PN WO200060077-A2.
 PD 12-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 40.7% Conservative: 25
 Best Local Similarity: 29.2% Mismatches: 66
 Query Match: 6.6% Indels: 62
 RESULT 459
 ID AAD23227 standard; cDNA; 2114 BP.
 DE Human lung tumour-specific protein SAL-104 cDNA.
 PN WO200172295-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 40.7% Conservative: 25
 Best Local Similarity: 29.2% Mismatches: 66
 Query Match: 6.6% Indels: 62
 RESULT 460
 ID ADD66466 standard; cDNA; 2114 BP.
 DE Human lung tumour-specific related cDNA, SEQ ID No 158.
 PN WO200292001-A2.
 PD 21-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 40.7% Conservative: 25
 Best Local Similarity: 29.2% Mismatches: 66
 Query Match: 6.6% Indels: 62
 RESULT 461
 ID ADE87720 standard; cDNA; 2114 BP.
 DE Human lung tumour antigen cDNA #105.
 PN US2003118599-A1.
 PD 26-JUN-2003.
 PA (CORI-) CORIXA CORP.

Percent Similarity: 40.7% Conservative: 25
 Best Local Similarity: 29.2% Mismatches: 66
 Query Match: 6.6% Indels: 62
 RESULT 462
 ID ADO08326 standard; cDNA; 2511 BP.
 DE Human MOVX polynucleotide #37.
 PN US2004018594-A1.
 PD 29-JAN-2004.
 PA (ALSO/) ALBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUNT/) GUNTHER E.
 PA (GUOX/) GUO X S.
 PA (KEKU/) KEKUDA R.
 PA (LEPL/) LEPLEY D M..
 PA (LILL/) LI L.
 PA (LIUX/) LIU X.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLER C E.
 PA (MILL/) MILLER I.
 PA (PADI/) PADIGARU M.
 PA (PATI/) PATURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SPYT/) SPYTEK K A.
 PA (TAUD/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERH/) ZERHUSEN B D.
 Percent Similarity: 33.7% Conservative: 35
 Best Local Similarity: 24.7% Mismatches: 155
 Query Match: 6.6% Indels: 104
 RESULT 463
 ID ABQ18250 standard; DNA; 7593 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4841.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 39.0% Conservative: 49
 Best Local Similarity: 23.8% Mismatches: 118
 Query Match: 6.6% Indels: 79
 RESULT 464
 ID ABQ18251 standard; DNA; 7593 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4842.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 39.0% Conservative: 49
 Best Local Similarity: 23.8% Mismatches: 118
 Query Match: 6.6% Indels: 79
 RESULT 465
 ID AAN91235 standard; DNA; 1368 BP.
 DE DNA sequence of preprospalmsin.
 PN DE3808456-A.
 PD 28-SEP-1989.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 Percent Similarity: 35.5% Conservative: 44
 Best Local Similarity: 23.5% Mismatches: 155
 Query Match: 6.6% Indels: 81
 RESULT 466
 ID ABL28829 standard; DNA; 2291 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37960.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.

Percent Similarity: 36.5% Conservative: 35
 Best Local Similarity: 25.2% Mismatches: 118
 Query Match: 6.6% Indels: 79
 RESULT 467
 ID AAA70157 standard; DNA; 9408 BP.
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:290.
 PN WO200025728-A2.
 PD 11-MAY-2000.
 PA (HOFF/) HOFFMAN S.
 PA (CARU/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J C.
 Percent Similarity: 35.7% Conservative: 56
 Best Local Similarity: 22.2% Mismatches: 158
 Query Match: 6.6% Indels: 108
 RESULT 468
 ID AAQ67190 standard; DNA; 9636 BP.
 DE P. falciparum transmission blocking target antigen Pfs230 DNA.
 PN WO9417187-A1.
 PD 04-AUG-1994.
 PA (USSH) US SEC DEPT HEALTH.
 Percent Similarity: 35.7% Conservative: 56
 Best Local Similarity: 22.2% Mismatches: 158
 Query Match: 6.6% Indels: 108
 RESULT 469
 ID ABL20354 standard; DNA; 13631 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12535.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 33.2% Conservative: 48
 Best Local Similarity: 19.8% Mismatches: 163
 Query Match: 6.6% Indels: 76
 RESULT 470
 ID ABQ76371 standard; cDNA; 2156 BP.
 DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 167.
 PN WO200264766-A2.
 PD 22-AUG-2002.
 PA (JANC) JANSSEN PHARM NV.
 Percent Similarity: 35.7% Conservative: 71
 Best Local Similarity: 21.1% Mismatches: 169
 Query Match: 6.5% Indels: 146
 RESULT 471
 ID ADI21446 standard; cDNA; 4115 BP.
 DE Novel human expressed sequence tag, EST #145.
 PN WO2003025148-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.3% Conservative: 62
 Best Local Similarity: 22.3% Mismatches: 148
 Query Match: 6.5% Indels: 111
 RESULT 472
 ID ADY34541 standard; cDNA; 4327 BP.
 DE DFCR1 (1393 amino acid form) coding sequence.
 PN WO2005019257-A1.
 PD 03-MAR-2005.
 PA (CLLT) CELLTech R & D LTD.
 Percent Similarity: 37.3% Conservative: 62
 Best Local Similarity: 22.3% Mismatches: 148
 Query Match: 6.5% Indels: 111
 RESULT 473
 ID ADN39109 standard; cDNA; 4383 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:427.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 37.3% Conservative: 62
 Best Local Similarity: 22.3% Mismatches: 148
 Query Match: 6.5% Indels: 111
 RESULT 474
 ID ADI21918 standard; cDNA; 5238 BP.
 DE Novel human protein cDNA #177.
 PN WO2003025148-A2.

PD 13-JUL-2000.
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 Percent Similarity: 49.4% Conservative: 39
 Best Local Similarity: 25.0% Mismatches: 69
 Query Match: 6.4% Indels: 13
 RESULT 492
 ID ADN07622 standard; cDNA; 12685 BP.
 DE Caenorhabditis elegans location of vulva (LOV) -1 cDNA.
 PN US6723557-B1.
 PD 20-APR-2004.
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 Percent Similarity: 49.4% Conservative: 39
 Best Local Similarity: 25.0% Mismatches: 69
 Query Match: 6.4% Indels: 13
 RESULT 493
 ID ADW79939 standard; DNA; 12685 BP.
 DE Nematode location of vulva (lov-1) gene.
 PN US6849717-B1.
 PD 01-FEB-2005.
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 Percent Similarity: 49.4% Conservative: 39
 Best Local Similarity: 25.0% Mismatches: 69
 Query Match: 6.4% Indels: 13
 RESULT 494
 ID ADY34543 standard; cDNA; 2293 BP.
 DE DPCR1 (715 amino acid form) coding sequence.
 PN WO2005019257-A1.
 PD 03-MAR-2005.
 PA (CLLT) CELLTech R & D LTD.
 Percent Similarity: 39.1% Conservative: 58
 Best Local Similarity: 22.6% Mismatches: 124
 Query Match: 6.4% Indels: 89
 RESULT 495
 ID ABL10403 standard; cDNA; 3263 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25691.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 38.0% Conservative: 44
 Best Local Similarity: 26.2% Mismatches: 147
 Query Match: 6.4% Indels: 87
 RESULT 496
 ID AEG97317 standard; DNA; 1905 BP.
 DE C. albicans hyphal growth regulator HWP1 DNA SEQ ID NO '86.
 PN WO2006036817-A2.
 PD 06-APR-2006.
 PA (MICK-) MICROBIA INC.
 Percent Similarity: 40.8% Conservative: 45
 Best Local Similarity: 24.3% Mismatches: 104
 Query Match: 6.4% Indels: 58
 RESULT 497
 ID AEL60498 standard; DNA; 2681 BP.
 DE Candida albicans hyphal wall protein 1 (HWP1) DNA.
 PN WO2006109283-A1.
 PD 19-OCT-2006.
 PA (UYNA-) UNIV NAT IRELAND GALWAY.
 Percent Similarity: 40.8% Conservative: 45
 Best Local Similarity: 24.3% Mismatches: 104
 Query Match: 6.4% Indels: 58
 RESULT 498
 ID AEL60483 standard; DNA; 2682 BP.
 DE Candida albicans hyphal wall protein 1 (HWP1) DNA SEQ ID NO 1.
 PN WO2006109283-A1.
 PD 19-OCT-2006.
 PA (UYNA-) UNIV NAT IRELAND GALWAY.
 Percent Similarity: 40.8% Conservative: 45
 Best Local Similarity: 24.3% Mismatches: 104
 Query Match: 6.4% Indels: 58
 RESULT 499
 ID ABA6656 standard; DNA; 3953 BP.
 DE Human foetal liver single exon nucleic acid probe #14961.
 PN WO200157277-A2.
 PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 500
 ID ABA48746 standard; DNA; 3953 BP.
 DE Human breast cell single exon nucleic acid probe #7441.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 501
 ID ABA33721 standard; DNA; 3953 BP.
 DE Probe #12187 for gene expression analysis in human heart cell sample.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 502
 ID AAK40813 standard; DNA; 3953 BP.
 DE Human bone marrow expressed single exon probe SEQ ID NO: 15370.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 503
 ID AAK15085 standard; DNA; 3953 BP.
 DE Human brain expressed single exon probe SEQ ID NO: 15076.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 504
 ID ABS40392 standard; DNA; 3953 BP.
 DE Human liver single exon probe, SEQ ID No 15382.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 505
 ID AAI07277 standard; DNA; 3953 BP.
 DE Probe #7268 used to measure gene expression in human breast sample.
 PN WO200157270-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 506
 ID ABS14767 standard; DNA; 3953 BP.
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 14758.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 36.9% Conservative: 59
 Best Local Similarity: 22.2% Mismatches: 145
 Query Match: 6.4% Indels: 108
 RESULT 507
 ID ACH87407 standard; DNA; 3953 BP.
 DE Human genome derived single exon probe #20602.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.

PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Percent Similarity: 36.9%
 Best Local Similarity: 35.9%
 Query Match: 145
 Indels: 108
 RESULT 508
 ID ABL05381 standard; cDNA; 2032 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10625.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.0%
 Best Local Similarity: 23.7%
 Query Match: 6.4%
 Indels: 55
 RESULT 509
 ID ABL05380 standard; cDNA; 4282 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10622.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 39.4%
 Best Local Similarity: 25.0%
 Query Match: 6.4%
 Indels: 46
 RESULT 510
 ID ABX07541 standard; DNA; 13152 BP.
 DE S. pneumoniae type 4 strain coding region #1829.
 PN WO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 511
 ID ABX07543 standard; DNA; 14328 BP.
 DE S. pneumoniae type 4 strain coding region #1831.
 PN WO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 512
 ID ADM91975 standard; DNA; 14328 BP.
 DE S. pneumoniae antigenic protein-encoding gene sequence SeqID172.
 PN WO2004020609-A2.
 PD 11-MAR-2004.
 PA (TUFT) UNIV TUFTS.
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 513
 ID ADT49995 standard; DNA; 14328 BP.
 DE S. pneumoniae hyperimmune serum reactive antigen DNA Seq 73.
 PN WO2004092209-A2.
 PD 28-OCT-2004.
 PA (INTE-) INTERCELL AG.
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 514
 ID ACA49624 standard; DNA; 14331 BP.
 DE Prokaryotic essential gene #31281.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 515
 ID AFK43399 standard; DNA; 107069 BP.
 DE Chlorothricin biological synthesis gene cluster.

PN CN1730657-A.
 PD 08-FEB-2006.
 PA (SHAN-) SHANGHAI ORGANIC CHEM INST.
 Percent Similarity: 33.5%
 Best Local Similarity: 23.5%
 Query Match: 6.4%
 Indels: 110
 RESULT 516
 Percent Similarity: 38.2%
 Best Local Similarity: 23.1%
 Query Match: 6.4%
 Indels: 80
 RESULT 517
 ID ABL07173 standard; cDNA; 6353 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 41.7%
 Best Local Similarity: 29.5%
 Query Match: 6.3%
 Indels: 61
 RESULT 518
 ID ABL07172 standard; cDNA; 8429 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 41.7%
 Best Local Similarity: 29.5%
 Query Match: 6.3%
 Indels: 61
 RESULT 519
 ID RAT96035 standard; cDNA; 1795 BP.
 DE Human kidney injury related molecule (KIM) cDNA clone H13-10-85.
 PN WO9744460-A1.
 PD 27-NOV-1997.
 PA (BIOJ) BIOGEN INC.
 Percent Similarity: 36.3%
 Best Local Similarity: 24.0%
 Query Match: 6.3%
 Indels: 82
 RESULT 520
 ID ABL10368 standard; cDNA; 3463 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25586.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 36.8%
 Best Local Similarity: 21.3%
 Query Match: 6.3%
 Indels: 76
 RESULT 521
 ID AAV20701 standard; DNA; 5318 BP.
 DE Cryptosporidium parvum GP900 antigen open reading frame and 3' region.
 PN WO9806430-A1.
 PD 19-FEB-1998.
 PA (REGC) UNIV CALIFORNIA.
 Percent Similarity: 36.2%
 Best Local Similarity: 22.8%
 Query Match: 6.3%
 Indels: 75
 RESULT 522
 ID ADZ51725 standard; DNA; 138203 BP.
 DE FR-008 polyketide gene cluster, SEQ ID 1.
 PN US2005089884-A1.
 PD 28-APR-2005.
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 PA (UYSH-) UNIV SHANGHAI JIAOTONG.
 Percent Similarity: 36.3%
 Best Local Similarity: 23.7%
 Query Match: 6.3%
 Indels: 87
 RESULT 523
 ID AEH46706 standard; DNA; 138203 BP.
 DE Streptomyces FR-008 polyketone synthesis gene cluster - SEQ ID 1.
 PN CN1667123-A.
 PD 14-SEP-2005.
 PA (UYSH-) UNIV SHANGHAI JIAOTONG.
 Percent Similarity: 36.3%
 Best Local Similarity: 23.7%
 Query Match: 6.3%
 Indels: 87

Query Match: 6.3% Indels: 87
RESULT 524
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 42.5%
Best Local Similarity: 30.7%
Query Match: 6.3%
Indels: 17
Conservative: 18
Mismatches: 71
Indels: 17
RESULT 525
ID AAX91461 standard; DNA; 867 BP.
DE T. gondii ntG867 reverse complement sequence.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 526
ID AAX91460 standard; DNA; 867 BP.
DE T. gondii immunogenic protein encoding DNA.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 527
ID AAS42783 standard; cDNA; 867 BP.
DE T. gondii cDNA encoding immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 528
ID AAS42784 standard; cDNA; 867 BP.
DE Reverse complement of T. gondii cDNA ntG288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 529
ID ADG17392 standard; DNA; 867 BP.
DE T. gondii protein DNA #86.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 530
ID ADG17390 standard; cDNA; 867 BP.
DE T. gondii protein cDNA #6.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 531
ID AEH92888 standard; DNA; 867 BP.
DE T. gondii polynucleotide ntG(867) SEQ ID NO: 342.
PN US2006115496-A1.
PD 01-JUN-2006.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35

RESULT 532
ID AEH92886 standard; cDNA; 867 BP.
DE T. gondii polynucleotide ntG(867) SEQ ID NO: 340.
PN US2006115496-A1.
PD 01-JUN-2006.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 533
ID ABL27929 standard; DNA; 1014 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35260.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.8%
Best Local Similarity: 29.7%
Query Match: 6.3%
Indels: 56
Conservative: 15
Mismatches: 77
Indels: 56
RESULT 534
ID AAX91462 standard; DNA; 1397 BP.
DE T. gondii immunogenic protein encoding DNA.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 535
ID AAX91463 standard; DNA; 1397 BP.
DE T. gondii ntG1397 reverse complement sequence.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 536
ID AAS42786 standard; cDNA; 1397 BP.
DE Reverse complement of T. gondii cDNA ntG1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 537
ID AAS42785 standard; cDNA; 1397 BP.
DE T. gondii cDNA encoding immunogenic protein PTg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 538
ID ADG17395 standard; DNA; 1397 BP.
DE T. gondii protein DNA #87.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 539
ID ADG17393 standard; cDNA; 1397 BP.
DE T. gondii protein cDNA #7.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 540
ID ABL27929 standard; DNA; 1014 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35260.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.8%
Best Local Similarity: 29.7%
Query Match: 6.3%
Indels: 56
Conservative: 15
Mismatches: 77
Indels: 56
RESULT 541
ID AAX91461 standard; DNA; 867 BP.
DE T. gondii ntG867 reverse complement sequence.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 542
ID AAX91460 standard; DNA; 867 BP.
DE T. gondii immunogenic protein encoding DNA.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 543
ID AAS42783 standard; cDNA; 867 BP.
DE T. gondii cDNA encoding immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 544
ID AAS42784 standard; cDNA; 867 BP.
DE Reverse complement of T. gondii cDNA ntG288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 545
ID ADG17392 standard; DNA; 867 BP.
DE T. gondii protein DNA #86.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 546
ID ADG17390 standard; cDNA; 867 BP.
DE T. gondii protein cDNA #6.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35
RESULT 547
ID AEH92888 standard; DNA; 867 BP.
DE T. gondii polynucleotide ntG(867) SEQ ID NO: 342.
PN US2006115496-A1.
PD 01-JUN-2006.
PA (MILH/) MILHAUSEN M J.
Percent Similarity: 38.6%
Best Local Similarity: 24.6%
Query Match: 6.3%
Indels: 35
Conservative: 33
Mismatches: 111
Indels: 35

Best Local Similarity:	22.3%	Mismatches:	204
Query Match:	6.3%	Indels:	77
RESULT 548			
ID	ABT04778 standard; DNA; 5163 BP.		
DE	C parvum GP900 gene fragment SEQ ID NO: 4.		
PN	WO200194631-A1.		
PD	13-DEC-2001.		
PA	(REGC) UNIV CALIFORNIA.		
Percent Similarity:	35.6%	Conservative:	58
Best Local Similarity:	22.3%	Mismatches:	204
Query Match:	6.3%	Indels:	77
RESULT 549			
ID	AA61848 standard; DNA; 5318 BP.		
DE	DE DNA encoding a portion of Cryptosporidium parvum NINC isolate GP900		
PN	US6071518-A.		
PD	06-JUN-2000.		
PA	(REGC) UNIV CALIFORNIA.		
Percent Similarity:	35.6%	Conservative:	58
Best Local Similarity:	22.3%	Mismatches:	204
Query Match:	6.3%	Indels:	77
RESULT 550			
ID	ABT04777 standard; DNA; 5318 BP.		
DE	C parvum GP900 gene fragment SEQ ID NO: 3.		
PN	WO200194631-A1.		
PD	13-DEC-2001.		
PA	(REGC) UNIV CALIFORNIA.		
Percent Similarity:	35.6%	Conservative:	58
Best Local Similarity:	22.3%	Mismatches:	204
Query Match:	6.3%	Indels:	77
RESULT 551			
ID	ABK94926 standard; cDNA; 5735 BP.		
DE	Human novel polynucleotide #37.		
PN	WO200244340-A2.		
PD	06-JUN-2002.		
PA	(HYSE-) HYSEQ INC.		
Percent Similarity:	40.2%	Conservative:	59
Best Local Similarity:	22.3%	Mismatches:	116
Query Match:	6.3%	Indels:	81
RESULT 552			
ID	ABK94980 standard; cDNA; 5735 BP.		
DE	Human novel polynucleotide #91.		
PN	WO200244340-A2.		
PD	06-JUN-2002.		
PA	(HYSE-) HYSEQ INC.		
Percent Similarity:	40.2%	Conservative:	59
Best Local Similarity:	22.3%	Mismatches:	116
Query Match:	6.3%	Indels:	81
RESULT 553			
ID	ABU24388 standard; DNA; 6116 BP.		
DE	Drosophila melanogaster genomic polynucleotide SEQ ID NO 24637.		
PN	WO200171042-A2.		
PD	27-SEP-2001.		
PA	(PEKE) PE CORP NY.		
Percent Similarity:	42.4%	Conservative:	29
Best Local Similarity:	28.1%	Mismatches:	54
Query Match:	6.3%	Indels:	63
RESULT 554			
ID	ADR18911 standard; DNA; 5985 BP.		
DE	Human mucin-like protein, SCS0004, coding sequence, SEQ ID 1.		
PN	WO2004069136-A2.		
PD	19-AUG-2004.		
PA	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.		
Percent Similarity:	40.0%	Conservative:	39
Best Local Similarity:	26.6%	Mismatches:	118
Query Match:	6.2%	Indels:	59
RESULT 555			
ID	AEB35716 standard; DNA; 162147 BP.		
DE	L. pneumophila DNA SEQ ID NO 48.		
PN	WO2005049642-A2.		
PD	02-JUN-2005.		
PA	(INSP) INST PASTEUR.		
PA	(INRM) INSERM INST NAT SANTE & RECH MEDICALE.		
PA	(UPLY-) UNIV LYON 1 BERNARD CLAUDE.		

RESULT 564

ID ADS47200 standard; cDNA; 1512 BP.
DE Bacterial polynucleotide #1943.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 45.5%
Best Local Similarity: 28.3%
Query Match: 6.2%
Conservative: 34
Mismatches: 102
Indels: 6

RESULT 565

ID ARG51911 standard; DNA; 1512 BP.
DE Stress-related protein, SRP, DNA SEQ ID NO 169.
PN WO2006032708-A2.
PD 30-MAR-2006.
PA (BADI) BASF PLANT SCI GMBH.
Percent Similarity: 45.5%
Best Local Similarity: 28.3%
Query Match: 6.2%
Conservative: 34
Mismatches: 102
Indels: 6

RESULT 566

ID ADF82805 standard; cDNA; 1923 BP.
DE Aspergillus niger phospholipase PLP34 coding sequence.
PN WO2003097825-A2.
PD 27-NOV-2003.
PA (STAM) DSM IP ASSETS BV.
Percent Similarity: 36.1%
Best Local Similarity: 23.8%
Query Match: 6.2%
Conservative: 59
Mismatches: 172
Indels: 135

RESULT 567

ID AAK52147 standard; cDNA; 3135 BP.
DE Human polynucleotide SEQ ID NO 692.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.7%
Best Local Similarity: 23.6%
Query Match: 6.2%
Conservative: 57
Mismatches: 162
Indels: 113

RESULT 568

ID ADF82804 standard; DNA; 3637 BP.
DE Aspergillus niger phospholipase PLP34 gene.
PN WO2003097825-A2.
PD 27-NOV-2003.
PA (STAM) DSM IP ASSETS BV.
Percent Similarity: 36.1%
Best Local Similarity: 23.8%
Query Match: 6.2%
Conservative: 59
Mismatches: 172
Indels: 135

RESULT 569

ID AEF87659 standard; DNA; 33359 BP.
DE Nucleotide sequence of plasmid pAD36delE1delB4Ad5Orf6.
PN WO2006086357-A2.
PD 17-AUG-2006.
PA (MERI) MERCK & CO INC.
Percent Similarity: 37.3%
Best Local Similarity: 25.1%
Query Match: 6.2%
Conservative: 48
Mismatches: 131
Indels: 117

RESULT 570

ID AEU87658 standard; DNA; 35152 BP.
DE Adenovirus serotype 36 genomic nucleotide sequence.
PN WO2006086357-A2.
PD 17-AUG-2006.
PA (MERI) MERCK & CO INC.
Percent Similarity: 37.3%
Best Local Similarity: 25.1%
Query Match: 6.2%
Conservative: 48
Mismatches: 131
Indels: 117

RESULT 571

ID ACU27913 standard; cDNA; 915 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:1869.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Percent Similarity: 36.6%	Conservative: 33	PA (SAGR-) SAGRES DISCOVERY.	Conservative: 55
Best Local Similarity: 25.4%	Mismatches: 127	Best Local Similarity: 34.7%	Mismatches: 159
Query Match: 6.2%	Indels: 60	Query Match: 6.2%	Indels: 123
RESULT 572		RESULT 579	
ID ADI57706 standard; cDNA; 1808 BP.		ID ADE82938 standard; DNA; 37487 BP.	
DE Human breast specific nucleic acid (BSNA) #77.		DE Human MYC genomic DNA sequence.	
PN WO2003106648-A2.		PN WO2003080808-A2.	
PD 24-DEC-2003.		PD 02-OCT-2003.	
PA (DIAD-) DIADEXUS INC.		PA (SAGR-) SAGRES DISCOVERY.	
Percent Similarity: 30.6%	Conservative: 41	Percent Similarity: 34.7%	Conservative: 55
Best Local Similarity: 21.7%	Mismatches: 146	Best Local Similarity: 21.9%	Mismatches: 159
Query Match: 6.2%	Indels: 174	Query Match: 6.2%	Indels: 123
RESULT 573		RESULT 580	
ID AEG97426 standard; DNA; 1905 BP.		ID ADE95746 standard; DNA; 37487 BP.	
DE C. albicans cell wall protein HWP1 DNA SEQ ID NO 195.		DE Human MYC gene genomic DNA sequence.	
PN WO2006036817-A2.		PN WO2003039484-A2.	
PD 06-APR-2006.		PD 15-MAY-2003.	
PA (MICR-) MICROBIA INC.		PA (SAGR-) SAGRES DISCOVERY.	
Percent Similarity: 40.4%	Conservative: 45	Percent Similarity: 34.7%	Conservative: 55
Best Local Similarity: 23.9%	Mismatches: 105	Best Local Similarity: 21.9%	Mismatches: 159
Query Match: 6.2%	Indels: 58	Query Match: 6.2%	Indels: 123
RESULT 574		RESULT 581	
ID AAZ32027 standard; DNA; 3015 BP.		ID AEK60017 standard; DNA; 37487 BP.	
DE Human METH1 related EST Z46970.		DE Human MYC genomic sequence, SEQ ID NO:4.	
PN WO9937660-A1.		PN US2006204982-A1.	
PD 29-JUL-1999.		PD 14-SEP-2006.	
PA (IRUE/) IRUELA-ARISPE L.		PA (ENG/) ENGELHARD E K.	
PA (HAST/) HASTINGS G A.		PA (MORR/) MORRIS D W.	
PA (RUBE/) RUBEN S M.		PA (ENG/) ENGELHARD E K.	
Percent Similarity: 34.7%	Conservative: 48	Percent Similarity: 34.7%	Conservative: 55
Best Local Similarity: 23.5%	Mismatches: 173	Best Local Similarity: 21.9%	Mismatches: 159
Query Match: 6.2%	Indels: 111	Query Match: 6.2%	Indels: 123
RESULT 575		RESULT 582	
ID AAC90084 standard; DNA; 3015 BP.		ID ADO25291 standard; cDNA; 191010 BP.	
DE Z46970 cDNA clone.		DE Human protein kinase C zeta I/zeta II genomic sequence.	
PN WO200071577-A1.		PN WO2004041212-A2.	
PD 30-NOV-2000.		PD 21-MAY-2004.	
PA (HUMA-) HUMAN GENOME SCI INC.		PA (SACK/) SACKTOR T C.	
PA (SMIK-) SMITHKLINE BEECHAM CORP.		PA (CRAR/) CRARY J F.	
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.		PA (HERN/) HERNANDEZ A I.	
PA (IRUE/) IRUELA-ARISPE L.		PA (MIRR/) MIRRA S.	
PA (HAST/) HASTINGS G A.		PA (SHAO/) SHAO C.	
PA (RUBE/) RUBEN S M.		Percent Similarity: 39.3%	Conservative: 66
PA (JONA/) JONAK Z L.		Best Local Similarity: 22.7%	Mismatches: 140
PA (TRUL/) TRULLI S H.		Query Match: 6.2%	Indels: 103
PA (FORN/) FORNWALD J A.		RESULT 583	
PA (TERP/) TERRETT J A.		ID AEI33649 standard; DNA; 889 BP.	
Percent Similarity: 34.7%	Conservative: 48	DE Soybean polymorphic locus, SEQ ID 6283.	
Best Local Similarity: 23.5%	Mismatches: 173	PN US2006135758-A1.	
Query Match: 6.2%	Indels: 111	PD 22-JUN-2006.	
RESULT 576		PA (WUKK/) WU K.	
ID ABT14863 standard; DNA; 6783 BP.		Percent Similarity: 42.2%	Conservative: 31
DE Pathogen specific antigen related staphylococcal DNA SEQ ID NO 8.		Best Local Similarity: 27.2%	Mismatches: 86
PN WO200259148-A2.		Query Match: 6.1%	Indels: 34
PD 01-AUG-2002.		RESULT 584	
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.		ID AEB65261 standard; DNA; 1718 BP.	
Percent Similarity: 41.5%	Conservative: 79	DE Rice genome derived DNA sequence, SEQ ID 406.	
Best Local Similarity: 21.3%	Mismatches: 192	PN JP2005185101-A.	
Query Match: 6.2%	Indels: 36	PD 14-JUL-2005.	
RESULT 577		PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.	
ID ADA02498 standard; DNA; 37487 BP.		PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.	
DE Human MYC carcinoma associated gene, SEQ ID NO:1016.		PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.	
PN WO2003057146-A2.		PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.	
PD 17-JUL-2003.		Percent Similarity: 37.9%	Conservative: 56
PA (SAGR-) SAGRES DISCOVERY.		Best Local Similarity: 22.0%	Mismatches: 124
Percent Similarity: 34.7%	Conservative: 55	Query Match: 6.1%	Indels: 96
Best Local Similarity: 21.9%	Mismatches: 159	RESULT 585	
Query Match: 6.2%	Indels: 123	ID ADU01973 standard; cDNA; 2328 BP.	
RESULT 578		DE Novel human polynucleotide seqid 440.	
ID ADB72236 standard; DNA; 37487 BP.		PN WO2004093804-A2.	
DE Human MYC gene.		PD 04-NOV-2004.	
PN WO2003008583-A2.		PA (FIVE-) FIVE PRIME THERAPEUTICS INC.	
PD 30-JAN-2003.		Percent Similarity: 45.3%	Conservative: 27

Best Local Similarity: 25.9% Mismatches: 73
 Query Match: 6.1% Indels: 3
 RESULT 586
 ID AD067406 standard; cDNA; 3089 BP.
 DE Novel human cDNA sequence #2379.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 39.0% Conservative: 55
 Best Local Similarity: 24.1% Mismatches: 135
 Query Match: 6.1% Indels: 91
 RESULT 587
 ID ABR89101 standard; DNA; 3949 BP.
 DE Aspergillus oryzae galactose oxidase gene.
 PN JP2002165596-A.
 PD 11-JUN-2002.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN SHURUI SOGO KENKY.
 PA (GEKK-) GEKKEIKAN KK.
 Percent Similarity: 33.7% Conservative: 57
 Best Local Similarity: 21.5% Mismatches: 181
 Query Match: 6.1% Indels: 129
 RESULT 588
 ID ABI20362 standard; DNA; 5396 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12559.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 38.0% Conservative: 50
 Best Local Similarity: 23.8% Mismatches: 117
 Query Match: 6.1% Indels: 104
 RESULT 589
 ID ACA19870 standard; DNA; 6816 BP.
 DE Prokaryotic essential gene #1527.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 40.7% Conservative: 76
 Best Local Similarity: 21.1% Mismatches: 195
 Query Match: 6.1% Indels: 35
 RESULT 590
 ID ABQ91845 standard; DNA; 349980 BP.
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1101.
 PN BP1227152-A1.
 PD 31-JUL-2002.
 PA (NEST-) SOC PROD NESTLE SA.
 Percent Similarity: 35.0% Conservative: 38
 Best Local Similarity: 24.6% Mismatches: 135
 Query Match: 6.1% Indels: 104
 RESULT 591
 ID ADT18751 standard; cDNA; 1131 BP.
 DE Plant cDNA, Seq ID 4077.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K.
 Percent Similarity: 44.0% Conservative: 31
 Best Local Similarity: 28.5% Mismatches: 75
 Query Match: 6.1% Indels: 38
 RESULT 592
 ID AAV1733 standard; DNA; 1140 BP.
 DE Codon-optimised Ramy3D signal fused to prosubtilisin BPN' DNA.
 PN WO9836085-A1.
 PD 20-AUG-1998.
 PA (PHT-) APPLIED PHYTOLOGICS INC.
 Percent Similarity: 41.3% Conservative: 44
 Best Local Similarity: 25.1% Mismatches: 94
 Query Match: 6.1% Indels: 66
 RESULT 593
 ID ABB5063 standard; DNA; 1475 BP.
 DE Rice genome derived DNA sequence, SEQ ID 208.
 PN JP2005185101-A.
 PD 14-JUL-2005.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.

PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
 PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
 Percent Similarity: 35.5% Conservative: 52
 Best Local Similarity: 22.2% Mismatches: 108
 Query Match: 6.1% Indels: 146
 RESULT 594
 ID ADQ84536 standard; cDNA; 2398 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1350.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH-) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 37.7% Conservative: 71
 Best Local Similarity: 22.7% Mismatches: 190
 Query Match: 6.1% Indels: 108
 RESULT 595
 ID ADQ86498 standard; cDNA; 2398 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3371.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH-) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Percent Similarity: 37.7% Conservative: 71
 Best Local Similarity: 22.7% Mismatches: 190
 Query Match: 6.1% Indels: 108
 RESULT 596
 ID ACH87318 standard; DNA; 2412 BP.
 DE Human genome derived single exon probe #20513.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANY/) HANZEL D K.
 Percent Similarity: 36.0% Conservative: 50
 Best Local Similarity: 23.1% Mismatches: 153
 Query Match: 6.1% Indels: 96
 RESULT 597
 ID ADY34547 standard; cDNA; 2425 BP.
 DE DPCRI (759 amino acid form) coding sequence.
 PN WO2005019257-A1.
 PD 03-MAR-2005.
 PA (CLLT-) CELLTech R & D LTD.
 Percent Similarity: 36.6% Conservative: 60
 Best Local Similarity: 22.0% Mismatches: 136
 Query Match: 6.1% Indels: 126
 RESULT 598
 ID ADC30653 standard; cDNA; 6614 BP.
 DE Human novel cDNA sequence, SEQ ID NO:735.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.2% Conservative: 37
 Best Local Similarity: 25.7% Mismatches: 135
 Query Match: 6.1% Indels: 69
 RESULT 599
 ID ABL03416 standard; cDNA; 9402 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4730.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 36.4% Conservative: 66
 Best Local Similarity: 20.7% Mismatches: 140
 Query Match: 6.1% Indels: 127
 RESULT 600
 ID ADF89954 standard; cDNA; 1446 BP.
 DE N. crassa del12-desaturase (Ncd12D) encoding cDNA.
 PN WO2003099216-A2.
 PD 04-DEC-2003.
 PA (MONS-) MONSANTO TECHNOLOGY LLC.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156

Query Match: 6.1% Indels: 142
 RESULT 601
 ID AEA10864 standard; DNA; 1446 BP.
 DE Neurospora crassa sub family 2 Delta-15 desaturase Nc2 DNA.
 PN WO2005047480-A2.
 PD 26-MAY-2005.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 602
 ID AEA12341 standard; cDNA; 1446 BP.
 DE DNA encoding delta12 desaturase polypeptide #8.
 PN WO2005047485-A2.
 PD 26-MAY-2005.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 603
 ID AEA14796 standard; DNA; 1446 BP.
 DE Sub-family 2 desaturase DNA SEQ ID NO 15.
 PN WO2005047479-A2.
 PD 26-MAY-2005.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 604
 ID AEH65581 standard; DNA; 1446 BP.
 DE N. crassa delta 12 desaturase DNA SEQ ID NO: 35.
 PN US2006094092-A1.
 PD 04-MAY-2006.
 PA (DAMU/) DAMUDE H G.
 PA (GILL/) GILLIES P J.
 PA (MACO/) MACCOOL D J.
 PA (PICA/) PICATAGGIO S K.
 PA (POLL/) POLLAK D M W.
 PA (RAGG/) RAGGHIANI J J.
 PA (XUEZ/) XUE Z.
 PA (YADA/) YADAV N S.
 PA (ZHAN/) ZHANG H.
 PA (ZHUQ/) ZHU Q Q.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 605
 ID AEI06008 standard; DNA; 1446 BP.
 DE Neurospora crassa delta 12 desaturase coding sequence, SEQ ID 35.
 PN US2006115881-A1.
 PD 01-JUN-2006.
 PA (DAMU/) DAMUDE H G.
 PA (GILL/) GILLIES P J.
 PA (MACO/) MACCOOL D J.
 PA (PICA/) PICATAGGIO S K.
 PA (POLL/) POLLAK D M W.
 PA (RAGG/) RAGGHIANI J J.
 PA (XUEZ/) XUE Z.
 PA (YADA/) YADAV N S.
 PA (ZHAN/) ZHANG H.
 PA (ZHUQ/) ZHU Q Q.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 606
 ID AEH96263 standard; DNA; 1446 BP.
 DE Delta-12 desaturase coding sequence - SEQ ID 40.
 PN US2006110806-A1.
 PD 25-MAY-2006.
 PA (DAMU/) DAMUDE H G.
 PA (GILL/) GILLIES P J.
 PA (MACO/) MACCOOL D J.
 PA (PICA/) PICATAGGIO S K.

PA (RAGG/) RAGGHIANI J J.
 PA (SEIP/) SEIP J E.
 PA (XUEZ/) XUE Z.
 PA (YADA/) YADAV N S.
 PA (ZHAN/) ZHANG H.
 PA (ZHUQ/) ZHU Q Q.
 Percent Similarity: 33.0% Conservative: 50
 Best Local Similarity: 21.7% Mismatches: 156
 Query Match: 6.1% Indels: 142
 RESULT 607
 ID AAD04178 standard; DNA; 1923 BP.
 DE Aspergillus niger lysophospholipase 1 (LLPL-1) DNA.
 PN WO200127251-A1.
 PD 19-APR-2001.
 PA (NOVO) NOVOZYMES AS.
 Percent Similarity: 36.1% Conservative: 59
 Best Local Similarity: 23.8% Mismatches: 172
 Query Match: 6.1% Indels: 135
 RESULT 608
 ID ABL32439 standard; DNA; 5337 BP.
 DE Human immune system associated gene SEQ ID NO: 412.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 38.8% Conservative: 51
 Best Local Similarity: 24.6% Mismatches: 131
 Query Match: 6.1% Indels: 89
 RESULT 609
 ID AEJ07211 standard; DNA; 9931 BP.
 DE pTrex3g_NSP24 vector containing Trichoderma reesei NSP24 gene.
 PN WO2006073839-A2.
 PD 13-JUL-2006.
 PA (GEMV) GENENCOR INT INC.
 Percent Similarity: 36.1% Conservative: 53
 Best Local Similarity: 23.2% Mismatches: 128
 Query Match: 6.1% Indels: 136
 RESULT 610
 ID AEK5957 standard; DNA; 9931 BP.
 DE NSP24 protease coding sequence contained within a plasmid - SEQ ID 4.
 PN WO2006073843-A2.
 PD 13-JUL-2006.
 PA (GEMV) GENENCOR INT INC.
 Percent Similarity: 36.1% Conservative: 53
 Best Local Similarity: 23.2% Mismatches: 128
 Query Match: 6.1% Indels: 136
 RESULT 611
 ID ADU47667 standard; DNA; 88400 BP.
 DE S. cyaneogriseus LU-F28249 compound full-length biosynthetic gene.
 PN EP1477563-A2.
 PD 17-NOV-2004.
 PA (AMHP) WYETH.
 PA (FORT-) FORT DODGE ANIMAL HEALTH.
 Percent Similarity: 35.6% Conservative: 30
 Best Local Similarity: 24.9% Mismatches: 113
 Query Match: 6.1% Indels: 68
 RESULT 612
 Percent Similarity: 39.7% Conservative: 38
 Best Local Similarity: 26.7% Mismatches: 129
 Query Match: 6.1% Indels: 47
 RESULT 613
 ID AAH68531 standard; DNA; 349980 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 7066.
 PN EP1108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 31.2% Conservative: 44
 Best Local Similarity: 22.8% Mismatches: 145
 Query Match: 6.1% Indels: 214
 RESULT 614
 ID AAH68532 standard; DNA; 349980 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 7067.
 PN EP1108790-A2.
 PD 20-JUN-2001.

PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 31.2% Conservative: 44
Best Local Similarity: 22.8% Mismatches: 145
Indels: 214
RESULT 615
ID AAS84303 standard; cDNA; 569 BP.
DE DNA encoding novel human diagnostic protein #20107.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC..
Percent Similarity: 50.4% Conservative: 23
Best Local Similarity: 32.6% Mismatches: 60
Indels: 5
Query Match:
RESULT 616
ID AAD33861 standard; cDNA; 837 BP.
DE Human secreted protein-encoding gene 17 cDNA clone HLDQZ72, SEQ ID NO:60.
PN WO200224719-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.3% Conservative: 31
Best Local Similarity: 25.4% Mismatches: 58
Indels: 79
Query Match:
RESULT 617
ID AAS80389 standard; cDNA; 1209 BP.
DE DNA encoding novel human diagnostic protein #16193.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 50.4% Conservative: 23
Best Local Similarity: 32.6% Mismatches: 60
Indels: 5
Query Match:
RESULT 618
ID AAS81401 standard; cDNA; 1209 BP.
DE DNA encoding novel human diagnostic protein #17205.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 50.4% Conservative: 23
Best Local Similarity: 32.6% Mismatches: 60
Indels: 5
Query Match:
RESULT 619
ID ADS48415 standard; cDNA; 1274 BP.
DE Bacterial polynucleotide #3158.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 34.4% Conservative: 32
Best Local Similarity: 23.3% Mismatches: 95
Indels: 94
Query Match:
RESULT 620
ID AEJ87551 standard; DNA; 1407 BP.
DE B. subtilis yaad-Xa-basf1-his fusion DNA.
PN WO2006082251-A2.
PD 10-AUG-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 621
ID AEK60806 standard; DNA; 1407 BP.
DE Hydrophobin fusion construct yaad-Xa-basf-1-his DNA.
PN WO2006082253-A2.
PD 10-AUG-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 622
ID AEL10480 standard; DNA; 1407 BP.
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.
PN DE102005015043-A1.
PD 05-OCT-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 623
ID AEL10520 standard; DNA; 1407 BP.
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.
PN WO2006103230-A1.
PD 05-OCT-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 624
ID AEL10590 standard; DNA; 1407 BP.
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.
PN WO2006103225-A1.
PD 05-OCT-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 625
ID AEL10555 standard; DNA; 1407 BP.
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.
PN WO2006103251-A1.
PD 05-OCT-2006.
PA (BADI) BASF AG.
Percent Similarity: 37.8% Conservative: 35
Best Local Similarity: 23.7% Mismatches: 82
Indels: 73
Query Match:
RESULT 626
ID ABL61038 standard; DNA; 3783 BP.
DE N. clavipes spidroin synthetic homologue S01S01.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Percent Similarity: 35.2% Conservative: 41
Best Local Similarity: 23.5% Mismatches: 111
Indels: 116
Query Match:
RESULT 627
ID ABL27121 standard; DNA; 4287 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.5% Conservative: 52
Best Local Similarity: 24.0% Mismatches: 126
Indels: 77
Query Match:
RESULT 628
ID ABL61040 standard; DNA; 5658 BP.
DE N. clavipes spidroin synthetic homologue S01SM12.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Percent Similarity: 35.2% Conservative: 41
Best Local Similarity: 23.5% Mismatches: 111
Indels: 116
Query Match:
RESULT 629
ID AAV52204 standard; DNA; 32768 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:71.
PN WO9818931-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.2% Conservative: 73
Best Local Similarity: 22.6% Mismatches: 187
Indels: 83
Query Match:
RESULT 630
ID ADQ54163 standard; DNA; 654 BP.
DE Novel canine microarray-related DNA sequence SeqID5465.

PN WO2004063324-A2.
 PD 29-JUL-2004.
 PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 34.3%
 Best Local Similarity: 24.9%
 Query Match: 6.0%
 RESULT 631
 ID ABZ68334 standard; DNA; 1098 BP.
 DE Nucleotide sequence of human TIM-1 allele 3.
 PN WO2003002722-A2.
 PD 09-JAN-2003.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 Percent Similarity: 37.5%
 Best Local Similarity: 24.3%
 Query Match: 6.0%
 RESULT 632
 ID ADY98076 standard; cDNA; 1098 BP.
 DE Human TIM-1 allele 3.
 PN WO2005027854-A2.
 PD 31-MAR-2005.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (DAND) DANA FARBEN CANCER INST INC.
 Percent Similarity: 37.5%
 Best Local Similarity: 24.3%
 Query Match: 6.0%
 RESULT 633
 ID AED60520 standard; DNA; 1098 BP.
 DE Human TIM-1, allele 3, DNA SEQ ID NO:28.
 PN WO2005097211-A2.
 PD 20-OCT-2005.
 PA (TELO-) TELOS PHARM INC.
 Percent Similarity: 37.5%
 Best Local Similarity: 24.3%
 Query Match: 6.0%
 RESULT 634
 ID AAT90038 standard; cDNA to mRNA; 1542 BP.
 DE Hepatocyte growth factor activator inhibitor cDNA.
 PN EP759467-A2.
 PD 26-FEB-1997.
 PA (MITU) MITSUBISHI CHEM CORP.
 Percent Similarity: 37.7%
 Best Local Similarity: 22.7%
 Query Match: 6.0%
 RESULT 635
 ID AAX02200 standard; DNA; 1542 BP.
 DE Human HAI-1 cDNA.
 PN JF11035480-A.
 PD 09-FEB-1999.
 PA (MITU) MITSUBISHI CHEM CORP.
 Percent Similarity: 37.7%
 Best Local Similarity: 22.7%
 Query Match: 6.0%
 RESULT 636
 ID ADS47275 standard; cDNA; 1671 BP.
 DE Bacterial polynucleotide #2018.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 41.5%
 Best Local Similarity: 22.6%
 Query Match: 6.0%
 RESULT 637
 ID APT42440 standard; DNA; 2636 BP.
 DE Toxicity modelling related rat gene SEQ ID No 2142.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 42.4%
 Conservative: 57
 Mismatches: 114
 Indels: 62
 Conservative: 71
 Mismatches: 190
 Indels: 108
 Conservative: 71
 Mismatches: 190
 Indels: 108
 Conservative: 57
 Mismatches: 114
 Indels: 62
 Conservative: 23

Best Local Similarity: 29.9%
 Query Match: 6.0%
 RESULT 638
 ID ADT47317 standard; cDNA; 3228 BP.
 DE Bacterial polynucleotide #22068.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 37.4%
 Best Local Similarity: 22.8%
 Query Match: 6.0%
 RESULT 639
 ID ABL28633 standard; DNA; 4777 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37372.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEXE) PE CORP NY.
 Percent Similarity: 31.8%
 Best Local Similarity: 20.2%
 Query Match: 6.0%
 RESULT 640
 Percent Similarity: 37.4%
 Best Local Similarity: 26.6%
 Query Match: 6.0%
 RESULT 641
 ID AAH77281 standard; cDNA; 1651 BP.
 DE Human hepatocyte growth factor activator inhibitor (HGF-AIh) #2 cDNA.
 PN WO200168707-A1.
 PD 20-SEP-2001.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 34.2%
 Best Local Similarity: 21.9%
 Query Match: 6.0%
 RESULT 642
 ID AAD28495 standard; cDNA; 2601 BP.
 DE Human extracellular messenger (XMES) -5 cDNA.
 PN WO200194587-A2.
 PD 13-DEC-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 34.2%
 Best Local Similarity: 21.9%
 Query Match: 6.0%
 RESULT 643
 ID AAH17836 standard; cDNA; 3260 BP.
 DE Human cDNA sequence SEQ ID NO:17520.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 34.2%
 Best Local Similarity: 21.9%
 Query Match: 6.0%
 RESULT 644
 ID ABX71379 standard; cDNA; 4082 BP.
 DE Human testes-derived cDNA from clone DKFZphtes3_2a11.
 PN WO200112659-A2.
 PD 22-FEB-2001.
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 Percent Similarity: 34.9%
 Best Local Similarity: 23.6%
 Query Match: 6.0%
 RESULT 645
 ID ADC30325 standard; cDNA; 4082 BP.
 DE Human novel cDNA sequence, SEQ ID NO:407.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 34.7%
 Best Local Similarity: 22.9%
 Query Match: 6.0%
 Conservative: 57
 Mismatches: 176
 Indels: 131
 Conservative: 57
 Mismatches: 176
 Indels: 131
 Conservative: 43
 Mismatches: 123
 Indels: 128
 Conservative: 56
 Mismatches: 174
 Indels: 141

RESULT 646
ID AD270350 standard; cDNA; 4082 BP.
DE Human cDNA from lung cancer marker gene FLJ12761.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Percent Similarity: 34.9%
Best Local Similarity: 23.6%
Query Match: 6.0%
Conservative: 43
Mismatch: 123
Indels: 128
RESULT 647
ID AD280791 standard; cDNA; 4154 BP.
DE Nucleotide sequence of human homologue of Drosophila gene CG11006.
PN WO2005039635-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS AG.
Percent Similarity: 34.9%
Best Local Similarity: 23.6%
Query Match: 6.0%
Conservative: 43
Mismatch: 123
Indels: 128
RESULT 648
ID ABL05017 standard; cDNA; 4667 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9533.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 33.6%
Best Local Similarity: 20.7%
Query Match: 6.0%
Conservative: 55
Mismatch: 152
Indels: 133
RESULT 649
ID ACP74294 standard; DNA; 6813 BP.
DE Staphylococcus aureus DNA #1974.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 41.1%
Best Local Similarity: 21.6%
Query Match: 6.0%
Conservative: 76
Mismatch: 192
Indels: 37
RESULT 650
ID AB222900 standard; DNA; 6852 BP.
DE Staphylococcus epidermidis DsqA encoding DNA SEQ ID NO:3.
PN WO2002102829-A2.
PD 27-DEC-2002.
PA (INHI-) INHIBITEX INC.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA (UWPA-) UNIV PAVIA.
Percent Similarity: 41.1%
Best Local Similarity: 21.6%
Query Match: 6.0%
Conservative: 76
Mismatch: 192
Indels: 37
RESULT 651
ID AAL07156 standard; DNA; 24387 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9844.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 35.6%
Best Local Similarity: 22.4%
Query Match: 6.0%
Conservative: 56
Mismatch: 140
Indels: 135
RESULT 652
ID ACH87193 standard; DNA; 461 BP.
DE Human genome derived single exon probe #20388.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 45.8%
Best Local Similarity: 26.0%
Query Match: 6.0%
Conservative: 26
Mismatch: 69
Indels: 2
RESULT 653
ID ABA35209 standard; DNA; 576 BP.
DE Probe #13675 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.4%
Best Local Similarity: 34.2%
Query Match: 6.0%
Conservative: 10
Mismatch: 66
Indels: 30
RESULT 654
ID AAK42331 standard; DNA; 576 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 16888.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.4%
Best Local Similarity: 34.2%
Query Match: 6.0%
Conservative: 10
Mismatch: 66
Indels: 30
RESULT 655
ID AAK16577 standard; DNA; 576 BP.
DE Human brain expressed single exon probe SEQ ID NO: 16568.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.4%
Best Local Similarity: 34.2%
Query Match: 6.0%
Conservative: 10
Mismatch: 66
Indels: 30
RESULT 656
ID AAI08759 standard; DNA; 576 BP.
DE Probe #8750 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.4%
Best Local Similarity: 34.2%
Query Match: 6.0%
Conservative: 10
Mismatch: 66
Indels: 30
RESULT 657
ID ACH91803 standard; DNA; 627 BP.
DE Human genome derived single exon probe #24998.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 40.4%
Best Local Similarity: 34.2%
Query Match: 6.0%
Conservative: 10
Mismatch: 66
Indels: 30
RESULT 658
ID AEB65941 standard; DNA; 1413 BP.
DE Rice genome derived DNA sequence, SEQ ID 1086.
PN JP2005185101-A.
PD 14-JUL-2005.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
Percent Similarity: 38.8%
Best Local Similarity: 26.2%
Query Match: 6.0%
Conservative: 41
Mismatch: 114
Indels: 86
RESULT 659
ID ABL61043 standard; DNA; 1908 BP.
DE N. clavipes spidroin synthetic homologue S01.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Percent Similarity: 36.7%
Best Local Similarity: 26.0%
Query Match: 6.0%
Conservative: 36
Mismatch: 154
Indels: 62
RESULT 660
ID ABQ61126 standard; cDNA; 2114 BP.
DE Human EXMAD-20 protein encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 32.9%
Best Local Similarity: 20.9%
Query Match: 6.0%
Conservative: 50
Mismatch: 124
Indels: 156
RESULT 661

ID AAZ45836 standard; cDNA; 2455 BP.
 DE cDNA of intestinal insect mucin isoform IIM14.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Percent Similarity: 40.6% Conservative: 15
 Best Local Similarity: 31.0% Mismatches: 78
 Query Match: 6.0% Indels: 14
 RESULT 662
 ID ADP04874 standard; cDNA; 2529 BP.
 DE Sea squirt cDNA with tissue specific expression in development Seq 469.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Percent Similarity: 32.8% Conservative: 59
 Best Local Similarity: 20.3% Mismatches: 151
 Query Match: 6.0% Indels: 169
 RESULT 663
 ID AAZ45837 standard; cDNA; 2821 BP.
 DE cDNA of intestinal insect mucin isoform IIM22.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Percent Similarity: 40.6% Conservative: 15
 Best Local Similarity: 31.0% Mismatches: 78
 Query Match: 6.0% Indels: 14
 RESULT 664
 ID ABL61039 standard; DNA; 2985 BP.
 DE N. clavipes spidroin synthetic homologue SOISM12.
 PN DE10113781-A1.
 PD 13-DEC-2001.
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
 Percent Similarity: 36.7% Conservative: 36
 Best Local Similarity: 26.0% Mismatches: 154
 Query Match: 6.0% Indels: 62
 RESULT 665
 ID ABT10922 standard; cDNA; 4669 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 1056.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.1% Conservative: 56
 Best Local Similarity: 22.8% Mismatches: 130
 Query Match: 6.0% Indels: 167
 RESULT 666
 ID AAA61847 standard; DNA; 5511 BP.
 DE Cryptosporidium parvum Iowa isolate GP900 ORF.
 PN US6071518-A.
 PD 06-JUN-2000.
 PA (REGC-) UNIV CALIFORNIA.
 Percent Similarity: 37.1% Conservative: 45
 Best Local Similarity: 23.3% Mismatches: 146
 Query Match: 6.0% Indels: 59
 RESULT 667
 ID ABT04776 standard; DNA; 5511 BP.
 DE C parvum GP900 gene fragment SEQ ID NO: 2.
 PN WO200194631-A1.
 PD 13-DEC-2001.
 PA (REGC-) UNIV CALIFORNIA.
 Percent Similarity: 37.1% Conservative: 45
 Best Local Similarity: 23.3% Mismatches: 146
 Query Match: 6.0% Indels: 59
 RESULT 668
 ID ADA83845 standard; DNA; 5610 BP.
 DE Human COL17A1 gene.
 PN WO2002103028-A2.
 PD 27-DEC-2002.
 PA (BIOW-) BIOMEDICAL CENT.
 Percent Similarity: 35.1% Conservative: 56
 Best Local Similarity: 22.8% Mismatches: 130
 Query Match: 6.0% Indels: 167
 RESULT 669
 ID ACN39117 standard; cDNA; 5610 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA325377, SEQ ID NO:3058.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH-) GEMENTECH INC.
 Percent Similarity: 35.1% Conservative: 56
 Best Local Similarity: 22.8% Mismatches: 130
 Query Match: 6.0% Indels: 167
 RESULT 670
 ID ABQ60955 standard; cDNA; 5714 BP.
 DE Bullock penhigold BP180 encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 35.1% Conservative: 57
 Best Local Similarity: 22.6% Mismatches: 130
 Query Match: 6.0% Indels: 167
 RESULT 671
 ID AED73234 standard; cDNA; 5796 BP.
 DE Human placental protein encoding cDNA SEQ ID NO:62.
 PN US2005255114-A1.
 PD 17-NOV-2005.
 PA (NUVE-) NUVELO INC.
 Percent Similarity: 35.1% Conservative: 56
 Best Local Similarity: 22.8% Mismatches: 130
 Query Match: 6.0% Indels: 167
 RESULT 672
 ID AAA61846 standard; DNA; 7334 BP.
 DE Cryptosporidium parvum Iowa isolate GP900 DNA.
 PN US6071518-A.
 PD 06-JUN-2000.
 PA (REGC-) UNIV CALIFORNIA.
 Percent Similarity: 37.1% Conservative: 45
 Best Local Similarity: 23.3% Mismatches: 146
 Query Match: 6.0% Indels: 59
 RESULT 673
 ID ABR04775 standard; DNA; 7334 BP.
 DE C parvum GP900 gene fragment SEQ ID NO: 1.
 PN WO200194631-A1.
 PD 13-DEC-2001.
 PA (REGC-) UNIV CALIFORNIA.
 Percent Similarity: 37.1% Conservative: 45
 Best Local Similarity: 23.3% Mismatches: 146
 Query Match: 6.0% Indels: 59
 RESULT 674
 ID ADN12161 standard; DNA; 172281 BP.
 DE Epstein-Barr virus genome B95-8.
 PN WO2004027036-A2.
 PD 01-APR-2004.
 PA (UYJO-) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Percent Similarity: 34.2% Conservative: 46
 Best Local Similarity: 21.6% Mismatches: 163
 Query Match: 6.0% Indels: 78
 RESULT 675
 ID ABQ93367 standard; cDNA; 12279 BP.
 DE Human cDNA SEQ ID NO 80.
 PN WO200218424-A2.
 PD 07-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 47.0% Conservative: 35
 Best Local Similarity: 28.1% Mismatches: 65
 Query Match: 5.9% Indels: 33
 RESULT 676
 ID ABE75855 standard; DNA; 73921 BP.
 DE Streptomyces tautomycin polyketide synthase enzyme gene cluster.
 PN WO2005118797-A2.
 PD 15-DEC-2005.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Percent Similarity: 41.8% Conservative: 36
 Best Local Similarity: 26.8% Mismatches: 105
 Query Match: 5.9% Indels: 34
 RESULT 677
 ID AAA44382 standard; cDNA; 716 BP.
 DE Human secreted expressed sequence tag SEQ ID NO:957.

PN	WO200021991-A1.				
PD	20-APR-2000.				
PA	(GEMY/) GENETICS INST INC.				
Percent Similarity:	38.2%	Conservative:	29		
Best Local Similarity:	26.7%	Mismatches:	94		
Query Match:	5.9%	Indels:	61		
RESULT 678					
ID	ADJ48292 standard; DNA; 1428 BP.				
DE	Maize oil-associated gene #110.				
PD	US2004025202-A1.				
PD	05-FEB-2004.				
PA	(LAUR/) LAURIE C C.				
PA	(RAVA/) RAVANELLO M.				
PA	(SAVA/) SAVAGE T.				
PA	(LEDE/) LEDEAUX J R.				
PA	(ROGE/) ROGERS J A.				
Percent Similarity:	38.1%	Conservative:	37		
Best Local Similarity:	27.1%	Mismatches:	111		
Query Match:	5.9%	Indels:	101		
RESULT 679					
ID	ADT17022 standard; cDNA; 1428 BP.				
DE	Plant cDNA, Seq ID 2348.				
PD	US2004216190-A1.				
PD	28-OCT-2004.				
PA	(KOVA/) KOVALIC D K.				
Percent Similarity:	38.1%	Conservative:	37		
Best Local Similarity:	27.1%	Mismatches:	111		
Query Match:	5.9%	Indels:	101		
RESULT 680					
ID	ADS47261 standard; cDNA; 2178 BP.				
DE	Bacterial polynucleotide #2004.				
PD	US200233675-A1.				
PD	18-DEC-2003.				
PA	(CAOY/) CAO Y.				
PA	(HINK/) HINKLE G J.				
PA	(SLAT/) SLATER S C.				
PA	(CHEN/) CHEN X.				
PA	(GOLD/) GOLDMAN B S.				
Percent Similarity:	33.6%	Conservative:	64		
Best Local Similarity:	19.5%	Mismatches:	185		
Query Match:	5.9%	Indels:	118		
RESULT 681					
ID	ADM72956 standard; DNA; 2391 BP.				
DE	Bread wheat strain identification-related 1Bx14 subunit DNA.				
PD	CN1428351-A.				
PD	09-JUL-2003.				
PA	(GENE-) INST GENETICS CHINESE ACAD SCI.				
Percent Similarity:	38.4%	Conservative:	57		
Best Local Similarity:	23.5%	Mismatches:	166		
Query Match:	5.9%	Indels:	72		
RESULT 682					
ID	ABS51504 standard; cDNA; 4468 BP.				
DE	Human cDNA encoding prey protein for Shigella ospC1 #29.				
PD	WO200257303-A2.				
PD	25-JUL-2002.				
PA	(HYBR-) HYBRIGENICS.				
Percent Similarity:	36.3%	Conservative:	45		
Best Local Similarity:	23.9%	Mismatches:	146		
Query Match:	5.9%	Indels:	87		
RESULT 683					
ID	ADR32198 standard; DNA; 4893 BP.				
DE	Yeast FLO11 open reading frame, SEQ ID NO:3.				
PD	WO2004067565-A1.				
PD	12-AUG-2004.				
PA	(OSBO-) OSBORNE DISTRIBUIDORA SA.				
PA	(UYDO/) UNIV DE OLAVIDE PABLO.				
Percent Similarity:	40.4%	Conservative:	38		
Best Local Similarity:	26.5%	Mismatches:	104		
Query Match:	5.9%	Indels:	61		
RESULT 684					
ID	ADS10393 standard; DNA; 7500 BP.				
DE	Human therapeutic DNA - SEQ ID 630.				
PD	WO2004080148-A2.				

PD 23-SEP-2004.			
PA (NUVE-) NUVELO INC.	36.3%	Conservative:	45
Percent Similarity:	23.9%	Mismatches:	146
Best Local Similarity:	5.9%	Indels:	87
Query Match:			
RESULT 685			
ID AEF92979 standard; DNA; 13125 BP.			
DE Human Hecth9 ORF DNA sequence.			
PN WO2006018654-A1.			
PD 23-FEB-2006.			
PA (CANC-) CANCER RES TECHNOLOGY LTD.			
Percent Similarity:	36.3%	Conservative:	45
Best Local Similarity:	23.9%	Mismatches:	146
Query Match:	5.9%	Indels:	87.
RESULT 686			
ID ADE79055 standard; DNA; 13855 BP.			
DE Human protein modification and maintenance molecule (PMM)-35 gene.			
PN WO2003063688-A2.			
PD 07-AUG-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Percent Similarity:	36.3%	Conservative:	45
Best Local Similarity:	23.9%	Mismatches:	146
Query Match:	5.9%	Indels:	87
RESULT 687			
ID AEF97928 standard; DNA; 13808 BP.			
DE Human cancer associated sequence HD11-024, SEQ ID 905.			
PN WO2004060304-A2.			
PD 22-JUL-2004.			
PA (SAGR-) SAGRES DISCOVERY INC.			
Percent Similarity:	41.1%	Conservative:	22
Best Local Similarity:	26.5%	Mismatches:	75
Query Match:	5.9%	Indels:	14
RESULT 688			
ID ACN44631 standard; cDNA; 1706 BP.			
DE Human mRNA sequence hCT1686293.			
PN WO2003073826-A2.			
PD 12-SEP-2003.			
PA (SAGR-) SAGRES DISCOVERY.			
Percent Similarity:	39.0%	Conservative:	51
Best Local Similarity:	25.5%	Mismatches:	118
Query Match:	5.9%	Indels:	112
RESULT 689			
ID ADM41104 standard; cDNA; 1924 BP.			
DE Human CD43 (stathophorin, leukosialin)-encoding cDNA, SEQ ID NO:5.			
PN WO2004026120-A2.			
PD 01-APR-2004.			
PA (GEO-) GEN HOSPITAL CORP.			
Percent Similarity:	39.0%	Conservative:	51
Best Local Similarity:	25.5%	Mismatches:	118
Query Match:	5.9%	Indels:	112
RESULT 690			
ID ABZ35214 standard; cDNA; 2166 BP.			
DE Human gene expression profile polynucleotide SEQ ID NO 326.			
PN WO200274979-A2.			
PD 26-SEP-2002.			
PA (ORTH-) ORTHO CLINICAL DIAGNOSTICS INC.			
Percent Similarity:	36.8%	Conservative:	57
Best Local Similarity:	22.6%	Mismatches:	139
Query Match:	5.9%	Indels:	113
RESULT 691			
ID ADX52983 standard; cDNA; 2220 BP.			
DE Plant full length insert polynucleotide seqid 27723.			
PN US2004034888-A1.			
PD 19-FEB-2004.			
PA (LIUO-) LIU J.			
PA (ZHOU-) ZHOU Y.			
PA (KOVA-) KOVALIC D K.			
PA (SCRE-) SCREEN S E.			
PA (TABA-) TABASKA J E.			
PA (CAOY-) CAO Y.			
Percent Similarity:	39.1%	Conservative:	46
Best Local Similarity:	23.6%	Mismatches:	136
Query Match:	5.9%	Indels:	45

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RESULT 692
ID AEK91705 standard; cDNA; 2235 BP.
DE Breast cancer antigen Muc-1 RT-PCR amplified nucleic acid.
PN WO2006105255-A2.
PD 05-OCT-2006.
PA (UNII ) UNIV ILLINOIS FOUND.
Percent Similarity: 36.8%
Best Local Similarity: 22.8%
Conservative: 57
Mismatches: 139
Indels: 113
Query Match: 5.9%
RESULT 693
ID ABL28816 standard; DNA; 2648 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37921.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Percent Similarity: 39.2%
Best Local Similarity: 25.1%
Conservative: 32
Mismatches: 104
Indels: 35
Query Match: 5.9%
RESULT 694
ID ADZ13126 standard; cDNA; 2696 BP.
DE Human cancer-associated cDNA #200.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR ) CHIRON CORP.
Percent Similarity: 39.0%
Best Local Similarity: 25.9%
Conservative: 51
Mismatches: 118
Indels: 112
Query Match: 5.9%
RESULT 695
ID AAT33007 standard; DNA; 10266 BP.
DE Mouse SVY-related gene.
PN JP08154685-A.
PD 18-JUN-1996.
PA (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.
Percent Similarity: 43.0%
Best Local Similarity: 24.6%
Conservative: 56
Mismatches: 136
Indels: 39
Query Match: 5.9%
RESULT 696
ID ADJ81505 standard; DNA; 14016 BP.
DE Plant retroelement associated sequence #66.
PN WO2003050259-A2.
PD 19-JUN-2003.
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
Percent Similarity: 36.4%
Best Local Similarity: 25.9%
Conservative: 40
Mismatches: 159
Indels: 83
Query Match: 5.9%
RESULT 697
ID AEK18770 standard; DNA; 1971884 BP.
DE T. parva strain Muguga chromosome 2 chr2_complete SEQ ID NO:70.
PN US2006210537-A1.
PD 21-SEP-2006.
PA (AUDO/) AUDONNET J F.
PA (LOOS/) LOOSMORE S M.
Percent Similarity: 32.3%
Best Local Similarity: 21.4%
Conservative: 41
Mismatches: 131
Indels: 126
Query Match: 5.9%
RESULT 698
ID ADJ39821 standard; cDNA; 947 BP.
DE Plant cDNA #821.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RICKÉ D.
PA (ZHUT/) ZHU T.
Percent Similarity: 36.0%
Best Local Similarity: 25.9%
Conservative: 29
Mismatches: 99

Query Match: 5.9% Indels: 84
RESULT 699
ID ADT18753 standard; cDNA; 1407 BP.
DE Plant cDNA, Seq ID 4079.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Percent Similarity: 39.1%
Best Local Similarity: 24.9%
Conservative: 37
Mismatches: 112
Indels: 48
Query Match: 5.9%
RESULT 700
ID ABT23249 standard; DNA; 1687 BP.
DE Seed development embryo/endosperm size alteration DNA SEQ ID 40.
PN WO200299063-A2.
PD 12-DEC-2002.
PA (DUFO ) DU PONT DE NEMOURS & CO E I.
Percent Similarity: 40.0%
Best Local Similarity: 25.8%
Conservative: 32
Mismatches: 105
Indels: 31
Query Match: 5.9%
RESULT 701
ID AEI36095 standard; DNA; 2042 BP.
DE Soybean polymorphic locus, SEQ ID 8729.
PN US2006135758-A1.
PD 22-JUN-2006.
PA (WUKK/) WU K.
Percent Similarity: 37.7%
Best Local Similarity: 24.9%
Conservative: 42
Mismatches: 113
Indels: 93
Query Match: 5.9%
RESULT 702
ID ADM02801 standard; cDNA; 2428 BP.
DE Human cDNA of the invention SEQ ID NO:1486.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.8%
Best Local Similarity: 23.2%
Conservative: 50
Mismatches: 128
Indels: 107
Query Match: 5.9%
RESULT 703
ID AEC85731 standard; cDNA; 2428 BP.
DE Human cDNA clone PROST20100460, SEQ ID 1486.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.8%
Best Local Similarity: 23.2%
Conservative: 50
Mismatches: 128
Indels: 107
Query Match: 5.9%
RESULT 704
ID AAZ58824 standard; DNA; 2872 BP.
DE Human MUC11 polypeptide encoding DNA.
PN WO200004142-A1.
PD 27-JAN-2000.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Percent Similarity: 34.9%
Best Local Similarity: 23.4%
Conservative: 41
Mismatches: 109
Indels: 123
Query Match: 5.9%
RESULT 705
ID AAI29501 standard; cDNA; 2872 BP.
DE C900P determined cDNA sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 34.9%
Best Local Similarity: 23.4%
Conservative: 41
Mismatches: 109
Indels: 123
Query Match: 5.9%
RESULT 706
ID ABZ33687 standard; cDNA; 2872 BP.
DE Human colon tumour cDNA for clone C900P SEQ ID NO:1055.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 34.9%
Best Local Similarity: 23.4%
Conservative: 41
Mismatches: 109
Indels: 123
Query Match: 5.9%

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Query Match: 5.9% Indels: 123

RESULT 707
ID ABL15838 standard; cDNA; 3983 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41996.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.3%
Best Local Similarity: 21.9%
Conservative: 44
Mismatch: 133
Indels: 80

Query Match: 5.9% Indels: 80

RESULT 708
ID ADQ29629 standard; DNA; 4707 BP.
DE Human colorectal cancer-associated protein coding sequence #51.
PN EPI439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 44
Mismatch: 122
Indels: 50

Query Match: 5.9% Indels: 50

RESULT 709
ID AED17896 standard; DNA; 4707 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 147.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UVFL) UNIV FLORIDA RES FOUND INC.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 44
Mismatch: 122
Indels: 50

Query Match: 5.9% Indels: 50

RESULT 710
ID AEF69941 standard; DNA; 4707 BP.
DE Colorectal cancer-associated marker DNA SEQ ID NO:119.
PN WO2006015047-A2.
PD 09-FEB-2006.
PA (FARB) BAYER HEALTHCARE LLC.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 44
Mismatch: 122
Indels: 50

Query Match: 5.9% Indels: 50

RESULT 711
ID AAF98223 standard; cDNA; 4718 BP.
DE Human EST-derived coding sequence SEQ ID NO: 80.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 44
Mismatch: 122
Indels: 50

Query Match: 5.9% Indels: 50

RESULT 712
ID ADI21512 standard; cDNA; 4718 BP.
DE Novel human expressed sequence tag, EST #211.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 44
Mismatch: 122
Indels: 50

Query Match: 5.9% Indels: 50

RESULT 713
ID AEG97264 standard; DNA; 5355 BP.
DE Cryptococcus neoformans CRV1 DNA homolog SEQ ID NO 33.
PN WO2006036817-A2.
PD 06-APR-2006.
PA (MICR-) MICROBIA INC.
Percent Similarity: 36.1%
Best Local Similarity: 24.2%
Conservative: 32
Mismatch: 112
Indels: 61

Query Match: 5.9% Indels: 61

RESULT 714
ID ACF74291 standard; DNA; 798 BP.
DE Staphylococcus aureus DNA #1971.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 42.8%
Conservative: 51

Best Local Similarity: 23.8%
Query Match: 5.9%
Indels: 23

RESULT 715
ID AAV75136 standard; DNA; 1099 BP.
DE Staphylococcus aureus contig SEQ ID #825.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.8%
Best Local Similarity: 23.8%
Conservative: 51
Mismatch: 131
Indels: 23

Query Match: 5.9% Indels: 23

RESULT 716
ID ADM99275 standard; DNA; 1719 BP.
DE C.heterostrophus strain C4 serine carboxypeptidase DNA SeqID 158.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Percent Similarity: 33.6%
Best Local Similarity: 24.5%
Conservative: 33
Mismatch: 148
Indels: 93

Query Match: 5.9% Indels: 93

RESULT 717
ID ABL28927 standard; DNA; 1767 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38254.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 48
Mismatch: 119
Indels: 69

Query Match: 5.9% Indels: 69

RESULT 718
ID AAS72679 standard; cDNA; 2922 BP.
DE DNA encoding novel human diagnostic protein #8483.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.1%
Best Local Similarity: 27.1%
Conservative: 22
Mismatch: 87
Indels: 52

Query Match: 5.9% Indels: 52

RESULT 719
ID ABL28926 standard; DNA; 3767 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38251.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.1%
Best Local Similarity: 23.5%
Conservative: 48
Mismatch: 119
Indels: 69

Query Match: 5.9% Indels: 69

RESULT 720
ID ABL10402 standard; cDNA; 16962 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25688.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 37.2%
Best Local Similarity: 26.3%
Conservative: 39
Mismatch: 150
Indels: 75

Query Match: 5.9% Indels: 75

RESULT 721
ID ADU06921 standard; DNA; 20425 BP.
DE Wheat plant genome region containing high molecular weight glutenin gene.
PN AU2003259589-A1.
PD 20-MAY-2004.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Percent Similarity: 40.2%
Best Local Similarity: 24.7%
Conservative: 40
Mismatch: 111
Indels: 45

Query Match: 5.9% Indels: 45

RESULT 722
ID ABZ68336 standard; DNA; 1095 BP.
DE Nucleotide sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 Percent Similarity: 37.5% Conservative: 42
 Best Local Similarity: 24.6% Mismatches: 144
 Query Match: 5.8% Indels: 60
 RESULT 723
 ID ADY98080 standard; cDNA; 1095 BP.
 DE Human TIM-1 allele 5.
 PN WO2005027854-A2.
 PD 31-MAR-2005.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (DAND) DANA FARBER CANCER INST INC.
 Percent Similarity: 37.5% Conservative: 42
 Best Local Similarity: 24.6% Mismatches: 144
 Query Match: 5.8% Indels: 60
 RESULT 724
 ID AED60524 standard; DNA; 1095 BP.
 DE Human TIM-1, allele 5, DNA SEQ ID NO:32.
 PN WO2005097211-A2.
 PD 20-OCT-2005.
 PA (TELO-) TELOS PHARM INC.
 Percent Similarity: 37.5% Conservative: 42
 Best Local Similarity: 24.6% Mismatches: 144
 Query Match: 5.8% Indels: 60
 RESULT 725
 ID ADL93906 standard; DNA; 1374 BP.
 DE Human FOXP2 ORF isoform VI nucleotide sequence.
 PN WO2004022104-A2.
 PD 18-MAR-2004.
 PA (ISIS-) ISIS INNOVATION LTD.
 Percent Similarity: 36.0% Conservative: 22
 Best Local Similarity: 26.7% Mismatches: 109
 Query Match: 5.8% Indels: 44
 RESULT 726
 ID AEI88287 standard; cDNA; 1752 BP.
 DE cDNA encoding glucoamylase, SEQ ID NO:41.
 PN WO2006069289-A2.
 PD 29-JUN-2006.
 PA (NOVO) NOVOZYMES NORTH AMERICA INC.
 PA (NOVO) NOVOZYMES AS.
 Percent Similarity: 37.5% Conservative: 39
 Best Local Similarity: 25.0% Mismatches: 142
 Query Match: 5.8% Indels: 54
 RESULT 727
 ID AAD09400 standard; cDNA; 1815 BP.
 DE Zea mays zeaxanthin cleavage enzyme, VP14 cDNA.
 PN EP1116794-A2.
 PD 18-JUL-2001.
 PA (RIKE) RIKEN KK.
 Percent Similarity: 34.3% Conservative: 36
 Best Local Similarity: 22.7% Mismatches: 116
 Query Match: 5.8% Indels: 88
 RESULT 728
 ID AAC43180 standard; DNA; 1893 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38322.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 36.4% Conservative: 41
 Best Local Similarity: 24.6% Mismatches: 140
 Query Match: 5.8% Indels: 81
 RESULT 729
 ID ADL93902 standard; DNA; 2223 BP.
 DE Human FOXP2 ORF isoform II nucleotide sequence.
 PN WO2004022104-A2.
 PD 18-MAR-2004.
 PA (ISIS-) ISIS INNOVATION LTD.
 Percent Similarity: 36.0% Conservative: 22
 Best Local Similarity: 26.7% Mismatches: 109
 Query Match: 5.8% Indels: 44
 RESULT 730
 ID AAF30256 standard; cDNA; 2249 BP.
 DE Human cDNA encoding protein associated with IgA nephropathy.
 PN WO200105803-A1.
 PD 25-JAN-2001.

PA (GENE-) GENE LOGIC INC..
 Percent Similarity: 37.7% Conservative: 55
 Best Local Similarity: 23.6% Mismatches: 162
 Query Match: 5.8% Indels: 82
 RESULT 731
 ID AEK56460 standard; cDNA; 2498 BP.
 DE Maize cDNA SEQ ID NO:17.
 PN WO2006098626-A2.
 PD 21-SEP-2006.
 PA (PLAN-) PLANT RES INT BV.
 PA (ROTH-) ROTHAMSTED RES LTD.
 Percent Similarity: 34.3% Conservative: 36
 Best Local Similarity: 22.7% Mismatches: 116
 Query Match: 5.8% Indels: 88
 RESULT 732
 ID ADS49143 standard; cDNA; 2714 BP.
 DE Bacterial polynucleotide #3886.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 38.5% Conservative: 44
 Best Local Similarity: 24.3% Mismatches: 133
 Query Match: 5.8% Indels: 58
 RESULT 733
 ID AEI34526 standard; DNA; 3020 BP.
 DE Soybean polymorphic locus, SEQ ID 7160.
 PN US2006135758-A1.
 PD 22-JUN-2006.
 PA (WURK/) WU K.
 Percent Similarity: 35.3% Conservative: 37
 Best Local Similarity: 23.9% Mismatches: 110
 Query Match: 5.8% Indels: 101
 RESULT 734
 ID AEH37864 standard; DNA; 3600 BP.
 DE Cryptosporidium hominis gene SEQ ID NO:955.
 PN WO2006044045-A2.
 PD 27-APR-2006.
 PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.
 Percent Similarity: 40.4% Conservative: 25
 Best Local Similarity: 24.4% Mismatches: 87
 Query Match: 5.8% Indels: 6
 RESULT 735
 ID AEA19839 standard; cDNA; 3809 BP.
 DE Novel human polynucleotide SEQ ID NO 533.
 PN WO2005049806-A2.
 PD 02-JUN-2005.
 PA (NUVE-) NUVELO INC.
 Percent Similarity: 34.6% Conservative: 40
 Best Local Similarity: 23.4% Mismatches: 110
 Query Match: 5.8% Indels: 123
 RESULT 736
 ID ADC30711 standard; cDNA; 3879 BP.
 DE Human novel cDNA sequence, SEQ ID NO:793.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 34.6% Conservative: 40
 Best Local Similarity: 23.4% Mismatches: 110
 Query Match: 5.8% Indels: 123
 RESULT 737
 ID AEA19838 standard; cDNA; 3893 BP.
 DE Novel human polynucleotide SEQ ID NO 532.
 PN WO2005049806-A2.
 PD 02-JUN-2005.
 PA (NUVE-) NUVELO INC.
 Percent Similarity: 34.6% Conservative: 40
 Best Local Similarity: 23.4% Mismatches: 110
 Query Match: 5.8% Indels: 123
 RESULT 738

ID AAS76405 standard; cDNA; 4074 BP.
 DE DNA encoding novel human diagnostic protein #12209.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 46.3%
 Best Local Similarity: 28.8%
 Query Match: 5.8%
 Indels: 33
 RESULT 739

ID ACC50985 standard; cDNA; 4209 BP.
 DE Human bladder cancer associated cDNA sequence SEQ ID NO:63.
 PN WO2003003906-A2.
 PD 16-JAN-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 35.6%
 Best Local Similarity: 24.0%
 Query Match: 5.8%
 Indels: 87
 RESULT 740

ID ADM98727 standard; DNA; 4725 BP.
 DE HMG-CoA reductase DNA #62.
 PN US2004072323-A1.
 PD 15-APR-2004.
 PA (MATS/) MATSUDA S P T.
 Percent Similarity: 43.2%
 Best Local Similarity: 28.4%
 Query Match: 5.8%
 Indels: 30
 RESULT 741

ID ABL29442 standard; DNA; 11847 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39799.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 39.8%
 Best Local Similarity: 24.1%
 Query Match: 5.8%
 Indels: 73
 RESULT 742

ID AAS57196 standard; DNA; 11847 BP.
 DE DNA encoding Drosophila G-protein coupled receptor, GPCR #63.
 PN WO200170980-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 39.8%
 Best Local Similarity: 24.1%
 Query Match: 5.8%
 Indels: 73
 RESULT 743

ID ADC35935 standard; DNA; 11847 BP.
 DE Drosophila G protein coupled receptor genomic DNA seq id 63.
 PN US2003092124-A1.
 PD 15-MAY-2003.
 PA (APPL-) APPLERA CORP.
 Percent Similarity: 39.8%
 Best Local Similarity: 24.1%
 Query Match: 5.8%
 Indels: 73
 RESULT 744

ID ABO41714 standard; DNA; 1127 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28305.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 40.6%
 Best Local Similarity: 31.1%
 Query Match: 5.8%
 Indels: 59
 RESULT 745

ID ABO41715 standard; DNA; 1127 BP.
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28306.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 40.6%
 Best Local Similarity: 31.1%
 Query Match: 5.8%
 Indels: 59
 RESULT 746

ID AAT63302 standard; cDNA to mRNA; 1538 BP.
 DE A. chrysogenum O-acetylhomoserine sulphydrylase coding sequence.
 PN JP08336391-A.
 PD 24-DEC-1996.
 PA (ASAH) ASahi KASEI KOGYO KK.
 Percent Similarity: 38.6%
 Best Local Similarity: 26.4%
 Query Match: 5.8%
 Indels: 103
 RESULT 747

ID AEJ43446 standard; DNA; 2391 BP.
 DE Wheat somatic cell like 13 gliutelin subunit related DNA.
 PN CN1710075-A.
 PD 21-DEC-2005.
 PA (UYSH-) UNIV SHANDONG.
 Percent Similarity: 39.7%
 Best Local Similarity: 24.0%
 Query Match: 5.8%
 Indels: 89
 RESULT 748

ID ACA30008 standard; DNA; 2880 BP.
 DE Prokaryotic essential gene #11665.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 36.1%
 Best Local Similarity: 21.4%
 Query Match: 5.8%
 Indels: 108
 RESULT 749

ID ADU01669 standard; cDNA; 3540 BP.
 DE Novel human polynucleotide seqid 136.
 PN WO2004093804-A2.
 PD 04-NOV-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Percent Similarity: 39.4%
 Best Local Similarity: 24.7%
 Query Match: 5.8%
 Indels: 92
 RESULT 750

ID AAH81794 standard; DNA; 4373 BP.
 DE Human differential transcription-associated cDNA SEQ ID 303.
 PN WO200157058-A2.
 PD 09-AUG-2001.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Percent Similarity: 35.0%
 Best Local Similarity: 22.3%
 Query Match: 5.8%
 Indels: 135
 RESULT 751

ID ABL20278 standard; DNA; 5162 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12307.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 34.3%
 Best Local Similarity: 23.6%
 Query Match: 5.8%
 Indels: 114
 RESULT 752

ID AED18170 standard; DNA; 5894 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 421.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Percent Similarity: 35.0%
 Best Local Similarity: 22.3%
 Query Match: 5.8%
 Indels: 135
 RESULT 753

ID AAH81795 standard; DNA; 9027 BP.
 DE Human differential transcription-associated cDNA SEQ ID 304.
 PN WO200157058-A2.
 PD 09-AUG-2001.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Percent Similarity: 35.0%
 Best Local Similarity: 22.3%
 Query Match: 5.8%
 Indels: 129
 RESULT 754

ID ADN60277 standard; cDNA; 9027 BP.

DE Human serine/arginine repetitive matrix 2 encoding cDNA.
 PN WO2004039955-A2.
 PD 13-MAY-2004.
 PA (RIGE-) RIGEL PHARM INC.
 Percent Similarity: 35.0% Conservative: 51
 Best Local Similarity: 22.3% Mismatches: 129
 Indels: 135
 Query Match: 5.8%
 RESULT 755
 ID ADP24101 standard; cDNA; 9027 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:1279.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 35.0% Conservative: 51
 Best Local Similarity: 22.3% Mismatches: 129
 Indels: 135
 Query Match: 5.8%
 RESULT 756
 ID ADY91654 standard; DNA; 9027 BP.
 DE Human prostatic cancer marker, splicing coactivator SRM300 DNA.
 PN JP2005080524-A.
 PD 31-MAR-2005.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
 Percent Similarity: 35.0% Conservative: 51
 Best Local Similarity: 22.3% Mismatches: 129
 Indels: 135
 Query Match: 5.8%
 RESULT 757
 ID ADZ49494 standard; DNA; 9027 BP.
 DE Insulin signaling pathway related gene, SEQ ID 823.
 PN US2005085436-A1.
 PD 21-APR-2005.
 PA (LIHH/) LI H.
 Percent Similarity: 35.0% Conservative: 51
 Best Local Similarity: 22.3% Mismatches: 129
 Indels: 135
 Query Match: 5.8%
 RESULT 758
 ID AEB49547 standard; cDNA; 9027 BP.
 DE Human ser/arg repetitive matrix 2 cDNA.
 PN WO2005116205-A1.
 PD 08-DEC-2005.
 PA (NICA-) JAPAN FOUND CANCER RES.
 Percent Similarity: 35.0% Conservative: 51
 Best Local Similarity: 22.3% Mismatches: 129
 Indels: 135
 Query Match: 5.8%
 RESULT 759
 ID AAK85753 standard; DNA; 9893 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40565.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 37.0% Conservative: 55
 Best Local Similarity: 23.0% Mismatches: 136
 Indels: 114
 Query Match: 5.8%
 RESULT 760
 ID ACN44303 standard; cDNA; 11895 BP.
 DE Human mRNA sequence hCT32001.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Percent Similarity: 36.7% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 141
 Indels: 66
 Query Match: 5.8%
 RESULT 761
 ID ACP42746 standard; cDNA; 12598 BP.
 DE Human ALMS1 cDNA sequence.
 PN WO2003034072-A2.
 PD 24-APR-2003.
 PA (UYSO-) UNIV SOUTHAMPTON.
 Percent Similarity: 36.7% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 141
 Indels: 66
 Query Match: 5.8%

RESULT 762
 ID AED20700 standard; cDNA; 12598 BP.
 DE Human ALMS1 encoding cDNA, SEQ ID 2.
 PN US2005214757-A1.
 PD 29-SEP-2005.
 PA (WILS/) WILSON D I.
 PA (HEAR/) HEARN T.
 PA (WALK/) WALKER M.
 Percent Similarity: 36.7% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 141
 Indels: 66
 Query Match: 5.8%
 RESULT 763
 ID AEH14311 standard; DNA; 12922 BP.
 DE Human alstrom syndrome 1 cDNA SEQ ID NO:1.
 PN FR2876705-A1.
 PD 21-APR-2006.
 PA (INMR) BIOMERIEUX SA.
 Percent Similarity: 36.7% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 141
 Indels: 66
 Query Match: 5.8%
 RESULT 764
 ID AAO20685 standard; DNA; 14704 BP.
 DE PKS 741 insert contg. Sry.
 PN WO9200375-A.
 PD 09-JAN-1992.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 Percent Similarity: 39.0% Conservative: 58
 Best Local Similarity: 21.2% Mismatches: 130
 Indels: 69
 Query Match: 5.8%
 RESULT 765
 ID AAK74017 standard; DNA; 15270 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28829.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 35.7% Conservative: 53
 Best Local Similarity: 21.9% Mismatches: 140
 Indels: 108
 Query Match: 5.8%
 RESULT 766
 ID AAK85754 standard; DNA; 15270 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40566.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 35.7% Conservative: 53
 Best Local Similarity: 21.9% Mismatches: 140
 Indels: 108
 Query Match: 5.8%
 RESULT 767
 ID AAA81457 standard; DNA; 49646 BP.
 DE N. meningitidis partial DNA sequence gnm_5 SEQ ID NO:5.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Percent Similarity: 37.2% Conservative: 62
 Best Local Similarity: 23.0% Mismatches: 145
 Indels: 131
 Query Match: 5.8%
 RESULT 768
 Percent Similarity: 37.2% Conservative: 62
 Best Local Similarity: 23.0% Mismatches: 145
 Indels: 131
 Query Match: 5.8%
 RESULT 769
 Percent Similarity: 36.7% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 141
 Indels: 66
 Query Match: 5.8%
 RESULT 770
 ID ADH69807 standard; DNA; 684973 BP.
 DE Human Vbeta gene.
 PN US2002150891-A1.
 PD 17-OCT-2002.
 PA (HOOD/) HOOD L E.
 PA (ROWE/) ROWEN L.
 Percent Similarity: 43.4% Conservative: 37
 Best Local Similarity: 25.9% Mismatches: 84
 Query Match: 25.9%

Query Match: 5.8% Indels: 36
 RESULT 771
 ID ACN44302 standard; DNA; 198073 BP.
 DE Human genomic sequence hCG40741.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Percent Similarity: 36.7%
 Best Local Similarity: 24.5%
 Query Match: 5.8%
 Indels: 66
 RESULT 772
 ID ABL68560 standard; DNA; 267156 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6897.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 43.4%
 Best Local Similarity: 25.9%
 Query Match: 5.8%
 Indels: 36
 RESULT 773
 ID AAF21607 standard; DNA; 349980 BP.
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:108.
 PN WO200066791-A1.
 PD 09-NOV-2000.
 PA (CHIR-) CHIRON CORP.
 Percent Similarity: 37.2%
 Best Local Similarity: 23.0%
 Query Match: 5.8%
 Indels: 131
 RESULT 774
 ID ADT47265 standard; cDNA; 1818 BP.
 DE Bacterial polynucleotide #22016.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 39.3%
 Best Local Similarity: 23.2%
 Query Match: 5.8%
 Indels: 42
 RESULT 775
 ID ADI57677 standard; cDNA; 1882 BP.
 DE Human breast specific nucleic acid (BSNA) #48.
 PN WO2003106648-A2.
 PD 24-DEC-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 33.7%
 Best Local Similarity: 23.3%
 Query Match: 5.8%
 Indels: 112
 RESULT 776
 ID ABL08459 standard; cDNA; 2885 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19859.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 40.9%
 Best Local Similarity: 22.0%
 Query Match: 5.8%
 Indels: 132

Query Match: 5.8% Indels: 41
 RESULT 779
 ID ADV97740 standard; cDNA; 3345 BP.
 DE cDNA sequence encoding a murine protein kinase Seq 60.
 PN WO2005000200-A2.
 PD 06-JAN-2005.
 PA (SUGE-) SUGEN INC.
 Percent Similarity: 35.6%
 Best Local Similarity: 23.5%
 Query Match: 5.8%
 Indels: 80
 RESULT 780
 ID AEG97266 standard; DNA; 3507 BP.
 DE Bremothecium gossypii CRV1 DNA homolog SEQ ID NO 35.
 PN WO2006036817-A2.
 PD 06-APR-2006.
 PA (MICR-) MICROBIA INC.
 Percent Similarity: 39.7%
 Best Local Similarity: 24.0%
 Query Match: 5.8%
 Indels: 41
 RESULT 781
 ID ABL08458 standard; cDNA; 5004 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19856.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 40.9%
 Best Local Similarity: 22.0%
 Query Match: 5.8%
 Indels: 41
 RESULT 782
 ID ADM47088 standard; DNA; 5615 BP.
 DE Ogataea minuta LEU2 gene.
 PN WO2003091431-A1.
 PD 06-NOV-2003.
 PA (KIRI-) KIRIN BEER KK.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Percent Similarity: 42.5%
 Best Local Similarity: 24.6%
 Query Match: 5.8%
 Indels: 38
 RESULT 783
 ID AEL31410 standard; DNA; 6138 BP.
 DE Mouse HCPC1 DNA SEQ ID NO 27.
 PN WO2006110264-A2.
 PD 19-OCT-2006.
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 Percent Similarity: 30.0%
 Best Local Similarity: 20.3%
 Query Match: 5.8%
 Indels: 210
 RESULT 784
 ID ADX62221 standard; cDNA; 6159 BP.
 DE Plant full length insert polynucleotide seqid 33064.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Percent Similarity: 36.5%
 Best Local Similarity: 22.7%
 Query Match: 5.8%
 Indels: 86
 RESULT 785
 Percent Similarity: 40.0%
 Best Local Similarity: 29.7%
 Query Match: 5.8%
 Indels: 31
 RESULT 786
 Percent Similarity: 40.0%
 Best Local Similarity: 29.7%
 Query Match: 5.8%
 Indels: 31
 RESULT 787
 ID ACH92224 standard; DNA; 572 BP.
 DE Human genome derived single exon probe #25419.
 PN US2003194704-A1.

PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 43.5% Conservative: 37
Best Local Similarity: 25.6% Mismatches: 83
Query Match: 5.8% Indels: 34
RESULT 798
ID ADE36591 standard; cDNA; 1017 BP.
DE Human NOV1a encoding cDNA SEQ ID NO:1.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 789
ID ADE36617 standard; DNA; 1017 BP.
DE Plasmid pCR2.1-CG57008-03-S843 15B nucleotide insert SEQ ID NO:27.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 790
ID AEC32060 standard; DNA; 1017 BP.
DE Human CG57008-03 DNA, SEQ ID NO: 5.
PN US2005197292-A1.
PD 08-SEP-2005.
PA (SMIT/) SMITHSON G.
PA (MESR/) MESRI M.
PA (STAR/) STARLING G.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 791
ID ACCT72709 standard; cDNA; 1080 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:48.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 792
ID ABZ68333 standard; DNA; 1080 BP.
DE Nucleotide sequence of human TIM-1 allele 2.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 793
ID ABZ68332 standard; DNA; 1080 BP.
DE Nucleotide sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 794
ID ADY98074 standard; cDNA; 1080 BP.
DE Human TIM-1 allele 2.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARRER CANCER INST INC.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65

RESULT 795
ID ADY98072 standard; cDNA; 1080 BP.
DE Human TIM-1 allele 1.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARRER CANCER INST INC.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 796
ID AED60516 standard; DNA; 1080 BP.
DE Human TIM-1, allele 1, DNA SEQ ID NO:24.
PN WO2005097211-A2.
PD 20-OCT-2005.
PA (TELO-) TELOS PHARM INC.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 797
ID AED60518 standard; DNA; 1080 BP.
DE Human TIM-1, allele 2, DNA SEQ ID NO:26.
PN WO2005097211-A2.
PD 20-OCT-2005.
PA (TELO-) TELOS PHARM INC.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 798
ID AEC32068 standard; DNA; 1099 BP.
DE Human CG57008-07 DNA, SEQ ID NO: 13.
PN US2005197292-A1.
PD 08-SEP-2005.
PA (SMIT/) SMITHSON G.
PA (MESR/) MESRI M.
PA (STAR/) STARLING G.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 799
ID AEC32070 standard; DNA; 1111 BP.
DE Human CG57008-08 DNA, SEQ ID NO: 15.
PN US2005197292-A1.
PD 08-SEP-2005.
PA (SMIT/) SMITHSON G.
PA (MESR/) MESRI M.
PA (STAR/) STARLING G.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 800
ID ACL38953 standard; cDNA; 1380 BP.
DE HAVCR1 coding sequence, SEQ ID 10.
PN WO2005001092-A2.
PD 06-JAN-2005.
PA (AMHP) WYETH.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 801
ID ADE36593 standard; cDNA; 1440 BP.
DE Human NOV1b encoding cDNA SEQ ID NO:3.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 36.9% Conservative: 42
Best Local Similarity: 24.0% Mismatches: 141
Query Match: 5.8% Indels: 65
RESULT 802
ID ADN38983 standard; cDNA; 1440 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:301.
PN WO2003042661-A2.
PD 22-MAY-2003.

DE Bacterial polynucleotide #1353.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 37.3%
Best Local Similarity: 22.5%
Query Match: 5.8%
Conservative: 58
Mismatches: 155
Indels: 91
RESULT 818
ID AAQ21604 standard; DNA; 4394 BP.
DE Alpha galactosidase gene.
PN GB2247238-A.
PD 26-FEB-1992.
PA (GNSS) GUINNESS & SON CO LTD ARTHUR.
Percent Similarity: 38.1%
Best Local Similarity: 25.0%
Query Match: 5.8%
Conservative: 46
Mismatches: 123
Indels: 96
RESULT 819
ID AAS84306 standard; cDNA; 10578 BP.
DE DNA encoding novel human diagnostic protein #20110.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 48.0%
Best Local Similarity: 27.6%
Query Match: 5.8%
Conservative: 40
Mismatches: 95
Indels: 8
RESULT 820
ID AAA92301 standard; DNA; 30690 BP.
DE S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.
PN WO200050605-A1.
PD 31-AUG-2000.
PA (KITA) KITASATO INST.
Percent Similarity: 37.3%
Best Local Similarity: 25.3%
Query Match: 5.8%
Conservative: 35
Mismatches: 130
Indels: 54
RESULT 821
ID AAH79277 standard; DNA; 30690 BP.
DE Streptomyces avermitilis coding sequences SEQ ID NO: 1.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 37.3%
Best Local Similarity: 25.3%
Query Match: 5.8%
Conservative: 35
Mismatches: 130
Indels: 54
RESULT 822
ID ADW43464 standard; DNA; 39912 BP.
DE S. avermitilis avermectin aglycon biosynthesis gene cluster aveA3-4 DNA.
PN WO200411230-A1.
PD 23-DEC-2004.
PA (KITA) KITASATO INST.
Percent Similarity: 37.3%
Best Local Similarity: 25.3%
Query Match: 5.8%
Conservative: 35
Mismatches: 130
Indels: 54
RESULT 823
ID ADI89084 standard; DNA; 80393 BP.
DE Arabidopsis thaliana T-DNA insertion mutant DNA, SALK041951.
PN US2004210962-A1.
PD 21-OCT-2004.
PA (UYNE-) UNIV NEBRASKA.
Percent Similarity: 40.9%
Best Local Similarity: 27.9%
Query Match: 5.8%
Conservative: 27
Mismatches: 93
Indels: 31
RESULT 824
ID AEL87435 standard; DNA; 80393 BP.
DE Thale cress T-DNA insertion mutant DNA SEQ ID: 4.
PN US2006248613-A1.
PD 02-NOV-2006.
PA (MACK/) MACKENZIE S.
PA (ABDE/) ABDELNOOR R V.
Percent Similarity: 40.9%
Best Local Similarity: 27.9%
Query Match: 5.8%
Conservative: 27
Mismatches: 93
Indels: 31
RESULT 825
ID AEL86867 standard; DNA; 80393 BP.
DE Thale cress T-DNA insertion mutant DNA SEQ ID: 4.
PN US2006248614-A1.
PD 02-NOV-2006.
PA (MACK/) MACKENZIE S.
PA (ABDE/) ABDELNOOR R V.
Percent Similarity: 40.9%
Best Local Similarity: 27.9%
Query Match: 5.8%
Conservative: 27
Mismatches: 93
Indels: 31
RESULT 826
ID ABQ81842 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 33.9%
Best Local Similarity: 21.1%
Query Match: 5.8%
Conservative: 58
Mismatches: 152
Indels: 146
RESULT 827
ID AAI23782 standard; DNA; 1667 BP.
DE Probe #13715 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 40
Mismatches: 109
Indels: 52
RESULT 828
ID ABA68895 standard; DNA; 1667 BP.
DE Human foetal liver single exon nucleic acid probe #17200.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 40
Mismatches: 109
Indels: 52
RESULT 829
ID AAI49092 standard; DNA; 1667 BP.
DE Probe #17778 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 40
Mismatches: 109
Indels: 52
RESULT 830
ID ABA50917 standard; DNA; 1667 BP.
DE Human breast cell single exon nucleic acid probe #9612.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 40
Mismatches: 109
Indels: 52
RESULT 831
ID ABA35846 standard; DNA; 1667 BP.
DE Probe #14312 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 40
Mismatches: 109
Indels: 52
RESULT 832
ID AAK43013 standard; DNA; 1667 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 17570.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 833
ID AAK17227 standard; DNA; 1667 BP.
DE Human brain expressed single exon probe SEQ ID NO: 17218.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 834
ID ABS42655 standard; DNA; 1667 BP.
DE Human liver single exon probe, SEQ ID NO 17645.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 835
ID AAI09388 standard; DNA; 1667 BP.
DE Probe #9379 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 836
ID AAA30736 standard; DNA; 1854 BP.
DE DNA encoding human mutant G protein-coupled receptor H3b (P236K).
PN WO20022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 837
ID ABZ81156 standard; cDNA; 1854 BP.
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:6.
PN WO2003006504-A2.
PD 23-JAN-2003.
PA (ALKU) AKZO NOBEL NV.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 838
ID ABZ81155 standard; cDNA; 1854 BP.
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:5.
PN WO2003006504-A2.
PD 23-JAN-2003.
PA (ALKU) AKZO NOBEL NV.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 839
ID ABZ81157 standard; cDNA; 1854 BP.
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:7.
PN WO2003006504-A2.
PD 23-JAN-2003.
PA (ALKU) AKZO NOBEL NV.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 840
ID ABZ81158 standard; cDNA; 1854 BP.
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:8.
PN WO2003006504-A2.
PD 23-JAN-2003.
PA (ALKU) AKZO NOBEL NV.
Percent Similarity: 39.6% Conservative: 40

Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 841
ID ADC22736 standard; cDNA; 1854 BP.
DE Human G protein-coupled receptor cDNA #67.
PN US6555339-B1.
PD 23-APR-2003.
PA (AREN-) ARENA PHARM INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 842
ID ADH14209 standard; cDNA; 1854 BP.
DE Mutated human H9b cDNA.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 843
ID AAI14586 standard; DNA; 1958 BP.
DE Probe #4519 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 844
ID ABA56312 standard; DNA; 1958 BP.
DE Human fetal liver single exon nucleic acid probe #4617.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 845
ID AAI35956 standard; DNA; 1958 BP.
DE Probe #4642 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 846
ID ABA45798 standard; DNA; 1958 BP.
DE Human breast cell single exon nucleic acid probe #4493.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 847
ID ABA25952 standard; DNA; 1958 BP.
DE Probe #4418 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.5% Mismatches: 109
Query Match: 5.7% Indels: 52
RESULT 848
ID AAK29990 standard; DNA; 1958 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 4547.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Percent Similarity: 39.6% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 109
 Query Match: 5.7% Indels: 52
 RESULT 849
 ID AAK04492 standard; DNA; 1958 BP.
 DE Human brain expressed single exon probe SEQ ID NO: 4483.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 39.6% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 109
 Query Match: 5.7% Indels: 52
 RESULT 850
 ID ABS29649 standard; DNA; 1958 BP.
 DE Human liver single exon probe, SEQ ID NO 4639.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 39.6% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 109
 Query Match: 5.7% Indels: 52
 RESULT 851
 ID AAI04397 standard; DNA; 1958 BP.
 DE Probe #4388 used to measure gene expression in human breast sample.
 PN WO200157270-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 39.6% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 109
 Query Match: 5.7% Indels: 52
 RESULT 852
 ID AEI34363 standard; DNA; 1967 BP.
 DE Soybean polymorphic locus, SEQ ID 6997.
 PN US2006135758-A1.
 PD 22-JUN-2006.
 PA (WUXK/) WU K.
 Percent Similarity: 33.5% Conservative: 50
 Best Local Similarity: 23.2% Mismatches: 178
 Query Match: 5.7% Indels: 148
 RESULT 853
 ID ACN43073 standard; cDNA; 2131 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1948.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 39.6% Conservative: 40
 Best Local Similarity: 24.5% Mismatches: 109
 Query Match: 5.7% Indels: 52
 RESULT 854
 ID ABL08537 standard; cDNA; 2175 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20093.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 34.1% Conservative: 53
 Best Local Similarity: 20.1% Mismatches: 122
 Query Match: 5.7% Indels: 127
 RESULT 855
 ID ADP07664 standard; DNA; 2335 BP.
 DE Human secreted protein encoding DNA, seq id 147.
 PN WO2004042000-A2.
 PD 21-MAY-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 35.7% Conservative: 43
 Best Local Similarity: 23.1% Mismatches: 132
 Query Match: 5.7% Indels: 89
 RESULT 856
 ID ADX26007 standard; DNA; 3378 BP.
 DE Novel cell pain response detection method-related mouse gene SeqID353.
 PN WO2005014849-A2.
 PD 17-FEB-2005.
 PA (EURO-) EUROCELTIQUE SA.
 Percent Similarity: 32.5% Conservative: 59

Best Local Similarity: 21.0% Mismatches: 137
 Query Match: 5.7% Indels: 208
 RESULT 857
 ID AEG97401 standard; DNA; 3783 BP.
 DE C. albicans cell wall protein ALS1b DNA SEQ ID NO 170.
 PN WO2006036817-A2.
 PD 06-APR-2006.
 PA (MICR-) MICROBIA INC.
 Percent Similarity: 36.4% Conservative: 64
 Best Local Similarity: 21.4% Mismatches: 181
 Query Match: 5.7% Indels: 90
 RESULT 858
 ID AAD62305 standard; DNA; 3786 BP.
 DE Candida albicans agglutinin-like sequence (ALS) 1 gene.
 PN US2003124134-A1.
 PD 03-JUL-2003.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 Percent Similarity: 36.4% Conservative: 64
 Best Local Similarity: 21.4% Mismatches: 181
 Query Match: 5.7% Indels: 90
 RESULT 859
 ID AEI26925 standard; DNA; 3786 BP.
 DE Candida albicans agglutinin-like sequence 1 gene, SEQ ID NO: 7.
 PN US7067138-B1.
 PD 27-JUN-2006.
 PA (ANGE-) LOS ANGELES BIOMEDICAL RES INST AT HARBO.
 Percent Similarity: 36.4% Conservative: 64
 Best Local Similarity: 21.4% Mismatches: 181
 Query Match: 5.7% Indels: 90
 RESULT 860
 ID AAS27718 standard; DNA; 3915 BP.
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1378.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.1% Conservative: 28
 Best Local Similarity: 25.2% Mismatches: 89
 Query Match: 5.7% Indels: 118
 RESULT 861
 ID ADB94521 standard; DNA; 3915 BP.
 DE Novel human protein DNA #130.
 PN US200218711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 Percent Similarity: 34.1% Conservative: 28
 Best Local Similarity: 25.2% Mismatches: 89
 Query Match: 5.7% Indels: 118
 RESULT 862
 ID ABA95683 standard; DNA; 7542 BP.
 DE Human protein kinase gene.
 PN WO200192492-A2.
 PD 06-DEC-2001.
 PA (APPL-) APPLERA CORP.
 Percent Similarity: 34.1% Conservative: 28
 Best Local Similarity: 25.2% Mismatches: 89
 Query Match: 5.7% Indels: 118
 RESULT 863
 ID ABL68626 standard; DNA; 10708 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6963.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 38.5% Conservative: 47
 Best Local Similarity: 24.2% Mismatches: 120
 Query Match: 5.7% Indels: 82
 RESULT 864
 ID ADS36503 standard; DNA; 24345 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1717.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.

Percent Similarity: 34.1% Conservative: 28
 Best Local Similarity: 25.2% Mismatches: 89
 Query Match: 5.7% Indels: 118
 RESULT 865
 ID ADS36474 standard; DNA; 40947 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Percent Similarity: 34.1% Conservative: 28
 Best Local Similarity: 25.2% Mismatches: 89
 Query Match: 5.7% Indels: 118
 RESULT 866
 ID AAH64966 standard; DNA; 349980 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 1.
 PN EPI108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 37.2% Conservative: 63
 Best Local Similarity: 22.3% Mismatches: 157
 Query Match: 5.7% Indels: 109
 RESULT 867
 ID AAT07199 standard; DNA; 913 BP.
 DE Cotton fibre-specific H6 protein gene.
 PN US5474925-A.
 PD 12-DEC-1995.
 PA (CETU) AGRACETUS INC.
 Percent Similarity: 42.3% Conservative: 31
 Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 868
 ID AAT13034 standard; cDNA; 913 BP.
 DE Cotton fibre-specific cDNA clone H6.
 PN US5495070-A.
 PD 27-FEB-1996.
 PA (CETU) AGRACETUS INC.
 Percent Similarity: 42.3% Conservative: 31
 Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 869
 ID AAT30253 standard; DNA; 913 BP.
 DE Cotton fibre cell-specific cDNA clone CKFB15A1-H6.
 PN US5521078-A.
 PD 28-MAY-1996.
 PA (CETU) AGRACETUS INC.
 Percent Similarity: 42.3% Conservative: 31
 Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 870
 ID AAT62610 standard; cDNA to mRNA; 913 BP.
 DE Cotton fibre specific cDNA clone CKFB15A1-H6.
 PN US5597718-A.
 PD 28-JAN-1997.
 PA (CETU) AGRACETUS.
 Percent Similarity: 42.3% Conservative: 31
 Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 871
 ID AAT70041 standard; cDNA; 913 BP.
 DE Cotton fibre specific cDNA clone H6.
 PN US5620882-A.
 PD 15-APR-1997.
 PA (CETU) AGRACETUS INC.
 Percent Similarity: 42.3% Conservative: 31
 Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 872
 ID AAZ35545 standard; DNA; 913 BP.
 DE cDNA sequence a cotton fibre gene from clone CDFB15A1H6.
 PN US5981834-A.
 PD 09-NOV-1999.
 PA (MONS) MONSANTO CO.
 Percent Similarity: 42.3% Conservative: 31

Best Local Similarity: 26.3% Mismatches: 80
 Query Match: 5.7% Indels: 33
 RESULT 873
 ID AEC32094 standard; DNA; 1440 BP.
 DE Human CG57008-01-SNP S51L DNA, SEQ ID NO: 39.
 PN US2005197292-A1.
 PD 08-SEP-2005.
 PA (SMIT/) SMITHSON G.
 PA (MESR/) MESRI M.
 PA (STAR/) STARLING G.
 Percent Similarity: 36.9% Conservative: 42
 Best Local Similarity: 24.0% Mismatches: 141
 Query Match: 5.7% Indels: 65
 RESULT 874
 ID AEC32092 standard; DNA; 1440 BP.
 DE Human CG57008-01-SNP V138I DNA, SEQ ID NO: 37.
 PN US2005197292-A1.
 PD 08-SEP-2005.
 PA (SMIT/) SMITHSON G.
 PA (MESR/) MESRI M.
 PA (STAR/) STARLING G.
 Percent Similarity: 36.9% Conservative: 43
 Best Local Similarity: 23.7% Mismatches: 141
 Query Match: 5.7% Indels: 65
 RESULT 875
 ID AEL57388 standard; cDNA; 1661 BP.
 DE Mouse podocalypsin-like protein 1 precursor gene, SEQ ID NO: 1851.
 PN US2006216722-A1.
 PD 28-SEP-2006.
 PA (BETS/) BETSHOLTZ C.
 PA (TRYG/) TRYGGVASON K.
 PA (TAKE/) TAKEMOTO M.
 PA (HELL/) HE L.
 PA (PATR/) PATRAKKAS J.
 Percent Similarity: 34.1% Conservative: 33
 Best Local Similarity: 23.1% Mismatches: 123
 Query Match: 5.7% Indels: 74
 RESULT 876
 ID ADY34545 standard; cDNA; 1804 BP.
 DE DPCR1 (552 amino acid form) coding sequence.
 PN WO2005019257-A1.
 PD 03-MAR-2005.
 PA (CLLT) CELUTECH R & D LTD.
 Percent Similarity: 37.2% Conservative: 51
 Best Local Similarity: 21.9% Mismatches: 134
 Query Match: 5.7% Indels: 75
 RESULT 877
 ID AAH25852 standard; DNA; 2131 BP.
 DE Murine PCLPI coding sequence.
 PN WO200134797-A1.
 PD 17-MAY-2001.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Percent Similarity: 34.1% Conservative: 33
 Best Local Similarity: 23.1% Mismatches: 123
 Query Match: 5.7% Indels: 74
 RESULT 878
 ID ADC01839 standard; DNA; 2217 BP.
 DE C. albicans DNA encoding dimorphism-specific protein 2400.
 PN DE10142743-A1.
 PD 13-MAR-2003.
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 Percent Similarity: 33.9% Conservative: 63
 Best Local Similarity: 19.7% Mismatches: 161
 Query Match: 5.7% Indels: 131
 RESULT 879
 ID ACL28658 standard; cDNA; 2403 BP.
 DE Rice abiotic stress responsive polynucleotide SEQ ID NO: 2614.
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 34.9% Conservative: 47
 Best Local Similarity: 21.9% Mismatches: 132
 Query Match: 5.7% Indels: 103

RESULT 880
ID AED11382 standard; DNA; 2800 BP.
DE Modified human CDH4 gene CpG island nucleotide sequence SEQ ID NO:3.
PN EP1584629-A1.
PD 12-OCT-2005.
PA (UYFE-) UNIV FERRARA.
Percent Similarity: 33.1%
Best Local Similarity: 25.2%
Query Match: 5.7%
Conservative: 21
Mismatch: 119
Indels: 60

RESULT 881
ID AEL57386 standard; DNA; 3981 BP.
DE Cryptosporidium hominis gene SEQ ID NO:1923.
PN WO2006044045-A2.
PD 27-APR-2006.
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.
Percent Similarity: 37.0%
Best Local Similarity: 24.0%
Query Match: 5.7%
Conservative: 44
Mismatch: 153
Indels: 65

RESULT 882
ID AEL57386 standard; cDNA; 5302 BP.
DE Mouse podocalyxin-like protein 1 precursor gene, SEQ ID NO: 1849.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS-) BETSHOLTZ C.
PA (TRYG-) TRYGGVASON K.
PA (TAKE-) TAKEMOTO M.
PA (HELL-) HE L.
PA (PATR-) PATRAKKAS J.
Percent Similarity: 34.1%
Best Local Similarity: 23.1%
Query Match: 5.7%
Conservative: 33
Mismatch: 123
Indels: 74

RESULT 883
ID AAS70562 standard; cDNA; 7715 BP.
DE DNA encoding novel human diagnostic protein #6366.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 32.2%
Best Local Similarity: 20.7%
Query Match: 5.7%
Conservative: 46
Mismatch: 123
Indels: 149

RESULT 884
ID ADO28931 standard; cDNA; 8194 BP.
DE Human novel GPCR PGR17 polynucleotide, SEQ ID NO:30.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Percent Similarity: 32.2%
Best Local Similarity: 20.7%
Query Match: 5.7%
Conservative: 46
Mismatch: 123
Indels: 149

RESULT 885
ID ADQ10013 standard; DNA; 8762 BP.
DE Borrelia afzelii strain ACAI vls silent cassette locus DNA SeqID 57.
PN WO2004058181-A2.
PD 15-JUL-2004.
PA (TEXA-) UNIV TEXAS SYSTEM.
Percent Similarity: 36.0%
Best Local Similarity: 23.2%
Query Match: 5.7%
Conservative: 58
Mismatch: 172
Indels: 119

RESULT 886
ID ABL08376 standard; cDNA; 11230 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19610.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 42.2%
Best Local Similarity: 29.4%
Query Match: 5.7%
Conservative: 23
Mismatch: 73
Indels: 31

RESULT 887
ID AAZ58381 standard; DNA; 12381 BP.
DE Streptomyces avermitilis avermectin polyketide synthase modules 1+2.
PN WO200001827-A2.
PD 13-JAN-2000.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.

PA (PFIZ-) PFIZER INC.
Percent Similarity: 35.3%
Best Local Similarity: 25.5%
Query Match: 5.7%
Conservative: 36
Mismatch: 155
Indels: 81

RESULT 888
ID ADB54255 standard; DNA; 12781 BP.
DE Pretreated genomic DNA region 179.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (BPIG-) EPIGENOMICS AG.
Percent Similarity: 34.6%
Best Local Similarity: 22.6%
Query Match: 5.7%
Conservative: 45
Mismatch: 156
Indels: 90

RESULT 889
ID ADY95168 standard; DNA; 1009 BP.
DE DNA of gene 118b from Lobiolly pine which encodes a glycine rich protein.
PN WO2005030988-A1.
PD 07-APR-2005.
PA (CELL-) CELLFOR INC.
Percent Similarity: 44.0%
Best Local Similarity: 29.3%
Query Match: 5.7%
Conservative: 22
Mismatch: 69
Indels: 15

RESULT 890
ID AAF08222 standard; cDNA; 1021 BP.
DE Fusarium venenatum EST SEQ ID NO:745.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO-) NOVO NORDISK BIOTECH INC.
Percent Similarity: 42.9%
Best Local Similarity: 30.6%
Query Match: 5.7%
Conservative: 24
Mismatch: 70
Indels: 43

RESULT 891
ID ADU52263 standard; cDNA; 1021 BP.
DE Fusarium venenatum CCl-3 EST, SEQ ID NO:745.
PN US2004229367-A1.
PD 18-NOV-2004.
PA (NOVO-) NOVOZYMES BIOTECH INC.
Percent Similarity: 42.9%
Best Local Similarity: 30.6%
Query Match: 5.7%
Conservative: 24
Mismatch: 70
Indels: 43

RESULT 892
ID ADZ90266 standard; cDNA; 1021 BP.
DE Fusarium venenatum expressed sequence tag cDNA SEQ ID NO 745.
PN US6902887-B1.
PD 07-JUN-2005.
PA (NOVO-) NOVOZYMES BIOTECH INC.
Percent Similarity: 42.9%
Best Local Similarity: 30.6%
Query Match: 5.7%
Conservative: 24
Mismatch: 70
Indels: 43

RESULT 893
ID ACL70863 standard; DNA; 1059 BP.
DE M. xanthus gene sequence, seq id 7326.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS-) MONSANTO TECHNOLOGY LLC.
Percent Similarity: 37.8%
Best Local Similarity: 26.7%
Query Match: 5.7%
Conservative: 24
Mismatch: 78
Indels: 57

RESULT 894
ID AAZ99653 standard; DNA; 1079 BP.
DE DNA coding for the extracellular domain of syndecan-3.
PN WO200014103-A1.
PD 16-MAR-2000.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Percent Similarity: 39.1%
Best Local Similarity: 26.2%
Query Match: 5.7%
Conservative: 32
Mismatch: 111
Indels: 40

RESULT 895
ID AAI21687 standard; DNA; 1161 BP.
DE Probe #11620 for gene expression analysis in human cervical cell sample.

PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 896
 ID ABA66765 standard; DNA; 1161 BP.
 DE Human foetal liver single exon nucleic acid probe #15070.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 897
 ID ABA46976 standard; DNA; 1161 BP.
 DE Probe #15662 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 898
 ID ABA48852 standard; DNA; 1161 BP.
 DE Human breast cell single exon nucleic acid probe #7547.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 899
 ID ABA33829 standard; DNA; 1161 BP.
 DE Probe #12295 for gene expression analysis in human heart cell sample.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 900
 ID AAK40921 standard; DNA; 1161 BP.
 DE Human bone marrow expressed single exon probe SEQ ID NO: 15478.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 901
 ID AAK15196 standard; DNA; 1161 BP.
 DE Human brain expressed single exon probe SEQ ID NO: 15187.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 902
 ID ABS40502 standard; DNA; 1161 BP.
 DE Human liver single exon probe, SEQ ID No 15492.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 903
 ID AAI07377 standard; DNA; 1161 BP.
 DE Probe #7368 used to measure gene expression in human breast sample.
 PN WO200157270-A2.

PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 35.9%
 Best Local Similarity: 22.1%
 Query Match: 5.7%
 RESULT 904
 ID ADS49128 standard; CDNA; 1239 BP.
 DE Bacterial polynucleotide #3871.
 PN US200323675-A1.
 PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 34.8%
 Best Local Similarity: 21.2%
 Query Match: 5.7%
 RESULT 905
 ID AAF11900 standard; CDNA; 1446 BP.
 DE Aspergillus oryzae EST SEQ ID NO:4423.
 PN WO200056762-A2.
 PD 28-SEP-2000.
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 33.1%
 Best Local Similarity: 22.8%
 Query Match: 5.7%
 RESULT 906
 ID ADU55941 standard; CDNA; 1446 BP.
 DE Aspergillus oryzae strain strain A1560/strain AL-1 EST, SEQ ID NO:4423.
 PN US2004229367-A1.
 PD 18-NOV-2004.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES INC AS.
 Percent Similarity: 33.1%
 Best Local Similarity: 22.8%
 Query Match: 5.7%
 RESULT 907
 ID ADZ93944 standard; CDNA; 1446 BP.
 DE Aspergillus oryzae expressed sequence tag CDNA SEQ ID NO 4423.
 PN US6902887-B1.
 PD 07-JUN-2005.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 Percent Similarity: 33.1%
 Best Local Similarity: 22.8%
 Query Match: 5.7%
 RESULT 908
 ID ADK41684 standard; CDNA; 1821 BP.
 DE Maize amino acid transporter gene.
 PN WO2003066879-A2.
 PD 14-AUG-2003.
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 Percent Similarity: 34.8%
 Best Local Similarity: 23.4%
 Query Match: 5.7%
 RESULT 909
 ID AAC69572 standard; DNA; 2084 BP.
 DE Human secreted protein gene 61 clone HAJBG14.
 PN WO200061623-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 36.9%
 Best Local Similarity: 23.0%
 Query Match: 5.7%
 RESULT 910
 ID ADA53108 standard; CDNA; 2256 BP.
 DE Human coding sequence, SEQ ID 676.
 PN EPI293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Conservative: 54
 Mismatches: 147
 Indels: 106

Conservative: 54
 Mismatches: 125
 Indels: 134

Conservative: 39
 Mismatches: 137
 Indels: 117

Conservative: 39
 Mismatches: 137
 Indels: 117

Conservative: 39
 Mismatches: 137
 Indels: 117

Conservative: 38
 Mismatches: 131
 Indels: 88

Conservative: 57
 Mismatches: 164
 Indels: 94

Percent Similarity: 34.2% Conservative: 43
Best Local Similarity: 22.9% Mismatches: 126
Query Match: 5.7% Indels: 127

RESULT 911
ID ABL08377 standard; cDNA; 2636 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19613.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Percent Similarity: 44.1% Conservative: 19
Best Local Similarity: 30.8% Mismatches: 64
Query Match: 5.7% Indels: 16

RESULT 912
ID ACN38055 standard; cDNA; 2733 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324424, SEQ ID NO:1338.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.6% Conservative: 38
Best Local Similarity: 25.4% Mismatches: 134
Query Match: 5.7% Indels: 62

RESULT 913
ID ADS48534 standard; cDNA; 3078 BP.
DE Bacterial polynucleotide #3277.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Percent Similarity: 35.7% Conservative: 40
Best Local Similarity: 25.3% Mismatches: 147
Query Match: 5.7% Indels: 102

RESULT 914
ID ABL23385 standard; DNA; 3906 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21628.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Percent Similarity: 33.2% Conservative: 46
Best Local Similarity: 22.0% Mismatches: 153
Query Match: 5.7% Indels: 122

RESULT 915
ID ACL64233 standard; DNA; 4039 BP.
DE M. xanthus DNA fragment, seq id 696.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Percent Similarity: 37.8% Conservative: 24
Best Local Similarity: 26.7% Mismatches: 78
Query Match: 5.7% Indels: 57

RESULT 916
ID ABL08392 standard; cDNA; 5296 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19658.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Percent Similarity: 35.4% Conservative: 39
Best Local Similarity: 21.3% Mismatches: 114
Query Match: 5.7% Indels: 66

RESULT 917
ID ADZ72162 standard; DNA; 5301 BP.
DE P. luminescens toxin A gene A0 with N- and C-terminal truncation.
PN US2005102713-A1.
PD 12-MAY-2005.
PA (MERL) MERLO D J.
PA (LIUD) LIU D.
PA (BURT) BURTON S L.
PA (GLAN) GLANCY T P.
Percent Similarity: 36.8% Conservative: 58
Best Local Similarity: 24.6% Mismatches: 165
Query Match: 5.7% Indels: 137

RESULT 918
ID ADZ72160 standard; DNA; 5561 BP.
DE P. luminescens toxin A full length gene A1 SEQ ID NO:7.
PN US2005102713-A1.
PD 12-MAY-2005.
PA (MERL) MERLO D J.
PA (LIUD) LIU D.
PA (BURT) BURTON S L.
PA (GLAN) GLANCY T P.
Percent Similarity: 36.8% Conservative: 58
Best Local Similarity: 24.6% Mismatches: 165
Query Match: 5.7% Indels: 137

RESULT 919
ID ADM10942 standard; cDNA; 5738 BP.
DE Human O645SgenomicContig2 cDNA.
PN US2003206918-A1.
PD 06-NOV-2003.
PA (CORI) CORIXA CORP.
Percent Similarity: 35.2% Conservative: 50
Best Local Similarity: 22.8% Mismatches: 153
Query Match: 5.7% Indels: 109

RESULT 920
ID ADJ11272 standard; DNA; 5738 BP.
DE Human ovarian tumour antigen DNA SeqID 273.
PN US2003232056-A1.
PD 18-DEC-2003.
PA (CORI) CORIXA CORP.
Percent Similarity: 35.2% Conservative: 50
Best Local Similarity: 22.8% Mismatches: 153
Query Match: 5.7% Indels: 109

RESULT 921
ID ADM43533 standard; DNA; 5738 BP.
DE Human ovarian cancer cDNA homologous DNA #18.
PN US2003129192-A1.
PD 10-JUL-2003.
PA (CORI) CORIXA CORP.
Percent Similarity: 35.2% Conservative: 50
Best Local Similarity: 22.8% Mismatches: 153
Query Match: 5.7% Indels: 109

RESULT 922
ID AEG35782 standard; DNA; 5738 BP.
DE Human ovarian tumor antigen O648S contig DNA sequence SEQ ID NO: 273.
PN US2006057141-A1.
PD 16-MAR-2006.
PA (CORI) CORIXA CORP.
Percent Similarity: 35.2% Conservative: 50
Best Local Similarity: 22.8% Mismatches: 153
Query Match: 5.7% Indels: 109

RESULT 923
ID ADZ72161 standard; DNA; 5816 BP.
DE P. luminescens toxin A gene A1 with C-terminal truncation SEQ ID NO:8.
PN US2005102713-A1.
PD 12-MAY-2005.
PA (MERL) MERLO D J.
PA (LIUD) LIU D.
PA (BURT) BURTON S L.
PA (GLAN) GLANCY T P.
Percent Similarity: 36.8% Conservative: 58
Best Local Similarity: 24.6% Mismatches: 165
Query Match: 5.7% Indels: 137

RESULT 924
ID AEG64418 standard; DNA; 5901 BP.
DE B. longum narrowly conserved hypothetical protein encoding DNA.
PN US2006068461-A1.
PD 30-MAR-2006.
PA (AJIN) AJINOMOTO CO INC.
Percent Similarity: 41.6% Conservative: 23
Best Local Similarity: 29.5% Mismatches: 72
Query Match: 5.7% Indels: 40

RESULT 925
ID ABL42510 standard; DNA; 5901 BP.
DE Bifidobacterium longum NCC2705 genomic DNA.
PN US2006223140-A1.

PA 05-OCT-2006.
PA (AJIN) AJINOMOTO CO INC.
Percent Similarity: 41.6%
Best Local Similarity: 29.5%
Query Match: 5.7%
Indels: 40
Conservative: 23
Mismatches: 72
Indels: 40

RESULT 926
ID ABL23384 standard; DNA; 5983 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21625.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 33.2%
Best Local Similarity: 22.0%
Query Match: 5.7%
Indels: 122
Conservative: 46
Mismatches: 153
Indels: 122

RESULT 927
ID AAD55736 standard; DNA; 6052 BP.
DE Plecteurys tristis fibroin 3 DNA.
PN WO2003020316-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Percent Similarity: 38.4%
Best Local Similarity: 22.0%
Query Match: 5.7%
Indels: 66
Conservative: 64
Mismatches: 177
Indels: 66

RESULT 928
ID ADZ72159 standard; DNA; 7302 BP.
DE P. luminescens toxin A gene A0 with N-terminal truncation SEQ ID NO:6.
PN US2005102713-A1.
PD 12-MAY-2005.
PA (MERL/) MERLO D J.
PA (LIUD/) LIU D.
PA (BURT/) BURTON S L.
PA (GLAN/) GLANCY T P.
Percent Similarity: 36.8%
Best Local Similarity: 24.6%
Query Match: 5.7%
Indels: 137
Conservative: 58
Mismatches: 165
Indels: 137

RESULT 929
ID ADZ72158 standard; DNA; 7560 BP.
DE P. luminescens toxin A full length gene A0 SEQ ID NO:5.
PN US2005102713-A1.
PD 12-MAY-2005.
PA (MERL/) MERLO D J.
PA (LIUD/) LIU D.
PA (BURT/) BURTON S L.
PA (GLAN/) GLANCY T P.
Percent Similarity: 36.8%
Best Local Similarity: 24.6%
Query Match: 5.7%
Indels: 137
Conservative: 58
Mismatches: 165
Indels: 137

RESULT 930
ID AAF58780 standard; DNA; 7577 BP.
DE Modified Photorhabdus tcdA toxin coding sequence.
PN WO200111029-A1.
PD 15-FEB-2001.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 36.8%
Best Local Similarity: 24.6%
Query Match: 5.7%
Indels: 137
Conservative: 58
Mismatches: 165
Indels: 137

RESULT 931
ID AAF58783 standard; DNA; 7621 BP.
DE TcdA toxin-zeln ER signal peptide fusion protein coding sequence.
PN WO200111029-A1.
PD 15-FEB-2001.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 36.8%
Best Local Similarity: 24.6%
Query Match: 5.7%
Indels: 137
Conservative: 58
Mismatches: 165
Indels: 137

RESULT 932
ID ABD33215 standard; DNA; 43865 BP.
DE Human cancer-associated (CA) gene HD07-034.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 33.2%
Best Local Similarity: 24.2%
Query Match: 5.7%
Indels: 159
Conservative: 33
Mismatches: 159

Query Match: 5.7%
Indels: 88
RESULT 933
ID ABEJ3218 standard; DNA; 43865 BP.
DE Cancer-associated gene sequence - SEQ ID 226.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (MALA/) MALANDRO M S.
Percent Similarity: 33.2%
Best Local Similarity: 24.2%
Query Match: 5.7%
Indels: 88
Conservative: 33
Mismatches: 159
Indels: 88

RESULT 934
ID ABQ81844 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1100.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 41.6%
Best Local Similarity: 29.5%
Query Match: 5.7%
Indels: 40
Conservative: 23
Mismatches: 72
Indels: 40

RESULT 935
ID ADT95863 standard; cDNA; 1111 BP.
DE Colon cancer associated human cDNA sequence #1382.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 43.0%
Best Local Similarity: 27.6%
Query Match: 5.7%
Indels: 55
Conservative: 42
Mismatches: 101
Indels: 55

RESULT 936
ID ADX42345 standard; cDNA; 1111 BP.
DE Human cDNA encoding colon cancer protein SEQ ID NO 1382.
PN WO200274156-A2.
PD 26-SEP-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 43.0%
Best Local Similarity: 27.6%
Query Match: 5.7%
Indels: 55
Conservative: 42
Mismatches: 101
Indels: 55

RESULT 937
ID AAQ75858 standard; DNA; 1352 BP.
DE Glucosylase gene.
PN JP06303984-A.
PD 01-NOV-1994.
PA (NISE) JAPAN TOBACCO INC.
Percent Similarity: 33.6%
Best Local Similarity: 23.2%
Query Match: 5.7%
Indels: 97
Conservative: 35
Mismatches: 126
Indels: 97

RESULT 938
ID ABT23537 standard; DNA; 1395 BP.
DE Cellobiohydrolase I activity polynucleotide SEQ ID No 49.
PN WO2003000941-A2.
PD 03-JAN-2003.
PA (NOVO) NOVOZYMES AS.
Percent Similarity: 36.0%
Best Local Similarity: 22.5%
Query Match: 5.7%
Indels: 97
Conservative: 52
Mismatches: 151
Indels: 97

RESULT 939
ID ABEI60832 standard; cDNA; 1541 BP.
DE Soybean coding sequence, SEQ ID NO: 5299.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Percent Similarity: 36.6%
Best Local Similarity: 24.1%
Query Match: 5.7%
Indels: 86
Conservative: 38
Mismatches: 106
Indels: 86

RESULT 940
ID ADQ23348 standard; DNA; 1679 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6168.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 36.8%
Best Local Similarity: 23.0%
Query Match: 5.7%
Indels: 143
Conservative: 45
Mismatches: 143

Query Match: 5.7% Indels: 64
 RESULT 941
 ID ADS61404 standard; cDNA; 1817 BP.
 DE Bacterial polynucleotide #13391.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 32.6%
 Best Local Similarity: 23.6%
 Query Match: 5.7%
 RESULT 942
 ID ADR96639 standard; DNA; 1860 BP.
 DE M. tuberculosis antigen Rv0312 DNA SEQ ID NO:65.
 PN WO2004083448-A2.
 PD 30-SEP-2004.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (STAT-) STATENS SERUM INST.
 Percent Similarity: 47.8%
 Best Local Similarity: 35.6%
 Query Match: 5.7%
 RESULT 943
 ID AB199688 standard; cDNA; 2215 BP.
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:726.
 PN WO200188188-A2.
 PD 22-NOV-2001.
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 Percent Similarity: 39.5%
 Best Local Similarity: 22.2%
 Query Match: 5.7%
 RESULT 944
 ID ACC46555 standard; cDNA; 2382 BP.
 DE Human dithp secreted/extracellular matrix protein-encoding cDNA.
 PN WO200297031-A2.
 PD 05-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 38.4%
 Best Local Similarity: 25.7%
 Query Match: 5.7%
 RESULT 945
 ID ABL28391 standard; DNA; 2532 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36646.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.5%
 Best Local Similarity: 23.9%
 Query Match: 5.7%
 RESULT 946
 ID ADH17161 standard; DNA; 2623 BP.
 DE Human gene of the invention NOV28k SEQ ID NO:657.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Query Match: 5.7%
 RESULT 947
 ID ADN00733 standard; DNA; 2671 BP.
 DE Human LDLR coding sequence, SEQ ID 6.
 PN WO2004024881-A2.
 PD 25-MAR-2004.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Query Match: 5.7%
 RESULT 948
 ID ABQ76406 standard; cDNA; 2717 BP.
 DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 237.
 PN WO200264766-A2.

PD 22-AUG-2002.
 PA (JANC) JANSSEN PHARM NV.
 Percent Similarity: 42.4%
 Best Local Similarity: 24.8%
 Query Match: 5.7%
 RESULT 949
 ID AAD07130 standard; cDNA; 2805 BP.
 DE Canine retinitis pigmentosa GTPase regulator (RPGR) cDNA.
 PN WO200138578-A1.
 PD 31-MAY-2001.
 PA (CORR) CORNELL RES FOUND INC.
 Percent Similarity: 36.4%
 Best Local Similarity: 19.4%
 Query Match: 5.7%
 RESULT 950
 ID ADR84702 standard; DNA; 2832 BP.
 DE Aspergillus fumigatus essential gene genomic sequence #513.
 PN WO2004067709-A2.
 PD 12-AUG-2004.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 35.8%
 Best Local Similarity: 21.3%
 Query Match: 5.7%
 RESULT 951
 ID AAA81463 standard; DNA; 78845 BP.
 DE N. meningitidis partial DNA sequence gnm_11 SEQ ID NO:11.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Percent Similarity: 36.1%
 Best Local Similarity: 22.9%
 Query Match: 5.7%
 RESULT 952
 ID ADU47667 standard; DNA; 88400 BP.
 DE S. cyaneogriseus LL-F28249 compound full-length biosynthetic gene.
 PN EPI477563-A2.
 PD 17-NOV-2004.
 PA (AMHP) WYETH.
 PA (FORT-) FORT DODGE ANIMAL HEALTH.
 Percent Similarity: 36.4%
 Best Local Similarity: 22.3%
 Query Match: 5.7%
 RESULT 953
 Percent Similarity: 36.1%
 Best Local Similarity: 22.9%
 Query Match: 5.7%
 RESULT 954
 Percent Similarity: 32.3%
 Best Local Similarity: 23.0%
 Query Match: 5.7%
 RESULT 955
 Percent Similarity: 38.4%
 Best Local Similarity: 26.4%
 Query Match: 5.7%
 RESULT 956
 ID AED46970 standard; DNA; 1242 BP.
 DE Membrane construction and membrane transport protein DNA SEQ ID 247.
 PN US2005244935-A1.
 PD 03-NOV-2005.
 PA (BADI) BASF AG.
 Percent Similarity: 36.7%
 Best Local Similarity: 22.0%
 Query Match: 5.7%
 RESULT 957
 ID ABK71704 standard; cDNA; 1430 BP.
 DE Human dithp polynucleotide #170.
 PN WO200220754-A2.
 PD 14-MAR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 36.9%
 Best Local Similarity: 23.8%
 Query Match: 5.7%
 RESULT 958
 ID ABQ76406 standard; cDNA; 2717 BP.
 DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 237.
 PN WO200264766-A2.

Conservative: 51
 Mismatches: 111
 Indels: 57
 Conservative: 72
 Mismatches: 139
 Indels: 131
 Conservative: 61
 Mismatches: 157
 Indels: 140
 Conservative: 65
 Mismatches: 162
 Indels: 134
 Conservative: 61
 Mismatches: 157
 Indels: 140
 Conservative: 38
 Mismatches: 142
 Indels: 135
 Conservative: 26
 Mismatches: 104
 Indels: 29
 Conservative: 62
 Mismatches: 159
 Indels: 109
 Conservative: 48
 Mismatches: 125
 Indels: 110

RESULT 958
 ID ADM86778 standard; cDNA; 1430 BP.
 DE Human cDNA #39 differentially expressed in lung cancer.
 PN US2003175704-A1.
 PD 18-SEP-2003.
 PA (LASE/) LASEK A K W.
 PA (SHYJ/) SHYJAN A W.
 PA (TURN/) TURNER C M.
 Percent Similarity: 36.9%
 Best Local Similarity: 23.8%
 Query Match: 5.7%
 RESULT 959
 ID ADL13149 standard; cDNA; 1430 BP.
 DE Human steroid-induced C3A liver cell cDNA #878.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 36.9%
 Best Local Similarity: 23.8%
 Query Match: 5.7%
 RESULT 960
 ID AAF07488 standard; cDNA; 1463 BP.
 DE Fusarium venenatum EST SEQ ID NO:11.
 PN WO200056762-A2.
 PD 28-SEP-2000.
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 39.3%
 Best Local Similarity: 21.9%
 Query Match: 5.7%
 RESULT 961
 ID ADU51529 standard; cDNA; 1463 BP.
 DE Fusarium venenatum CCL-3 EST, SEQ ID NO:11.
 PN US2004229367-A1.
 PD 18-NOV-2004.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES INC AS.
 Percent Similarity: 39.3%
 Best Local Similarity: 21.9%
 Query Match: 5.7%
 RESULT 962
 ID ADZ89532 standard; cDNA; 1463 BP.
 DE Fusarium venenatum expressed sequence tag cDNA SEQ ID NO 11.
 PN US6902887-B1.
 PD 07-JUN-2005.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 Percent Similarity: 39.3%
 Best Local Similarity: 21.9%
 Query Match: 5.7%
 RESULT 963
 ID ABL16653 standard; DNA; 1529 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1432.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NV.
 Percent Similarity: 40.4%
 Best Local Similarity: 29.2%
 Query Match: 5.7%
 RESULT 964
 ID AAI49456 standard; DNA; 1887 BP.
 DE Probe #18142 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 965
 ID ABA51281 standard; DNA; 1887 BP.
 DE Human breast cell single exon nucleic acid probe #9976.
 PN WO200157271-A2.
 PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 966
 ID ABS17477 standard; DNA; 1887 BP.
 DE Human genome-derived single exon probe ORF from lung SEQ ID NO 17468.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 967
 ID AAI36327 standard; DNA; 1972 BP.
 DE Probe #5013 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 968
 ID ABA46169 standard; DNA; 1972 BP.
 DE Human breast cell single exon nucleic acid probe #4864.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 969
 ID ABS04966 standard; DNA; 1972 BP.
 DE Human genome-derived single exon probe from lung SEQ ID NO 4957.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.7%
 RESULT 970
 ID ACC61564 standard; DNA; 2000 BP.
 DE Gene sequence #SEQ ID 1910.
 PN EP1258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.
 Percent Similarity: 42.6%
 Best Local Similarity: 27.7%
 Query Match: 5.7%
 RESULT 971
 ID ADK64447 standard; DNA; 2000 BP.
 DE Disease treating protein complex-derived gene #1152.
 PN EP1338608-A2.
 PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Percent Similarity: 42.6%
 Best Local Similarity: 27.7%
 Query Match: 5.7%
 RESULT 972
 ID AAT17864 standard; DNA; 2093 BP.
 DE Hepatitis A virus receptor DNA.
 PN WO9604376-A1.
 PD 15-FEB-1996.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Percent Similarity: 41.0%
 Best Local Similarity: 23.4%
 Query Match: 5.7%
 RESULT 973
 ID AAI60599 standard; cDNA; 2177 BP.
 DE Human polynucleotide SEQ ID NO 4588.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.

Conservative: 62
 Mismatches: 147
 Indels: 78

Conservative: 62
 Mismatches: 147
 Indels: 78

Conservative: 62
 Mismatches: 147
 Indels: 78

Conservative: 62
 Mismatches: 147
 Indels: 78

Conservative: 62
 Mismatches: 147
 Indels: 78

Conservative: 42
 Mismatches: 126
 Indels: 37

Conservative: 43
 Mismatches: 110
 Indels: 35

Percent Similarity: 39.1% Conservative: 46
Best Local Similarity: 23.5% Mismatches: 117
Query Match: 5.7% Indels: 63
RESULT 974
ID AAD30798 standard; DNA; 2337 BP.
DE Saccharomyces diastaticus-derived glucoamylase gene, STAL.
PN WO200212509-A1.
PD 14-FEB-2002.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Percent Similarity: 35.8% Conservative: 35
Best Local Similarity: 22.8% Mismatches: 86
Query Match: 5.7% Indels: 87
RESULT 975
ID AAV02953 standard; DNA; 2753 BP.
DE S. diastaticus STAL genomic DNA.
PN JP09299090-A.
PD 25-NOV-1997.
PA (SUNR) SUNTORY LTD.
Percent Similarity: 35.8% Conservative: 35
Best Local Similarity: 22.8% Mismatches: 86
Query Match: 5.7% Indels: 87
RESULT 976
ID AAN60834 standard; DNA; 2764 BP.
DE Sequence of plasmid pSTAL.
PN JP60262593-A.
PD 25-DEC-1985.
PA (MITK) MITSUI TOATSU CHEM INC.
Percent Similarity: 35.8% Conservative: 35
Best Local Similarity: 22.8% Mismatches: 86
Query Match: 5.7% Indels: 87
RESULT 977
ID ADM10463 standard; DNA; 2818 BP.
DE Colon proliferative disorder associated human DNA fragment, SEQ ID 268.
PN US2004265833-A1.
PD 30-DEC-2004.
PA (LOFT/) LOFTON-DAY C.
PA (SLED/) SLEDZIEWSKI A.
PA (THOM/) THOMAS J.
PA (DAYR/) DAY R W.
PA (TONN/) TONNES-PRIDDY L.
PA (CARD/) CARDON K.
Percent Similarity: 34.9% Conservative: 43
Best Local Similarity: 21.7% Mismatches: 138
Query Match: 5.7% Indels: 76
RESULT 978
ID ADW10457 standard; DNA; 2818 BP.
DE Colon proliferative disorder associated human DNA fragment, SEQ ID 262.
PN US2004265833-A1.
PD 30-DEC-2004.
PA (LOFT/) LOFTON-DAY C.
PA (SLED/) SLEDZIEWSKI A.
PA (THOM/) THOMAS J.
PA (DAYR/) DAY R W.
PA (TONN/) TONNES-PRIDDY L.
PA (CARD/) CARDON K.
Percent Similarity: 34.9% Conservative: 43
Best Local Similarity: 21.7% Mismatches: 138
Query Match: 5.7% Indels: 76
RESULT 979
ID ABN92052 standard; DNA; 2835 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1515.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.5% Conservative: 76
Best Local Similarity: 20.5% Mismatches: 160
Query Match: 5.7% Indels: 66
RESULT 980
ID ABL25807 standard; DNA; 3381 BP.
DE Drosohila melanogaster genomic polynucleotide SEQ ID NO 28894.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Percent Similarity: 33.9% Conservative: 51
Best Local Similarity: 22.1% Mismatches: 158
Query Match: 5.7% Indels: 130
RESULT 981
ID ABN92222 standard; DNA; 3561 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1685.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.5% Conservative: 76
Best Local Similarity: 20.5% Mismatches: 160
Query Match: 5.7% Indels: 66
RESULT 982
ID ADS02014 standard; DNA; 3561 BP.
DE Staphylococcus epidermis polynucleotide segid 1309.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Percent Similarity: 40.5% Conservative: 76
Best Local Similarity: 20.5% Mismatches: 160
Query Match: 5.7% Indels: 66
RESULT 983
ID AEI08097 standard; DNA; 3561 BP.
DE Staphylococcus epidermidis protein coding sequence - SEQ ID 1309.
PN US7060458-B1.
PD 13-JUN-2006.
PA (AMHP) WYETH.
Percent Similarity: 40.5% Conservative: 76
Best Local Similarity: 20.5% Mismatches: 160
Query Match: 5.7% Indels: 66
RESULT 984
ID ABL16652 standard; DNA; 3591 BP.
DE Drosohila melanogaster genomic polynucleotide SEQ ID NO 1429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.4% Conservative: 31
Best Local Similarity: 29.2% Mismatches: 119
Query Match: 5.7% Indels: 47
RESULT 985
ID AAAS9701 standard; DNA; 4998 BP.
DE DNA encoding murine neural plakophilin related armidillo protein.
PN WO200047615-A2.
PD 17-AUG-2000.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
Percent Similarity: 34.9% Conservative: 62
Best Local Similarity: 22.0% Mismatches: 193
Query Match: 5.7% Indels: 122
RESULT 986
ID ABL25806 standard; DNA; 5381 BP.
DE Drosohila melanogaster genomic polynucleotide SEQ ID NO 28891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 33.9% Conservative: 51
Best Local Similarity: 22.1% Mismatches: 158
Query Match: 5.7% Indels: 130
RESULT 987
ID ABN92163 standard; DNA; 6414 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1626.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.5% Conservative: 76
Best Local Similarity: 20.5% Mismatches: 160
Query Match: 5.7% Indels: 66
RESULT 988
ID ADS01884 standard; DNA; 6414 BP.
DE Staphylococcus epidermis polynucleotide segid 1179.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.

PA (BUSH/) BUSH D.
Percent Similarity: 40.5%
Best Local Similarity: 20.5%
Query Match: 5.7%
Conservative: 76
Mismatch: 160
Indels: 66
RESULT 989
ID AE107967 standard; DNA; 6414 BP.
DE Staphylococcus epidermidis protein coding sequence - SEQ ID 1179.
PN US7060458-B1.
PD 13-JUN-2006.
PA (AMHP-) WYETH.
Percent Similarity: 40.5%
Best Local Similarity: 20.5%
Query Match: 5.7%
Conservative: 76
Mismatch: 160
Indels: 66
RESULT 990
ID AAS84050 standard; cDNA; 6458 BP.
DE DNA encoding novel human diagnostic protein #19854.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.2%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 43
Mismatch: 119
Indels: 95
RESULT 991
ID ADZ13121 standard; cDNA; 8382 BP.
DE Murine cancer-associated cDNA #70.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 37.6%
Best Local Similarity: 23.9%
Query Match: 5.7%
Conservative: 47
Mismatch: 138
Indels: 76
RESULT 992
ID AAS68117 standard; cDNA; 9012 BP.
DE DNA encoding novel human diagnostic protein #3921.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.0%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 62
Mismatch: 147
Indels: 78
RESULT 993
ID AAS72748 standard; cDNA; 9012 BP.
DE DNA encoding novel human diagnostic protein #8552.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.0%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 62
Mismatch: 147
Indels: 78
RESULT 994
ID ACN40983 standard; cDNA; 9633 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA327008, SEQ ID NO:6123.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 41.0%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 62
Mismatch: 147
Indels: 78
RESULT 995
ID AAS88071 standard; cDNA; 10184 BP.
DE DNA encoding novel human diagnostic protein #23875.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.0%
Best Local Similarity: 24.5%
Query Match: 5.7%
Conservative: 62
Mismatch: 147
Indels: 78
RESULT 996
ID ADA02558 standard; DNA; 21526 BP.
DE Human ly6E carcinoma associated gene, SEQ ID NO:1076.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.

Percent Similarity: 34.6%
Best Local Similarity: 22.9%
Query Match: 5.7%
Conservative: 42
Mismatch: 137
Indels: 98
RESULT 997
ID ADB72296 standard; DNA; 21526 BP.
DE Human LY6E gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 34.6%
Best Local Similarity: 22.9%
Query Match: 5.7%
Conservative: 42
Mismatch: 137
Indels: 98
RESULT 998
ID ADE95806 standard; DNA; 21526 BP.
DE Human LY6E gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 34.6%
Best Local Similarity: 22.9%
Query Match: 5.7%
Conservative: 42
Mismatch: 137
Indels: 98
RESULT 999
ID AEK60077 standard; DNA; 21526 BP.
DE Human LY6E genomic sequence, SEQ ID NO: 64.
PN US2006204982-A1.
PD 14-SEP-2006.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 34.6%
Best Local Similarity: 22.9%
Query Match: 5.7%
Conservative: 42
Mismatch: 137
Indels: 98
RESULT 1000
ID ABD32538 standard; DNA; 46030 BP.
DE Mouse cancer-associated genomic DNA MD7-023.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 39.4%
Best Local Similarity: 27.3%
Query Match: 5.7%
Conservative: 35
Mismatch: 116
Indels: 59
RESULT 1001
Percent Similarity: 35.5%
Best Local Similarity: 26.3%
Query Match: 5.7%
Conservative: 27
Mismatch: 112
Indels: 77
RESULT 1002
Percent Similarity: 35.5%
Best Local Similarity: 26.3%
Query Match: 5.7%
Conservative: 27
Mismatch: 112
Indels: 77
RESULT 1003
ID ABN77933 standard; cDNA; 702 BP.
DE Human ORF2880 cDNA, SEQ ID NO:5759.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.9%
Best Local Similarity: 28.5%
Query Match: 5.6%
Conservative: 34
Mismatch: 98
Indels: 27
RESULT 1004
ID AEI57142 standard; cDNA; 1209 BP.
DE Thale cress coding sequence, SEQ ID NO: 1609.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Percent Similarity: 36.9%
Best Local Similarity: 23.6%
Query Match: 5.6%
Conservative: 41
Mismatch: 125
Indels: 71
RESULT 1005
ID AAQ82821 standard; cDNA; 1425 BP.
DE A. aculeatus protease II gene.
PN WO9502044-A1.
PD 19-JAN-1995.
PA (NOVO) NOVO-NORDISK AS.
Percent Similarity: 31.4%
Conservative: 26

Best Local Similarity: 24.9% Mismatches: 133
 Query Match: 5.6% Indels: 145
 RESULT 1006
 ID ABL19993 standard; DNA; 1439 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11452.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEXE) PE CORP NY.
 Percent Similarity: 35.0% Conservative: 32
 Best Local Similarity: 24.5% Mismatches: 103
 Query Match: 5.6% Indels: 96
 RESULT 1007
 ID ADQ96833 standard; DNA; 1944 BP.
 DE CrtWcrty nucleotide sequence.
 PN CN1380415-A.
 PD 20-NOV-2002.
 PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
 Percent Similarity: 35.4% Conservative: 41
 Best Local Similarity: 23.1% Mismatches: 120
 Query Match: 5.6% Indels: 96
 RESULT 1008
 ID ADQ96933 standard; DNA; 1966 BP.
 DE CrtWcrty nucleotide sequence.
 PN CN1380415-A.
 PD 20-NOV-2002.
 PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
 Percent Similarity: 35.4% Conservative: 41
 Best Local Similarity: 23.1% Mismatches: 120
 Query Match: 5.6% Indels: 96
 RESULT 1009
 ID AED70477 standard; DNA; 2175 BP.
 DE Corynebacterium glutamicum MCP gene SEQ ID NO:653.
 PN US6962989-B1.
 PD 08-NOV-2005.
 PA (BADI) BASF AG.
 Percent Similarity: 31.7% Conservative: 34
 Best Local Similarity: 22.9% Mismatches: 110
 Query Match: 5.6% Indels: 153
 RESULT 1010
 ID AED70479 standard; DNA; 2175 BP.
 DE Corynebacterium glutamicum MCP gene SEQ ID NO:655.
 PN US6962989-B1.
 PD 08-NOV-2005.
 PA (BADI) BASF AG.
 Percent Similarity: 31.7% Conservative: 34
 Best Local Similarity: 22.9% Mismatches: 110
 Query Match: 5.6% Indels: 153
 RESULT 1011
 ID AAQ80010 standard; DNA; 2414 BP.
 DE Genomic DNA encoding cystathionine gamma lyase.
 PN JP06292586-A.
 PD 21-OCT-1994.
 PA (ASAH) ASAHI KASEI KOGYO KK.
 Percent Similarity: 38.1% Conservative: 49
 Best Local Similarity: 24.4% Mismatches: 153
 Query Match: 5.6% Indels: 70
 RESULT 1012
 ID ADC30199 standard; cDNA; 3007 BP.
 DE Human novel cDNA sequence, SEQ ID NO:281.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSPO INC.
 Percent Similarity: 36.0% Conservative: 32
 Best Local Similarity: 25.3% Mismatches: 111
 Query Match: 5.6% Indels: 81
 RESULT 1013
 ID ADZ03671 standard; cDNA; 3117 BP.
 DE PRG4-Lub.3 cDNA construct.
 PN WO2005016130-A2.
 PD 24-FEB-2005.
 PA (AMHP) WYETH.
 Percent Similarity: 38.2% Conservative: 59
 Best Local Similarity: 23.4% Mismatches: 162

Query Match: 5.6% Indels: 85
 RESULT 1014
 ID AEP99542 standard; cDNA; 3891 BP.
 DE C. botulinum active BoNT/A modified open reading frame, SEQ ID NO:29.
 PN WO2006017749-A2.
 PD 16-FEB-2006.
 PA (ALLR) ALLERGAN INC.
 Percent Similarity: 36.6% Conservative: 38
 Best Local Similarity: 23.8% Mismatches: 137
 Query Match: 5.6% Indels: 52
 RESULT 1015
 ID ADT87027 standard; DNA; 3921 BP.
 DE Yeast Stress-related protein gene YR014W.
 PN WO2004092398-A2.
 PD 28-OCT-2004.
 PA (BADI) BASF PLANT SCI GMBH.
 Percent Similarity: 39.4% Conservative: 51
 Best Local Similarity: 23.2% Mismatches: 146
 Query Match: 5.6% Indels: 45
 RESULT 1016
 ID AEJ50086 standard; DNA; 3921 BP.
 DE Saccharomyces cerevisiae stress-related protein coding seq - SEQ ID 5.
 PN US2006137043-A1.
 PD 22-JUN-2006.
 PA (BADI) BASF PLANT SCI GMBH.
 Percent Similarity: 39.4% Conservative: 51
 Best Local Similarity: 23.2% Mismatches: 146
 Query Match: 5.6% Indels: 45
 RESULT 1017
 ID AED53819 standard; DNA; 8994 BP.
 DE Ulkenia sp. PUFA-PKS DNA fragment SEQ ID NO 3.
 PN WO2005097982-A2.
 PD 20-OCT-2005.
 PA (NUTR-) NUTRINOVA NUTRITION SPECIALTIES & FOOD.
 Percent Similarity: 40.5% Conservative: 56
 Best Local Similarity: 24.2% Mismatches: 142
 Query Match: 5.6% Indels: 64
 RESULT 1018
 ID AED53817 standard; DNA; 43372 BP.
 DE Cosmid containing PUFA-PKS open reading frames SEQ ID NO 1.
 PN WO2005097982-A2.
 PD 20-OCT-2005.
 PA (NUTR-) NUTRINOVA NUTRITION SPECIALTIES & FOOD.
 Percent Similarity: 40.5% Conservative: 56
 Best Local Similarity: 24.2% Mismatches: 142
 Query Match: 5.6% Indels: 64
 RESULT 1019
 Percent Similarity: 37.6% Conservative: 49
 Best Local Similarity: 21.9% Mismatches: 96
 Query Match: 5.6% Indels: 99
 RESULT 1020
 ID ABQ81849 standard; DNA; 349980 BP.
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.
 PN EPI227152-A1.
 PD 31-JUL-2002.
 PA (NEST) SOC PROD NESTLE SA.
 Percent Similarity: 33.2% Conservative: 41
 Best Local Similarity: 22.0% Mismatches: 137
 Query Match: 5.6% Indels: 109
 RESULT 1021
 ID ADX28535 standard; cDNA; 865 BP.
 DE Plant full length insert polynucleotide seqid 11355.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ) LIU J.
 PA (ZHOU) ZHOU Y.
 PA (KOVA) KOVALIC D K.
 PA (SCRE) SCREEN S E.
 PA (TABA) TABASKA J E.
 PA (CAOY) CAO Y.
 Percent Similarity: 41.1% Conservative: 27
 Best Local Similarity: 26.5% Mismatches: 72
 Query Match: 5.6% Indels: 37

RESULT 1022
 ID ACH87528 standard; DNA; 1083 BP.
 DE Human genome derived single exon probe #20723.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Percent Similarity: 38.3%
 Best Local Similarity: 25.8%
 Mismatches: 79
 Indels: 0
 Query Match:
 RESULT 1023
 ID AAS92828 standard; cDNA; 1200 BP.
 DE DNA encoding novel human diagnostic protein #28632.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 46.2%
 Best Local Similarity: 27.3%
 Mismatches: 71
 Indels: 8
 Query Match:
 RESULT 1024
 ID AEB67470 standard; DNA; 1351 BP.
 DE Rice genome derived DNA sequence, SEQ ID 2615.
 PN JP2005185101-A.
 PD 14-JUL-2005.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
 PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
 PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
 Percent Similarity: 38.6%
 Best Local Similarity: 26.0%
 Mismatches: 105
 Indels: 91
 Query Match:
 RESULT 1025
 ID ADS48557 standard; cDNA; 1451 BP.
 DE Bacterial polynucleotide #3300.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 37.2%
 Best Local Similarity: 23.7%
 Mismatches: 147
 Indels: 82
 Query Match:
 RESULT 1026
 ID ADT18746 standard; cDNA; 1463 BP.
 DE Plant cDNA, Seq ID 4072.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K.
 Percent Similarity: 42.9%
 Best Local Similarity: 27.0%
 Mismatches: 70
 Indels: 38
 Query Match:
 RESULT 1027
 ID AAH78220 standard; DNA; 1464 BP.
 DE Nucleotide sequence of a human secreted polypeptide.
 PN WO200166690-A2.
 PD 13-SEP-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Percent Similarity: 36.0%
 Best Local Similarity: 23.8%
 Mismatches: 160
 Indels: 97
 Query Match:
 RESULT 1028
 ID AD005413 standard; DNA; 1795 BP.
 DE Human GPR50 polymorphic genomic fragment, SEQ ID NO:43.
 PN WO2003104381-A2.
 PD 18-DEC-2003.
 PA (ASTR) ASTRAZENECA AB.
 PA (ASTR) ASTRAZENECA UK LTD.
 Percent Similarity: 38.9%
 Best Local Similarity: 24.2%
 Mismatches: 39
 Indels: 111

Query Match:
 RESULT 1029
 ID AEH37863 standard; DNA; 2199 BP.
 DE Cryptosporidium hominis gene SEQ ID NO:954.
 PN WO2006044045-A2.
 PD 27-APR-2006.
 PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.
 Percent Similarity: 36.3%
 Best Local Similarity: 24.4%
 Mismatches: 86
 Indels: 0
 Query Match:
 RESULT 1030
 ID ABL01969 standard; cDNA; 2268 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 389.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 31.8%
 Best Local Similarity: 23.0%
 Mismatches: 157
 Indels: 162
 Query Match:
 RESULT 1031
 ID AAH15971 standard; cDNA; 2566 BP.
 DE Human cDNA sequence SEQ ID NO:14580.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 39.3%
 Best Local Similarity: 26.5%
 Mismatches: 82
 Indels: 84
 Query Match:
 RESULT 1032
 ID ADK60438 standard; DNA; 2566 BP.
 DE Angiogenesis differentially expressed gene GS-N13.
 PN FR2836687-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Percent Similarity: 39.3%
 Best Local Similarity: 26.5%
 Mismatches: 82
 Indels: 84
 Query Match:
 RESULT 1033
 ID ADK60739 standard; DNA; 2566 BP.
 DE Angiogenesis differentially expressed gene GS-N13.
 PN FR2836686-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Percent Similarity: 39.3%
 Best Local Similarity: 26.5%
 Mismatches: 82
 Indels: 84
 Query Match:
 RESULT 1034
 ID ADP73061 standard; DNA; 2566 BP.
 DE Angiogenesis inhibitor human DNA sequence, GS-N13.
 PN FR2843753-A1.
 PD 27-FEB-2004.
 PA (GENE/) GENE S.
 PA (ALMS/) AL M S.
 Percent Similarity: 39.3%
 Best Local Similarity: 26.5%
 Mismatches: 82
 Indels: 84
 Query Match:
 RESULT 1035
 ID AAN60473 standard; DNA; 2790 BP.
 DE Sequence encoding the Falciparum Interspersed Repeat Antigen (FIRA).
 PN WO8601802-A.
 PD 27-MAR-1986.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 Percent Similarity: 39.3%
 Best Local Similarity: 25.4%
 Mismatches: 104
 Indels: 44
 Query Match:
 RESULT 1036
 ID ADB62373 standard; cDNA; 2821 BP.
 DE Human cDNA encoding clone FCBBF30125460.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 38.5% Conservative: 63
 Best Local Similarity: 22.8% Mismatches: 160
 Query Match: 5.6% Indels: 87
 RESULT 1037
 ID ADM99269 standard; DNA; 3002 BP.
 DE C heterostrophus strain C4 serine carboxypeptidase gene SeqID 152.
 PN WO2004033668-A2.
 PD 22-APR-2004.
 PA (DIVE-) DIVERSA CORP.
 Percent Similarity: 32.0% Conservative: 45
 Best Local Similarity: 22.5% Mismatches: 189
 Query Match: 5.6% Indels: 132
 RESULT 1038
 ID ABZ11405 standard; cDNA; 3429 BP.
 DE Human polynucleotide seq ID NO 287.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 39.3% Conservative: 35
 Best Local Similarity: 26.5% Mismatches: 82
 Query Match: 5.6% Indels: 84
 RESULT 1039
 ID ADM43923 standard; cDNA; 3604 BP.
 DE Novel human arginine-rich protein cDNA #287.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (KURA/) XUE A.
 PA (DRWA/) DRWANAC R.
 Percent Similarity: 39.3% Conservative: 35
 Best Local Similarity: 26.5% Mismatches: 82
 Query Match: 5.6% Indels: 84
 RESULT 1040
 ID ADX64026 standard; cDNA; 4072 BP.
 DE Plant full length insert polynucleotide seqid 34869.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREIN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Percent Similarity: 35.5% Conservative: 75
 Best Local Similarity: 20.4% Mismatches: 144
 Query Match: 5.6% Indels: 177
 RESULT 1041
 ID ADS48728 standard; cDNA; 4566 BP.
 DE Bacterial polynucleotide #3471.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 34.4% Conservative: 54
 Best Local Similarity: 22.4% Mismatches: 181
 Query Match: 5.6% Indels: 116
 RESULT 1042
 ID ADY18478 standard; DNA; 5095 BP.
 DE DNA encoding a PRO polypeptide, SEQ ID NO 4284.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH/) GENENTECH INC.
 Percent Similarity: 39.3% Conservative: 35
 Best Local Similarity: 26.5% Mismatches: 82
 Query Match: 5.6% Indels: 84
 RESULT 1043
 ID ABX72552 standard; cDNA; 5465 BP.
 DE Human CA125 cDNA encoding the amino terminal domain.
 PN WO200283866-A2.

PD 24-OCT-2002.
 PA (UYAR-) UNIV ARKANSAS.
 Percent Similarity: 37.3% Conservative: 46
 Best Local Similarity: 23.5% Mismatches: 103
 Query Match: 5.6% Indels: 107
 RESULT 1044
 ID ADO28933 standard; cDNA; 7710 BP.
 DE Mouse novel GPCR PGR17 polynucleotide, SEQ ID NO:32.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 PA (PRIN-) PRIMAL INC.
 Percent Similarity: 37.3% Conservative: 57
 Best Local Similarity: 22.6% Mismatches: 158
 Query Match: 5.6% Indels: 86
 RESULT 1045
 ID AAD53014 standard; DNA; 18404 BP.
 DE Human mucin (MUC-16B) DNA.
 PN WO200292836-A2.
 PD 21-NOV-2002.
 PA (SLOK/) SLOAN KETTERING INST CANCER RES.
 Percent Similarity: 37.3% Conservative: 46
 Best Local Similarity: 23.5% Mismatches: 103
 Query Match: 5.6% Indels: 107
 RESULT 1046
 ID ACL68541 standard; DNA; 24459 BP.
 DE M. xanthus gene sequence, seq id 5004.
 PN US6833447-B1.
 PD 21-DEC-2004.
 PA (MONS/) MONSANTO TECHNOLOGY LLC.
 Percent Similarity: 35.7% Conservative: 66
 Best Local Similarity: 21.7% Mismatches: 162
 Query Match: 5.6% Indels: 141
 RESULT 1047
 ID ACL64784 standard; DNA; 32241 BP.
 DE M. xanthus DNA fragment, seq id 1247.
 PN US6833447-B1.
 PD 21-DEC-2004.
 PA (MONS/) MONSANTO TECHNOLOGY LLC.
 Percent Similarity: 35.7% Conservative: 66
 Best Local Similarity: 21.7% Mismatches: 162
 Query Match: 5.6% Indels: 141
 RESULT 1048
 ID AAI21781 standard; DNA; 1075 BP.
 DE Probe #11714 for gene expression analysis in human cervical cell sample.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 44.2% Conservative: 24
 Best Local Similarity: 25.6% Mismatches: 69
 Query Match: 5.6% Indels: 3
 RESULT 1049
 ID ABA66852 standard; DNA; 1075 BP.
 DE Human foetal liver single exon nucleic acid probe #15157.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 44.2% Conservative: 24
 Best Local Similarity: 25.6% Mismatches: 69
 Query Match: 5.6% Indels: 3
 RESULT 1050
 ID AAI47064 standard; DNA; 1075 BP.
 DE Probe #15750 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Percent Similarity: 44.2% Conservative: 24
 Best Local Similarity: 25.6% Mismatches: 69
 Query Match: 5.6% Indels: 3
 RESULT 1051
 ID ABA48937 standard; DNA; 1075 BP.
 DE Human breast cell single exon nucleic acid probe #7632.
 PN WO200157271-A2.
 PD 09-AUG-2001.

Best Local Similarity: 25.6% Mismatches: 69
Query Match: 5.6% Indels: 3
RESULT 1068
ID AA102498 standard; DNA; 1403 BP.
DE Probe #2489 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.2%
Best Local Similarity: 25.6%
Query Match: 5.6%
Indels: 3
RESULT 1069
ID ABS02482 standard; DNA; 1403 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 2473.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 44.2%
Best Local Similarity: 25.6%
Query Match: 5.6%
Indels: 3
RESULT 1070
ID ADA70624 standard; DNA; 1755 BP.
DE Rice gene, SEQ ID 3947.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 44.1%
Best Local Similarity: 29.3%
Query Match: 5.6%
Indels: 24
RESULT 1071
ID ADJ39721 standard; cDNA; 1755 BP.
DE Plant cDNA #721.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW) BUDWORTH P.
PA (MOUG) MOUGHAMER T.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZERBROOK J.
PA (GOFF) GOFF S A.
PA (KATA) KATAGIRI F.
PA (KREP) KREPS J.
PA (PROV) PROVANT N.
PA (RICK) RICKIE D.
PA (ZHUT) ZHU T.
Percent Similarity: 44.1%
Best Local Similarity: 29.3%
Query Match: 5.6%
Indels: 24
RESULT 1072
ID ADC30239 standard; cDNA; 2139 BP.
DE Human novel cDNA sequence, SEQ ID NO:321.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.1%
Best Local Similarity: 23.2%
Query Match: 5.6%
Indels: 140
RESULT 1073
ID AAH98444 standard; cDNA; 2283 BP.
DE Yeast EST-derived coding sequence SEQ ID NO: 301.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.7%
Best Local Similarity: 26.0%
Query Match: 5.6%
Indels: 43
RESULT 1074
ID ABK5571 standard; cDNA; 2474 BP.
DE Human cDNA encoding NOV5f.
PN WO200216600-A2.
PD 28-FEB-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.2%
Best Local Similarity: 27.3%
Query Match: 5.6%
Indels: 57
Conservative: 27
Mismatches: 117

Best Local Similarity: 20.0% Mismatches: 158
Query Match: 5.6% Indels: 117
RESULT 1075
ID ADH71753 standard; DNA; 2474 BP.
DE Human gene of the invention NOV28g SEQ ID NO:649.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.2%
Best Local Similarity: 20.0%
Query Match: 5.6%
Indels: 117
Conservative: 81
Mismatches: 158
RESULT 1076
ID ADD93417 standard; cDNA; 2856 BP.
DE Human lipid-associated molecule LIPAM-5 polynucleotide.
PN WO2003083081-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 38.2%
Best Local Similarity: 20.0%
Query Match: 5.6%
Indels: 117
Conservative: 81
Mismatches: 158
RESULT 1077
ID ADI27140 standard; DNA; 2892 BP.
DE Human LRP binding family protein DNA #16.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Percent Similarity: 38.2%
Best Local Similarity: 20.0%
Query Match: 5.6%
Indels: 117
Conservative: 81
Mismatches: 158
RESULT 1078
ID ABN68049 standard; DNA; 2910 BP.
DE Streptococcus polynucleotide SEQ ID NO 4011.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 37.9%
Best Local Similarity: 22.6%
Query Match: 5.6%
Indels: 91
Conservative: 60
Mismatches: 151
RESULT 1079
ID ABK55569 standard; cDNA; 3039 BP.
DE Human cDNA encoding NOV5d.
PN WO200216600-A2.
PD 28-FEB-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.2%
Best Local Similarity: 20.0%
Query Match: 5.6%
Indels: 117
Conservative: 81
Mismatches: 158
RESULT 1080
ID ADH71749 standard; DNA; 3039 BP.
DE Human gene of the invention NOV28e SEQ ID NO:645.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.2%
Best Local Similarity: 20.0%
Query Match: 5.6%
Indels: 117
Conservative: 81
Mismatches: 158
RESULT 1081
ID ABL15152 standard; cDNA; 3090 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39938.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 37.1%
Best Local Similarity: 27.3%
Query Match: 5.6%
Indels: 57
Conservative: 27
Mismatches: 117
RESULT 1082
ID ADN00734 standard; DNA; 3322 BP.
DE Human LDLR coding sequence, SEQ ID 7.
PN WO2004024881-A2.
PD 25-MAR-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 38.2%
Conservative: 81

Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1083
 ID ABL02901 standard; cDNA; 3401 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3185.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 34.2%
 Best Local Similarity: 22.6%
 Mismatches: 149
 Indels: 121
 Query Match: 5.6%
 RESULT 1084
 ID AEE02823 standard; DNA; 3795 BP.
 DE Human S-100 beta binding protein encoding DNA, SEQ ID NO:66.
 PN WO2005106473-A1.
 PD 10-NOV-2005.
 PA (ONOV) ONO PHARM CO LTD.
 Percent Similarity: 36.1%
 Best Local Similarity: 23.2%
 Mismatches: 127
 Indels: 140
 Query Match: 5.6%
 RESULT 1085
 ID ADN00730 standard; DNA; 4097 BP.
 DE Human LDLR coding sequence, SEQ ID 3.
 PN WO2004024891-A2.
 PD 25-MAR-2004.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1086
 ID ADY19819 standard; DNA; 4097 BP.
 DE DNA encoding a PRO polypeptide, SEQ ID NO 5625.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1087
 ID AEE49594 standard; cDNA; 4097 BP.
 DE Human LDL receptor-related protein cDNA.
 PN WO2005116205-A1.
 PD 08-DEC-2005.
 PA (NICA-) JAPAN FOUND CANCER RES.
 PA (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.
 PA (YOSH/) YOSHIMOTO M.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1088
 ID ADD93421 standard; cDNA; 4099 BP.
 DE Human lipid-associated molecule LIPAM-9 polynucleotide.
 PN WO2003083081-A2.
 PD 09-OCT-2003.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1089
 ID ABK55572 standard; cDNA; 4150 BP.
 DE Human cDNA encoding NOV5g.
 PN WO200216600-A2.
 PD 28-FEB-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1090
 ID ADH71755 standard; DNA; 4150 BP.
 DE Human gene of the invention NOV28h SEQ ID NO:651.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.

Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 158
 Indels: 117
 Query Match: 5.6%
 RESULT 1091
 ID ABK55573 standard; cDNA; 4180 BP.
 DE Human cDNA encoding NOV5h.
 PN WO200216600-A2.
 PD 28-FEB-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 158
 Indels: 117
 Query Match: 5.6%
 RESULT 1092
 ID ADH71757 standard; DNA; 4180 BP.
 DE Human gene of the invention NOV28i SEQ ID NO:653.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 158
 Indels: 117
 Query Match: 5.6%
 RESULT 1093
 ID ADQ64490 standard; cDNA; 4240 BP.
 DE Novel human cDNA sequence #1651.
 PN EPI440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 36.1%
 Best Local Similarity: 23.2%
 Mismatches: 53
 Indels: 140
 Query Match: 5.6%
 RESULT 1094
 ID ABK55574 standard; cDNA; 4294 BP.
 DE Human cDNA encoding NOV5i.
 PN WO200216600-A2.
 PD 28-FEB-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1095
 ID ADH71767 standard; DNA; 4294 BP.
 DE Human gene of the invention NOV28n SEQ ID NO:663.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1096
 ID ADH71741 standard; DNA; 4294 BP.
 DE Human gene of the invention NOV28a SEQ ID NO:637.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1097
 ID ADH71765 standard; DNA; 4294 BP.
 DE Human gene of the invention NOV28m SEQ ID NO:661.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1098
 ID ADD93420 standard; cDNA; 4309 BP.
 DE Human lipid-associated molecule LIPAM-8 polynucleotide.
 PN WO2003083081-A2.
 PD 09-OCT-2003.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 38.2%
 Best Local Similarity: 20.0%
 Mismatches: 81
 Indels: 117
 Query Match: 5.6%
 RESULT 1099
 ID ADH71755 standard; DNA; 4150 BP.
 DE Human gene of the invention NOV28h SEQ ID NO:651.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.

Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1099
 ID ABL28909 standard; DNA; 4443 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38200.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEXE) PE CORP NY.
 Percent Similarity: 38.0% Conservative: 49
 Best Local Similarity: 24.7% Mismatches: 129
 Query Match: 5.6% Indels: 100
 RESULT 1100
 ID ABL66481 standard; DNA; 4468 BP.
 DE Lung cancer related gene sequence SEQ ID NO:4818.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1101
 ID ADN00732 standard; DNA; 4468 BP.
 DE Human LDLR coding sequence, SEQ ID 5.
 PN WO2004024881-A2.
 PD 25-MAR-2004.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1102
 ID AEC82956 standard; cDNA; 4468 BP.
 DE Breast cancer associated cDNA SEQ ID NO 524.
 PN WO2005083429-A2.
 PD 09-SEP-2005.
 PA (VERI-) VERIDEX LLC.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1103
 ID ADH71763 standard; DNA; 4607 BP.
 DE Human gene of the invention NOV281 SEQ ID NO:659.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1104
 ID ADN00728 standard; DNA; 4607 BP.
 DE Human LDLR coding sequence, SEQ ID 1.
 PN WO2004024881-A2.
 PD 25-MAR-2004.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1105
 ID ADO19503 standard; cDNA; 4607 BP.
 DE Human PRO polynucleotide #217.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1106
 ID ADY15957 standard; DNA; 4607 BP.
 DE DNA encoding a PRO polypeptide, SEQ ID NO 1763.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158

Query Match: 5.6% Indels: 117
 RESULT 1107
 ID AEG59841 standard; cDNA; 4607 BP.
 DE Human breast cancer marker gene, SEQ ID NO:146.
 PN WO2006015312-A2.
 PD 09-FEB-2006.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Percent Similarity: 38.2% Conservative: 81
 Best Local Similarity: 20.0% Mismatches: 158
 Query Match: 5.6% Indels: 117
 RESULT 1108
 ID ABL34357 standard; DNA; 5660 BP.
 DE Human immune system associated gene SEQ ID NO: 2330.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 39.7% Conservative: 43
 Best Local Similarity: 24.5% Mismatches: 102
 Query Match: 5.8% Indels: 68
 RESULT 1109
 ID ABL02900 standard; cDNA; 6007 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3182.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 34.2% Conservative: 47
 Best Local Similarity: 22.6% Mismatches: 149
 Query Match: 5.6% Indels: 121
 RESULT 1110
 ID ADM10522 standard; DNA; 17220 BP.
 DE Colon proliferative disorder associated human DNA fragment, SEQ ID 327.
 PN US2004265833-A1.
 PD 30-DEC-2004.
 PA (LOFT/) LOFTON-DAY C.
 PA (SLED/) SLEDZIEWSKI A.
 PA (THOM/) THOMAS J.
 PA (DAYR/) DAY R W.
 PA (TONN/) TONNES-PRIDDY L.
 PA (CARD/) CARDON K.
 Percent Similarity: 35.5% Conservative: 41
 Best Local Similarity: 23.8% Mismatches: 136
 Query Match: 5.6% Indels: 92
 RESULT 1111
 ID ABS79084 standard; DNA; 48012 BP.
 DE E. coli CFT073 genomic sequence #251.
 PN WO200259320-A2.
 PD 01-AUG-2002.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 Percent Similarity: 35.6% Conservative: 69
 Best Local Similarity: 22.0% Mismatches: 143
 Query Match: 5.6% Indels: 188
 RESULT 1112
 ID ADH80651 standard; DNA; 48012 BP.
 DE Escherichia coli CFT073 genome contig #251.
 PN US2003165870-A1.
 PD 04-SEP-2003.
 PA (BLAT/) BLATTNER F R.
 PA (WELC/) WELCH R A.
 PA (BURL/) BURLAND V D.
 Percent Similarity: 35.6% Conservative: 69
 Best Local Similarity: 22.0% Mismatches: 143
 Query Match: 5.6% Indels: 188
 RESULT 1113
 ID AED32653 standard; DNA; 117750 BP.
 DE Human cancer-associated genomic DNA HD13-060.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.

Percent Similarity: 35.2% Conservative: 34
 Best Local Similarity: 25.1% Mismatches: 136
 Query Match: 5.6% Indels: 84
 RESULT 1115
 ID ABL22175 standard; DNA; 1110 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17998.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEXE) PE CORP NY.
 Percent Similarity: 34.8% Conservative: 40
 Best Local Similarity: 23.8% Mismatches: 141
 Query Match: 5.6% Indels: 98
 RESULT 1116
 ID ADS56260 standard; cDNA; 1398 BP.
 DE Bacterial polynucleotide #8247.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Percent Similarity: 36.8% Conservative: 19
 Best Local Similarity: 27.8% Mismatches: 85
 Query Match: 5.6% Indels: 49
 RESULT 1117
 ID AAQ29276 standard; cDNA; 1452 BP.
 DE Encodes transmembrane form of H23-ETA antigen.
 PN WO20207000-A1.
 PD 30-APR-1992.
 PA (TRGE) TRANSGENE SA.
 Percent Similarity: 35.3% Conservative: 26
 Best Local Similarity: 26.2% Mismatches: 107
 Query Match: 5.6% Indels: 78
 RESULT 1118
 ID AAD30794 standard; DNA; 1614 BP.
 DE Hansenula polymorpha GPI cell wall anchor protein gene, Hpgasl.
 PN WO200212509-A1.
 PD 14-FEB-2002.
 PA (KORE) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 Percent Similarity: 36.4% Conservative: 62
 Best Local Similarity: 23.1% Mismatches: 173
 Query Match: 5.6% Indels: 127
 RESULT 1119
 ID AAQ29277 standard; DNA; 1709 BP.
 DE Encodes secreted form of H23-ETA antigen.
 PN WO20207000-A1.
 PD 30-APR-1992.
 PA (TRGE) TRANSGENE SA.
 Percent Similarity: 35.3% Conservative: 29
 Best Local Similarity: 25.2% Mismatches: 107
 Query Match: 5.6% Indels: 78
 RESULT 1120
 ID ABK64853 standard; DNA; 1830 BP.
 DE Human benign prostatic hyperplasia gene #748.
 PN WO200212440-A2.
 PD 14-FEB-2002.
 PA (GENE) GENE LOGIC INC.
 PA (NISH) JAPAN TOBACCO INC.
 Percent Similarity: 38.2% Conservative: 47
 Best Local Similarity: 24.8% Mismatches: 133
 Query Match: 5.6% Indels: 86
 RESULT 1121
 ID ACL28401 standard; cDNA; 2469 BP.
 DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2357.
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 33.9% Conservative: 43
 Best Local Similarity: 21.7% Mismatches: 114
 Query Match: 5.6% Indels: 119
 RESULT 1122
 ID AAF30055 standard; cDNA; 2482 BP.

DE Human cDNA encoding PRO256.
 PN WO200105972-A1.
 PD 25-JAN-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1123
 ID AAD16721 standard; cDNA; 2482 BP.
 DE Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.
 PN WO200159100-A2.
 PD 16-AUG-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1124
 ID ABK40259 standard; cDNA; 2482 BP.
 DE cDNA encoding human PRO256 polypeptide.
 PN WO200153486-A1.
 PD 26-JUL-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1125
 ID ABL88092 standard; cDNA; 2482 BP.
 DE Human PRO256 cDNA sequence SEQ ID NO:41.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1126
 ID ABK69965 standard; DNA; 2482 BP.
 DE cDNA encoding human Pro peptide #5.
 PN WO200224888-A2.
 PD 28-MAR-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1127
 ID ABL95581 standard; cDNA; 2482 BP.
 DE Human angiogenesis related cDNA PRO256 SEQ ID NO: 41.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1128
 ID ADA01277 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003068779-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1129
 ID ADA43706 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003064474-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1130
 ID ADA43474 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003073196-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1131
 ID ADA01149 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003068782-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1132
 ID ADA01033 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003068780-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1133
 ID ADA43590 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003073190-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1134
 ID ADA06852 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003068781-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1135
 ID ADA08340 standard; cDNA; 2482 BP.
 DE Novel human secreted and transmembrane protein PRO256 cDNA.
 PN US2003068783-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1136
 ID ADB99633 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide SEQ ID 9.
 PN US2003082728-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54

Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1137
 ID ADB86916 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003082726-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1138
 ID ADB66071 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003082729-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1139
 ID ADB99749 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide SEQ ID 9.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1140
 ID ADB99404 standard; cDNA; 2482 BP.
 DE Novel human secreted and transmembrane protein PRO256 cDNA.
 PN US2003082731-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1141
 ID ADB65955 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003082732-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1142
 ID ADC23353 standard; cDNA; 2482 BP.
 DE Human cDNA clone (SeqID 9) encoding the transmembrane PRO protein.
 PN US2003073193-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1143
 ID ADC26046 standard; cDNA; 2482 BP.
 DE Human PRO256 cDNA.
 PN US2003073194-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173
 RESULT 1144
 ID ADD10330 standard; cDNA; 2482 BP.
 DE Human secreted/transmembrane PRO polypeptide cDNA #21.
 PN US2003105011-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3% Conservative: 54
 Best Local Similarity: 20.8% Mismatches: 143
 Query Match: 5.6% Indels: 173

Query Match: 5.6% Indels: 173
RESULT 1145
ID ADD11290 standard; cDNA; 2482 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #21.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1146
ID ADD37083 standard; cDNA; 2482 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #21.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1147
ID ADE04873 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1148
ID ADE11179 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1149
ID ADD88110 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1150
ID ADD95405 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1151
ID ADE06335 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1152
ID ADE38110 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173

RESULT 1153
ID ADD88226 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1154
ID ADD90807 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1155
ID ADF99362 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1156
ID ADG06455 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1157
ID ADG05406 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1158
ID ADG82407 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.8%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1159
ID ADJ37292 standard; cDNA; 2482 BP.
DE Human tumour therapy associated PRO256 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1160
ID ADE51660 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1161
ID ADE38110 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Indels: 173
Conservative: 54
Mismatches: 143
Indels: 173

ID ADE51776 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1162
ID ADE37634 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1163
ID ADE37518 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1164
ID ADD95289 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1165
ID ADE37989 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1166
ID ADE76078 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1167
ID ADE39401 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1168
ID ADE04205 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1169
ID ADE39802 standard; cDNA; 2482 BP.

DE Human PRO polynucleotide #5.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1170
ID ADE19667 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1171
ID ADE77245 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1172
ID ADE65353 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1173
ID ADE75962 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1174
ID ADE37873 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1175
ID ADE64483 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1176
ID ADE41291 standard; cDNA; 2482 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #21.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Conservative: 54
Mismatches: 143
Indels: 173
Query Match:
RESULT 1177
ID ADE38818 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.

PN US2003096363-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1178
 ID ADE51892 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003104562-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1179
 ID ADD90923 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003138902-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1180
 ID ADE38702 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003108956-A1.
 PD 12-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1181
 ID ADE37402 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003104563-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1182
 ID ADE06219 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003138898-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1183
 ID ADD90078 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003138904-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1184
 ID ADE38586 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003119086-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1185
 ID ADE39517 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003119118-A1.

PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1186
 ID ADD89122 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003138897-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1187
 ID ADD88889 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003138899-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1188
 ID ADE19783 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003138900-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1189
 ID ADE77361 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003124667-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1190
 ID ADE65237 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003119113-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1191
 ID ADE39285 standard; cDNA; 2482 BP.
 DE Human PRO polynucleotide #5.
 PN US2003119115-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1192
 ID ADE38470 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003104559-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 RESULT 1193
 ID ADG11023 standard; cDNA; 2482 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
 PN US2003170809-A1.
 PD 11-SEP-2003.

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

Conservative: 54
 Mismatches: 143
 Indels: 173

PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1194
ID ADG10907 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US200307743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1195
ID ADH31435 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1196
ID ADH38683 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1197
ID ADH29318 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1198
ID ADH23621 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1199
ID ADH26951 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1200
ID ADH38219 standard; cDNA; 2482 BP.
DE Novel human secreted and transmembrane protein PRO256 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1201
ID ADH26835 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1202
ID ADH38103 standard; cDNA; 2482 BP.
DE Novel human secreted and transmembrane protein PRO256 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1203
ID ADG68216 standard; cDNA; 2482 BP.
DE Human PRO polypeptide cDNA #6.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1204
ID ADH38799 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1205
ID ADH23737 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1206
ID ADH40113 standard; cDNA; 2482 BP.
DE Human PRO256 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1207
ID ADH39997 standard; cDNA; 2482 BP.
DE Human PRO256 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1208
ID ADH31319 standard; cDNA; 2482 BP.
DE Human PRO polynucleotide #5.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1209
ID ADH29197 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.3%
Best Local Similarity: 20.8%
Query Match: 5.6%
Conservative: 54
Mismatches: 143
Indels: 173
RESULT 1210
ID ADH26835 standard; cDNA; 2482 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match: 5.6% Indels: 173
 RESULT 1226
 ID AEG73262 standard; cDNA; 2482 BP.
 DE Human PRO256 cDNA clone, DNA35880-1160.
 PN US2006073551-A1.
 PD 06-APR-2006.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 Indels: 173
 Conservative: 54
 Mismatches: 143
 RESULT 1227
 ID AEG74506 standard; cDNA; 2482 BP.
 DE Human PRO256 encoding cDNA SEQ ID NO:9.
 PN US2006073552-A1.
 PD 06-APR-2006.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 Indels: 173
 Conservative: 54
 Mismatches: 143
 RESULT 1228
 ID ADT19106 standard; cDNA; 2552 BP.
 DE Plant cDNA, Seq ID 4432.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVN/) KOVALIC D K.
 Percent Similarity: 42.2%
 Best Local Similarity: 29.5%
 Query Match: 5.6%
 Indels: 28
 Conservative: 22
 Mismatches: 72
 RESULT 1229
 ID ADP81020 standard; DNA; 2679 BP.
 DE Human ovarian specific gene, SEQ ID NO 54.
 PN WO2004053079-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 Indels: 173
 Conservative: 54
 Mismatches: 143
 RESULT 1230
 ID AAT02504 standard; DNA; 2717 BP.
 DE Pectin-lyase-I gene expression system.
 PN EP683228-A2.
 PD 22-NOV-1995.
 PA (CIBA) CIBA GEIGY AG.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERWALTUNGS GMBH.
 Percent Similarity: 34.0%
 Best Local Similarity: 22.4%
 Query Match: 5.6%
 Indels: 154
 Conservative: 56
 Mismatches: 185
 RESULT 1231
 ID AD203663 standard; cDNA; 2946 BP.
 DE PRG4-Lub:1 cDNA construct.
 PN WO2005016130-A2.
 PD 24-FEB-2005.
 PA (AMHP) WYETH.
 Percent Similarity: 38.7%
 Best Local Similarity: 24.0%
 Query Match: 5.6%
 Indels: 96
 Conservative: 55
 Mismatches: 135
 RESULT 1232
 ID ACL28243 standard; cDNA; 2958 BP.
 DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2199.
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 37.0%
 Best Local Similarity: 22.0%
 Query Match: 5.6%
 Indels: 118
 Conservative: 65
 Mismatches: 155
 RESULT 1233
 ID ABD32539 standard; cDNA; 2969 BP.
 DE Mouse cancer-associated cDNA MR7-023.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRIS DISCOVERY INC.
 Percent Similarity: 42.1%
 Indels: 29
 Conservative: 29

Best Local Similarity: 27.2%
 Query Match: 5.6%
 Indels: 85
 Mismatches: 28
 RESULT 1234
 ID ADP81021 standard; DNA; 3125 BP.
 DE Human ovarian specific gene, SEQ ID NO 55.
 PN WO2004053079-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 32.3%
 Best Local Similarity: 20.8%
 Query Match: 5.6%
 Indels: 173
 Conservative: 54
 Mismatches: 143
 RESULT 1235
 ID ADS48485 standard; cDNA; 3309 BP.
 DE Bacterial polynucleotide #3228.
 PN US200333675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Percent Similarity: 38.9%
 Best Local Similarity: 23.2%
 Query Match: 5.6%
 Indels: 96
 Conservative: 61
 Mismatches: 142
 RESULT 1236
 ID AEF99566 standard; cDNA; 3891 BP.
 DE C. Botulinum BONT/A modified open reading frame, SEQ ID NO:53.
 PN WO2006017749-A2.
 PD 16-FEB-2006.
 PA (ALLR) ALLERGAN INC.
 Percent Similarity: 35.6%
 Best Local Similarity: 21.6%
 Query Match: 5.6%
 Indels: 109
 Conservative: 55
 Mismatches: 144
 RESULT 1237
 ID ABL33102 standard; DNA; 7758 BP.
 DE Human immune system associated gene SEQ ID NO: 1075.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Percent Similarity: 44.6%
 Best Local Similarity: 33.1%
 Query Match: 5.6%
 Indels: 18
 Conservative: 16
 Mismatches: 59
 RESULT 1238
 ID AD203662 standard; DNA; 8049 BP.
 DE Vector PTmed2 with PRG4-Lub:1 cDNA construct.
 PN WO2005016130-A2.
 PD 24-FEB-2005.
 PA (AMHP) WYETH.
 Percent Similarity: 38.7%
 Best Local Similarity: 24.0%
 Query Match: 5.6%
 Indels: 96
 Conservative: 55
 Mismatches: 135
 RESULT 1239
 ID AAK72613 standard; DNA; 8298 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27425.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 42.1%
 Best Local Similarity: 30.8%
 Query Match: 5.6%
 Indels: 6
 Conservative: 15
 Mismatches: 71
 RESULT 1240
 ID AAD08215 standard; DNA; 114793 BP.
 DE Human genome from BAC clone, hbm168.
 PN WO200142434-A1.
 PD 14-JUN-2001.
 PA (MERI) MERCK & CO INC.
 Percent Similarity: 39.6%
 Best Local Similarity: 26.6%
 Query Match: 5.6%
 Indels: 40
 Conservative: 25
 Mismatches: 78
 RESULT 1241
 ID ADD17541 standard; DNA; 578 BP.
 DE DNA (SeqID 1609) that confers an altered visual phenotype in plants.
 PN WO2003020741-A1.

PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 42.7%
Best Local Similarity: 27.1%
Query Match: 5.5%
Conservative: 30
Mismatches: 55
Indels: 56

RESULT 1242
ID ADK52960 standard; DNA; 578 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #343.
PD WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 42.7%
Best Local Similarity: 27.1%
Query Match: 5.5%
Conservative: 30
Mismatches: 55
Indels: 56

RESULT 1243
ID ADX28417 standard; cDNA; 818 BP.
DE Plant full length insert polynucleotide seqid 11237.
PD US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Percent Similarity: 39.9%
Best Local Similarity: 27.3%
Query Match: 5.5%
Conservative: 23
Mismatches: 70
Indels: 40

RESULT 1244
ID AEI30716 standard; DNA; 982 BP.
DE Soybean polymorphic locus, SEQ ID 3350.
PD US2006135758-A1.
PD 22-JUN-2006.
PA (WURK/) WU K.
Percent Similarity: 39.9%
Best Local Similarity: 27.3%
Query Match: 5.5%
Conservative: 23
Mismatches: 70
Indels: 40

RESULT 1245
ID AAF12769 standard; cDNA; 1042 BP.
DE Aspergillus oryzae EST SEQ ID NO:5292.
PD WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Percent Similarity: 36.8%
Best Local Similarity: 23.5%
Query Match: 5.5%
Conservative: 31
Mismatches: 99
Indels: 49

RESULT 1246
ID ADU56810 standard; cDNA; 1042 BP.
DE Aspergillus oryzae strain AL1560/strain AL-1 EST, SEQ ID NO:5292.
PD US2004229367-A1.
PD 18-NOV-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES INC AS.
Percent Similarity: 36.8%
Best Local Similarity: 23.5%
Query Match: 5.5%
Conservative: 31
Mismatches: 99
Indels: 49

RESULT 1247
ID ADZ94813 standard; cDNA; 1042 BP.
DE Aspergillus oryzae expressed sequence tag cDNA SEQ ID NO 5292.
PD US6902987-B1.
PD 07-JUN-2005.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Percent Similarity: 36.8%
Best Local Similarity: 23.5%
Query Match: 5.5%
Conservative: 31
Mismatches: 99
Indels: 49

RESULT 1248
ID AEI59414 standard; cDNA; 1348 BP.
DE Zea mays coding sequence, SEQ ID NO: 2881.
PD US2006143729-A1.

PD	29-JUN-2006.
PA	(CERE-) CERES INC.
Percent Similarity:	37.6%
Best Local Similarity:	24.1%
Query Match:	5.5%
RESULT 1249	
ID	ADT47341 standard; cDNA; 1428 BP.
DE	Bacterial polynucleotide #22092.
PN	US2003233675-A1.
PD	18-DEC-2003.
PA	(CAOV/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
Percent Similarity:	39.7%
Best Local Similarity:	25.5%
Query Match:	5.5%
RESULT 1250	
ID	ABS67721 standard; cDNA; 1555 BP.
DE	DNA encoding primate LP282.
PN	WO200263009-A2.
PD	15-AUG-2002.
PA	(ELIL) LILLY & CO ELI.
Percent Similarity:	35.3%
Best Local Similarity:	22.1%
Query Match:	5.5%
RESULT 1251	
ID	ADT46663 standard; cDNA; 1638 BP.
DE	Bacterial polynucleotide #21414.
PN	US2003233675-A1.
PD	18-DEC-2003.
PA	(CAOV/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
Percent Similarity:	40.0%
Best Local Similarity:	25.2%
Query Match:	5.5%
RESULT 1252	
ID	AKG60090 standard; DNA; 1640 BP.
DE	Plant DNA sequence which confers altered metabolic c
PN	WO2003020936-A1.
PD	13-MAR-2003.
PA	(DOWC) DOW CHEM CO.
PA	(DOWC) DOW AGROSCIENCES LLC.
Percent Similarity:	37.1%
Best Local Similarity:	21.3%
Query Match:	5.5%
RESULT 1253	
ID	AAA64661 standard; cDNA; 2126 BP.
DE	cDNA encoding TBP associated factor (TAFII68).
PN	WO2000050595-A2.
PD	31-AUG-2000.
PA	(GOUT/) GOUT I.
PA	(RODN/) RODIN N.
PA	(FILO/) FILOENKO V.
PA	(NATS/) MATSUKA G.
PA	(SCAN/) SCANLAN M.
PA	(OLDL) OLD L.
PA	(BILY/) BILYSKY B.
Percent Similarity:	42.6%
Best Local Similarity:	23.4%
Query Match:	5.5%
RESULT 1254	
ID	ADB62594 standard; cDNA; 2335 BP.
DE	Human cDNA encoding clone HLJNG20083480.
PN	EPI308459-A2.
PD	07-MAY-2003.
PA	(HELI-) HELIX RES INST.
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:	41.5%
Conservative:	51
Mismatches:	89
Indels:	64
Conservative:	37
Mismatches:	112
Indels:	60
Conservative:	43
Mismatches:	114
Indels:	70
Conservative:	58
Mismatches:	171
Indels:	114
Conservative:	45
Mismatches:	121
Indels:	64
Conservative:	56
Mismatches:	124
Indels:	100
Conservative:	51
Mismatches:	89
Indels:	64
Conservative:	49

Best Local Similarity: 24.6% Mismatches: 111
 Query Match: 5.5% Indels: 59
 RESULT 1255
 ID ABA15398 standard; cDNA; 2352 BP.
 DE Human polynucleotide cDNA; 2352 BP.
 PN WO2005047534-A2.
 PD 26-MAY-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Percent Similarity: 36.6%
 Best Local Similarity: 22.7% Mismatches: 146
 Indels: 78
 Query Match: 5.5%
 RESULT 1256
 ID AAI59413 standard; cDNA; 2421 BP.
 DE Human polynucleotide SEQ ID NO 1616.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 32.8%
 Best Local Similarity: 24.2% Mismatches: 135
 Indels: 124
 Query Match: 5.5%
 RESULT 1257
 ID ACC59980 standard; cDNA; 2526 BP.
 DE Human PMW-22 encoding cDNA SEQ ID NO:53.
 PN WO2003025131-A2.
 PD 27-MAR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 35.3%
 Best Local Similarity: 22.1% Mismatches: 174
 Indels: 111
 Query Match: 5.5%
 RESULT 1258
 ID AAT12337 standard; DNA; 3004 BP.
 DE A. cellulolyticus E1 endoglucanase gene.
 PN WO9602551-A1.
 PD 01-FEB-1996.
 PA (MIDE) MIDWEST RES INST.
 Percent Similarity: 36.6%
 Best Local Similarity: 23.8% Mismatches: 115
 Indels: 69
 Query Match: 5.5%
 RESULT 1259
 ID AAZ55924 standard; DNA; 3004 BP.
 DE Acidothermus cellulolyticus E1 endoglucanase gene.
 PN CA2226898-A1.
 PD 25-SEP-1999.
 PA (MIDE) MIDWEST RES INST.
 Percent Similarity: 36.6%
 Best Local Similarity: 23.8% Mismatches: 115
 Indels: 69
 Query Match: 5.5%
 RESULT 1260
 ID ABK36729 standard; cDNA; 3004 BP.
 DE A. cellulolyticus cellulase E1 beta-1,4-endoglucanase precursor cDNA, e1.
 PN WO200234926-A2.
 PD 02-MAY-2002.
 PA (UNMS) UNIV MICHIGAN STATE.
 Percent Similarity: 36.6%
 Best Local Similarity: 23.8% Mismatches: 115
 Indels: 69
 Query Match: 5.5%
 RESULT 1261
 ID ADU48443 standard; DNA; 3004 BP.
 DE Acidothermus cellulolyticus endoglucanase E1 DNA.
 PN US6818803-B1.
 PD 16-NOV-2004.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 Percent Similarity: 36.6%
 Best Local Similarity: 23.8% Mismatches: 115
 Indels: 69
 Query Match: 5.5%
 RESULT 1262
 ID ABX63016 standard; cDNA; 3125 BP.
 DE Human cDNA #16 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Percent Similarity: 41.5%
 Best Local Similarity: 24.6% Mismatches: 111

Query Match: 5.5% Indels: 59
 RESULT 1263
 ID AAI61199 standard; cDNA; 3138 BP.
 DE Human polynucleotide SEQ ID NO 5188.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 32.8%
 Best Local Similarity: 24.2% Mismatches: 135
 Indels: 124
 Query Match: 5.5%
 RESULT 1264
 ID AAQ22202 standard; DNA; 3306 BP.
 DE A. chrysogenum phosphoglycerate kinase.
 PN EP474273-A.
 PD 11-MAR-1992.
 PA (ASAH) ASahi Kasei Kogyo KK.
 Percent Similarity: 38.2%
 Best Local Similarity: 22.2% Mismatches: 113
 Indels: 89
 Query Match: 5.5%
 RESULT 1265
 ID AAQ23005 standard; DNA; 3306 BP.
 DE Phosphoglycerate kinase gene (incl. promoter).
 PN JP04058891-A.
 PD 25-FEB-1992.
 PA (ASAH) ASahi Kasei Kogyo KK.
 Percent Similarity: 38.2%
 Best Local Similarity: 22.2% Mismatches: 113
 Indels: 89
 Query Match: 5.5%
 RESULT 1266
 ID RAD51687 standard; cDNA; 3840 BP.
 DE Human nucleic acid associated protein (NAAP)-13 encoding cDNA.
 PN WO200299115-A2.
 PD 12-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 41.5%
 Best Local Similarity: 24.6% Mismatches: 111
 Indels: 59
 Query Match: 5.5%
 RESULT 1267
 ID AEL55888 standard; cDNA; 3967 BP.
 DE Mouse MKIAA1930 coding sequence, SEQ ID NO: 349.
 PN US2006216722-A1.
 PD 28-SEP-2006.
 PA (BETS/) BETSHOLTZ C.
 PA (TRYG/) TRYGGVASON K.
 PA (TAKE/) TAKEMOTO M.
 PA (HELL/) HE L. KIKAS J.
 PA (PATR/) PATRAKAS J.
 Percent Similarity: 35.6%
 Best Local Similarity: 20.9% Mismatches: 138
 Indels: 122
 Query Match: 5.5%
 RESULT 1268
 ID ADE71196 standard; DNA; 4815 BP.
 DE Novel human protein coding sequence #12.
 PN JP2002345493-A.
 PD 03-DEC-2002.
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
 Percent Similarity: 41.2%
 Best Local Similarity: 24.6% Mismatches: 112
 Indels: 59
 Query Match: 5.5%
 RESULT 1269
 ID ADV97761 standard; cDNA; 6432 BP.
 DE cDNA sequence encoding a murine protein kinase Seq 81.
 PN WO200500200-A2.
 PD 06-JAN-2005.
 PA (SUGE-) SUGEN INC.
 Percent Similarity: 33.9%
 Best Local Similarity: 23.9% Mismatches: 31
 Indels: 80
 Query Match: 5.5%
 RESULT 1270
 ID AAS54978 standard; DNA; 7035 BP.
 DE Staphylococcus aureus DNA for cellular proliferation protein #1290.
 PN WO200170955-A2.

PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.1%
Best Local Similarity: 20.6%
Query Match: 5.5%
RESULT 1271
ID AEB96869 standard; cDNA; 7035 BP.
DE Human cancer associated cDNA SEQ ID NO 162.
PN WO2006033664-A1.
PD 30-MAR-2006.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 35.8%
Best Local Similarity: 22.4%
Query Match: 5.5%
RESULT 1272
ID AED50861 standard; DNA; 11040 BP.
DE S. cellulosum strain So ce 307 jerangolid biosynthetic cluster jerB gene.
PN US2005233369-A1.
PD 20-OCT-2005.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 32.3%
Best Local Similarity: 21.2%
Query Match: 5.5%
RESULT 1273
ID AEB56305 standard; DNA; 11517 BP.
DE Enterobacter cloacae protein coding sequence - SEQ ID 4475.
PN US7041814-B1.
PD 09-MAY-2006.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 34.8%
Best Local Similarity: 24.1%
Query Match: 5.5%
RESULT 1274
ID ABL03868 standard; cDNA; 31562 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6086.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Percent Similarity: 30.8%
Best Local Similarity: 21.8%
Query Match: 5.5%
RESULT 1275
ID AED50859 standard; DNA; 67323 BP.
DE S. cellulosum strain So ce 307 jerangolid biosynthetic gene cluster.
PN US2005233369-A1.
PD 20-OCT-2005.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 32.3%
Best Local Similarity: 21.2%
Query Match: 5.5%
RESULT 1276
ID ABV75557 standard; DNA; 75236 BP.
DE Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 1.
PN WO200279477-A2.
PD 10-OCT-2002.
PA (DOWC-) DOW AGROSCIENCES LLC.
Percent Similarity: 37.4%
Best Local Similarity: 21.2%
Query Match: 5.5%
RESULT 1277
ID AAI24837 standard; DNA; 531 BP.
DE Probe #14770 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 36.0%
Best Local Similarity: 24.5%
Query Match: 5.5%
RESULT 1278
ID AAI24837 standard; DNA; 531 BP.
DE Probe #14770 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 33.8%
Best Local Similarity: 19.5%
Query Match: 5.5%
RESULT 1279
ID AAI24837 standard; DNA; 531 BP.
DE Probe #14770 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 33.8%
Best Local Similarity: 19.5%
Query Match: 5.5%
RESULT 1280
ID ABA70232 standard; DNA; 531 BP.
DE Human foetal liver single exon nucleic acid probe #18537.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1281
ID AAI50362 standard; DNA; 531 BP.
DE Probe #19048 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1282
ID ABA36961 standard; DNA; 531 BP.
DE Probe #15427 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1283
ID AAK44363 standard; DNA; 531 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 18920.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1284
ID AAK18458 standard; DNA; 531 BP.
DE Human brain expressed single exon probe SEQ ID NO: 18449.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1285
ID ABS44020 standard; DNA; 531 BP.
DE Human liver single exon probe, SEQ ID No 19010.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1286
ID ABS18599 standard; DNA; 531 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 18590.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 45.4%
Best Local Similarity: 27.0%
Query Match: 5.5%
RESULT 1287
ID AAO12218 standard; DNA; 836 BP.
DE SMUC-41 intestinal mucin cDNA clone.
PN WO9108217-A.
PD 13-JUN-1991.
PA (REGC-) UNIV CALIFORNIA.
Percent Similarity: 35.2%
Conservative: 36
Mismatches: 77
Indels: 13

Best Local Similarity: 23.3% Mismatches: 108
 Query Match: 5.5% Indels: 87
 RESULT 1288
 ID ADX15294 standard; cDNA; 846 BP.
 DE Plant full length insert polynucleotide seqid 9869.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Percent Similarity: 41.1%
 Best Local Similarity: 25.9% Conservative: 28
 Mismatches: 72
 Indels: 37
 Query Match: 5.5%
 RESULT 1289
 ID ADX14720 standard; cDNA; 862 BP.
 DE Plant full length insert polynucleotide seqid 9295.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Percent Similarity: 41.1%
 Best Local Similarity: 25.9% Conservative: 28
 Mismatches: 72
 Indels: 37
 Query Match: 5.5%
 RESULT 1290
 ID ADT17667 standard; cDNA; 864 BP.
 DE Plant cDNA, Seq ID 2993.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K.
 Percent Similarity: 40.3% Conservative: 30
 Best Local Similarity: 26.7% Mismatches: 78
 Indels: 55
 Query Match: 5.5%
 RESULT 1291
 ID AEI30715 standard; DNA; 930 BP.
 DE Soybean polymorphic locus, SEQ ID 3349.
 PN US2006135758-A1.
 PD 22-JUN-2006.
 PA (WUKK/) WU K.
 Percent Similarity: 41.1% Conservative: 28
 Best Local Similarity: 25.9% Mismatches: 72
 Indels: 37
 Query Match: 5.5%
 RESULT 1292
 ID AAF12775 standard; cDNA; 1347 BP.
 DE Aspergillus oryzae EST SEQ ID NO:5298.
 PN WO200056762-A2.
 PD 28-SEP-2000.
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 36.0% Conservative: 23
 Best Local Similarity: 24.6% Mismatches: 66
 Indels: 64
 Query Match: 5.5%
 RESULT 1293
 ID ADU56816 standard; cDNA; 1347 BP.
 DE Aspergillus oryzae strain strain A1560/strain AL-1 EST, SEQ ID NO:5298.
 PN US2004229367-A1.
 PD 18-NOV-2004.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES INC AS.
 Percent Similarity: 36.0% Conservative: 23
 Best Local Similarity: 24.6% Mismatches: 66
 Indels: 64
 Query Match: 5.5%
 RESULT 1294
 ID ADZ94819 standard; cDNA; 1347 BP.
 DE Aspergillus oryzae expressed sequence tag cDNA SEQ ID NO 5298.
 PN US6902887-B1.
 PD 07-JUN-2005.

PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 Percent Similarity: 36.0% Conservative: 23
 Best Local Similarity: 24.6% Mismatches: 66
 Indels: 64
 Query Match: 5.5%
 RESULT 1295
 ID ADA69781 standard; DNA; 1650 BP.
 DE Rice gene, SEQ ID 3104.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 36.6% Conservative: 48
 Best Local Similarity: 24.0% Mismatches: 152
 Indels: 92
 Query Match: 5.5%
 RESULT 1296
 ID ADI57686 standard; cDNA; 1712 BP.
 DE Human breast specific nucleic acid (BSNA) #57.
 PN WO2003106648-A2.
 PD 24-DEC-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 30.2% Conservative: 40
 Best Local Similarity: 21.3% Mismatches: 134
 Indels: 178
 Query Match: 5.5%
 RESULT 1297
 ID ADI57673 standard; cDNA; 1755 BP.
 DE Human breast specific nucleic acid (BSNA) #44.
 PN WO2003106648-A2.
 PD 24-DEC-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 32.6% Conservative: 37
 Best Local Similarity: 22.6% Mismatches: 124
 Indels: 124
 Query Match: 5.5%
 RESULT 1298
 ID ADI57672 standard; cDNA; 1918 BP.
 DE Human breast specific nucleic acid (BSNA) #43.
 PN WO2003106648-A2.
 PD 24-DEC-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 32.6% Conservative: 37
 Best Local Similarity: 22.6% Mismatches: 124
 Indels: 124
 Query Match: 5.5%
 RESULT 1299
 ID ABL04769 standard; cDNA; 2241 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8789.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.6% Conservative: 39
 Best Local Similarity: 24.0% Mismatches: 131
 Indels: 48
 Query Match: 5.5%
 RESULT 1300
 ID ACH89449 standard; DNA; 2329 BP.
 DE Human genome derived single exon probe #22644.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Percent Similarity: 35.8% Conservative: 50
 Best Local Similarity: 22.8% Mismatches: 152
 Indels: 96
 Query Match: 5.5%
 RESULT 1301
 ID ACA92438 standard; DNA; 2352 BP.
 DE DNA encoding human PMM-23.
 PN WO2003031939-A2.
 PD 17-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 32.7% Conservative: 54
 Best Local Similarity: 20.5% Mismatches: 130
 Indels: 169
 Query Match: 5.5%
 RESULT 1302
 ID ABL04347 standard; cDNA; 3188 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7523.

PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 33.9%
 Best Local Similarity: 21.7%
 Query Match: 5.5%
 RESULT 1303
 ID AD67427 standard; cDNA; 3538 BP.
 DE Novel human cDNA sequence #2400.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 41.9%
 Best Local Similarity: 24.8%
 Query Match: 5.5%
 RESULT 1304
 ID AD128073 standard; cDNA; 4111 BP.
 DE ECWAD gene clone 553744CB1.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 39.6%
 Best Local Similarity: 26.7%
 Query Match: 5.5%
 RESULT 1305
 ID ADK65923 standard; DNA; 4447 BP.
 DE Y lipolytica isocitrate lyase vector fragment #1.
 PN WO2004009828-A1.
 PD 29-JAN-2004.
 PA (UYDR) UNIV DRESDEN TECH.
 Percent Similarity: 35.2%
 Best Local Similarity: 23.8%
 Query Match: 5.5%
 RESULT 1306
 ID AB211844 standard; cDNA; 4573 BP.
 DE Human polynucleotide SEQ ID NO 726.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 36.7%
 Best Local Similarity: 23.3%
 Query Match: 5.5%
 RESULT 1307
 ID ADP55703 standard; cDNA; 4839 BP.
 DE Human PRO cDNA sequence SEQ ID NO:1679.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 39.6%
 Best Local Similarity: 26.7%
 Query Match: 5.5%
 RESULT 1308
 ID ABL04768 standard; cDNA; 4864 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8786.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.6%
 Best Local Similarity: 24.0%
 Query Match: 5.5%
 RESULT 1309
 ID ADM44362 standard; cDNA; 5323 BP.
 DE Novel human arginine-rich protein cDNA #726.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRNA/) DRMANAC R T.
 Percent Similarity: 36.7%
 Best Local Similarity: 23.3%
 Query Match: 5.5%
 RESULT 1310
 ID ABL25205 standard; DNA; 5931 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 31.0%
 Best Local Similarity: 21.5%
 Query Match: 5.5%
 RESULT 1311
 ID ABL25204 standard; DNA; 7931 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 31.0%
 Best Local Similarity: 21.5%
 Query Match: 5.5%
 RESULT 1312
 ID AD080813 standard; DNA; 9163 BP.
 DE Porcine enterotoxigenic E coli resistance gene contig 132.
 PN WO2004048606-A2.
 PD 10-JUN-2004.
 PA (KGLV-) DEN KGL VETERINAER OG LANDBOHJSKOLE.
 Percent Similarity: 35.7%
 Best Local Similarity: 23.8%
 Query Match: 5.5%
 RESULT 1313
 ID ADK65925 standard; DNA; 9300 BP.
 DE Y lipolytica isocitrate lyase vector fragment #3.
 PN WO2004009828-A1.
 PD 29-JAN-2004.
 PA (UYDR) UNIV DRESDEN TECH.
 Percent Similarity: 35.2%
 Best Local Similarity: 23.8%
 Query Match: 5.5%
 RESULT 1314
 ID ADK65924 standard; DNA; 10056 BP.
 DE Y lipolytica isocitrate lyase vector fragment #2.
 PN WO2004009828-A1.
 PD 29-JAN-2004.
 PA (UYDR) UNIV DRESDEN TECH.
 Percent Similarity: 35.2%
 Best Local Similarity: 23.8%
 Query Match: 5.5%
 RESULT 1315
 ID ACC00398 standard; cDNA; 10569 BP.
 DE Human cell adhesion and extracellular matrix protein, CAECM-7, DNA.
 PN WO2003027230-A2.
 PD 03-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 41.0%
 Best Local Similarity: 24.5%
 Query Match: 5.5%
 RESULT 1316
 ID ADW42645 standard; DNA; 31967 BP.
 DE Simian adenovirus 18 polynucleotide.
 PN WO2005001103-A2.
 PD 06-JAN-2005.
 PA (UYPE-) UNIV PENNSYLVANIA.
 Percent Similarity: 34.1%
 Best Local Similarity: 22.7%
 Query Match: 5.5%
 RESULT 1317
 ID ABL18214 standard; DNA; 34712 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6115.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 35.2%
 Best Local Similarity: 22.2%
 Query Match: 5.5%
 RESULT 1318
 ID ADM43175 standard; DNA; 35167 BP.
 DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.


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PD 13-SEP-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1335
ID ABK33649 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO protein, Seq ID No 227.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1336
ID ADV31967 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1337
ID ACA03678 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1338
ID ABX89216 standard; cDNA; 2164 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4322.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1339
ID ACD41870 standard; cDNA; 2164 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #76.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1340
ID ACA86610 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1341
ID ACA04099 standard; cDNA; 2164 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 151.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1342
ID ADA45670 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1343
ID ADA76101 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1344
ID ABT44339 standard; cDNA; 2164 BP.
DE Human PRO4322 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1345
ID ADA18751 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1346
ID ADA61374 standard; cDNA; 2164 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1347
ID ADB19159 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1348
ID ADB27700 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1349
ID ADA86179 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1350
ID ADB15743 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.

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Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1351
ID ADA47529 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1352
ID ADA67324 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1353
ID ADB30331 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1354
ID ADA85627 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1355
ID ADA96839 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1356
ID ADA79143 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1357
ID ADA87282 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1358
ID ADB16484 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33

Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1359
ID ADA91576 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1360
ID ADB14639 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1361
ID ADB18600 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1362
ID ADA93815 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1363
ID ADB19711 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1364
ID ADB13023 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1365
ID ACD98499 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1366
ID ADA74277 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33
Best Local Similarity: 24.2% Mismatches: 135
Query Match: 5.5% Indels: 124
RESULT 1367
ID ADB16484 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8% Conservative: 33

Query Match: 5.5% Indels: 124
RESULT 1367
ID ADA24510 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide SEQ ID NO 151.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1368
ID ADA82034 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1369
ID ADA74997 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1370
ID ADA85075 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1371
ID ADA84523 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1372
ID ADB29779 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1373
ID ADA80307 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1374
ID ADA75549 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124

RESULT 1375
ID ADA46774 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1376
ID ADB25070 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide SEQ ID NO 151.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1377
ID ADA93246 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1378
ID ADB26596 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1379
ID ADB30883 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1380
ID ABT44622 standard; cDNA; 2164 BP.
DE Human PRO4322 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1381
ID ADA60811 standard; cDNA; 2164 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1382
ID ADB23958 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide SEQ ID NO 151.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124
RESULT 1383
ID ADB23958 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide SEQ ID NO 151.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135
Indels: 124

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ID ADA96287 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082630-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1384
ID ADA80859 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1385
ID ADA95735 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1386
ID ADB26044 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1387
ID ADB21529 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1388
ID ACD82289 standard; cDNA; 2164 BP.
DE Human secreted/transmembrane polypeptide PRO 4322 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1389
ID ADA77308 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1390
ID ADB18048 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003077110-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1391
ID ADA86731 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1392
ID ADA87834 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1393
ID ADA46222 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1394
ID ADB28252 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1395
ID ADB28804 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1396
ID ADA76756 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1397
ID ADA88386 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1398
ID ADA97391 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1399
ID ADB27148 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.

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RESULT 1432
ID ADC36956 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1433
ID ADC21946 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #114.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1434
ID ADC50192 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1435
ID ADC71739 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1436
ID ADC59718 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1437
ID ADC49977 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1438
ID ADC49176 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1439
ID ADC49693 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1440
ID ADC58854 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1441
ID ADC52725 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1442
ID ADC57079 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1443
ID ADC60270 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1444
ID ADC50745 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1445
ID ADC65272 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1446
ID ADC54370 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1447
ID ADC53331 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1448
ID ADC58854 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
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DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PD US2003087359-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1449
ID ADC55732 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PD US2003087360-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1450
ID ADC58302 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID151.
PD US2003087346-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1451
ID ADC47299 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003105288-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1452
ID ADD02976 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003092104-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1453
ID ADC89968 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003087348-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1454
ID ADC69387 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PD US2003194770-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1455
ID ADC48276 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PD US2003194773-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1456
ID ADD09805 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.

PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1457
ID ADC78174 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003096972-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1458
ID ADD04380 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003087354-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1459
ID ADD06409 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003073816-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1460
ID ADC80336 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003092103-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1461
ID ADD10843 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PD US2003194774-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1462
ID ADC47724 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PD US2003194771-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1463
ID ADC77928 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003088066-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Conservative: 33
Mismatch: 135
Indels: 124
RESULT 1464
ID ADC79784 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PD US2003087358-A1.

PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1473			
ID ADD02352 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #76.			
PN US2003203431-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1474			
ID ADD50618 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #114.			
PN US2003096971-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1475			
ID ADD01786 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #76.			
PN US2003203430-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1476			
ID ADD53968 standard; cDNA; 2164 BP.			
DE Novel human secreted and transmembrane protein PRO4322 cDNA.			
PN US2003203432-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1477			
ID ADD50372 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #114.			
PN US2003096970-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1478			
ID ADD51383 standard; cDNA; 2164 BP.			
DE Novel human secreted and transmembrane protein PRO4322 cDNA.			
PN US2003105289-A1.			
PD 05-JUN-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1479			
ID ADD92385 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #76.			
PN US2003199030-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124
RESULT 1480			
ID ADD91181 standard; cDNA; 2164 BP.			
DE Human PRO polynucleotide #76.			
PN US2003199055-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	32.8%		Conservative: 33
Best Local Similarity:	24.2%		Mismatches: 135
Query Match:	5.5%		Indels: 124

Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1481
 ID ADE03795 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199057-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1482
 ID ADE32092 standard; cDNA; 2164 BP.
 DE Novel human secreted and transmembrane protein PRO4322 cDNA.
 PN US2003194765-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1483
 ID ADE22024 standard; cDNA; 2164 BP.
 DE cDNA encoding human PRO polypeptide #76.
 PN US2003199056-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1484
 ID ADD79248 standard; cDNA; 2164 BP.
 DE cDNA encoding human PRO polypeptide #76.
 PN US2003203428-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1485
 ID ADE41784 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003194772-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1486
 ID ADE17601 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199023-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1487
 ID ADD91733 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199053-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1488
 ID ADE33196 standard; cDNA; 2164 BP.
 DE Novel human secreted and transmembrane protein PRO4322 cDNA.
 PN US2003194767-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33

Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1489
 ID ADE33748 standard; cDNA; 2164 BP.
 DE Novel human secreted and transmembrane protein PRO4322 cDNA.
 PN US2003194791-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1490
 ID ADD79800 standard; cDNA; 2164 BP.
 DE cDNA encoding human PRO polypeptide #76.
 PN US2003207417-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1491
 ID ADD92837 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003194768-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1492
 ID ADE19257 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199025-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1493
 ID ADE18705 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199026-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1494
 ID ADE42901 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199033-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1495
 ID ADD95690 standard; cDNA; 2164 BP.
 DE Human PRO polynucleotide #76.
 PN US2003199059-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1496
 ID ADE22576 standard; cDNA; 2164 BP.
 DE cDNA encoding human PRO polypeptide #76.
 PN US2003199064-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33
 Best Local Similarity: 24.2% Mismatches: 135
 Query Match: 5.5% Indels: 124
 RESULT 1497
 ID ADE33196 standard; cDNA; 2164 BP.
 DE Novel human secreted and transmembrane protein PRO4322 cDNA.
 PN US2003194767-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.8% Conservative: 33

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Query Match: 5.5% Indels: 124
RESULT 1497
ID ADD78694 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135

Query Match:
RESULT 1498
ID ADE32644 standard; cDNA; 2164 BP.
DE Novel human secreted and transmembrane protein PRO4322 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135

Query Match:
RESULT 1499
ID ADE42336 standard; cDNA; 2164 BP.
DE Human PRO polynucleotide #76.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135

Query Match:
RESULT 1500
ID ADD80352 standard; cDNA; 2164 BP.
DE cDNA encoding human PRO polypeptide #76.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.8%
Best Local Similarity: 24.2%
Query Match: 5.5%
Indels: 124
Conservative: 33
Mismatches: 135

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c 81	146	6.6	767677	3	US-09-949-016-12147	Sequence 12147, A	154	132.5	6.0	617	5	US-10-703-032-77253	Sequence 77253, A
c 82	146	6.6	767677	3	US-09-949-016-17361	Sequence 17361, A	155	132.5	6.0	792	5	US-10-703-032-2920	Sequence 2920, Ap
c 83	145.5	6.6	2114	3	US-09-370-838-158	Sequence 158, App	156	132.5	6.0	6852	3	US-10-172-502-3	Sequence 3, Appli
c 84	145.5	6.6	2114	3	US-09-854-133-158	Sequence 158, App	157	132	6.0	532	5	US-10-703-032-98728	Sequence 98728, A
c 85	145	6.6	1088	5	US-10-703-032-103747	Sequence 103747	158	132	6.0	585	5	US-10-703-032-77269	Sequence 77269, A
c 86	145	6.6	9636	2	US-08-323-170B-1	Sequence 1, Appli	159	132	6.0	613	5	US-10-703-032-105228	Sequence 105228, A
c 87	145	6.6	9636	2	US-08-954-441-1	Sequence 1, Appli	160	132	6.0	615	5	US-10-703-032-65933	Sequence 65933, A
c 88	144.5	6.5	2156	5	US-10-451-467A-167	Sequence 167, App	161	132	6.0	814	5	US-10-703-032-4517	Sequence 4517, Ap
c 89	144.5	6.5	3423	3	US-09-614-221A-91	Sequence 91, Appl	162	132	6.0	1230	5	US-10-703-032-2320	Sequence 2320, Ap
c 90	143	6.5	720	5	US-10-703-032-14434	Sequence 14434, A	163	132	6.0	2455	3	US-09-103-429A-1	Sequence 1, Appli
c 91	142	6.4	12685	3	US-09-479-467A-3	Sequence 3, Appli	164	132	6.0	2455	3	US-09-294-663-1	Sequence 1, Appli
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c 93	141.5	6.4	3486	3	US-09-614-221A-292	Sequence 292, App	166	132	6.0	2821	3	US-09-294-663-2	Sequence 2, Appli
c 94	140.5	6.4	1490	5	US-10-703-032-8641	Sequence 8641, Ap	167	132	6.0	5511	3	US-08-928-361B-2	Sequence 2, Appli
c 95	139.5	6.3	1795	3	US-09-197-970B-6	Sequence 6, Appli	168	132	6.0	5511	3	US-09-588-995A-2	Sequence 1, Appli
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c 97	139	6.3	867	3	US-09-216-393B-340	Sequence 340, App	170	132	6.0	7334	3	US-09-588-995A-1	Sequence 1, Appli
c 98	139	6.3	867	3	US-09-216-393B-342	Sequence 342, App	171	131.5	5.9	688	5	US-10-703-032-74240	Sequence 74240, A
c 99	139	6.3	867	3	US-09-321-856-340	Sequence 340, App	172	131	5.9	993	5	US-10-703-032-30891	Sequence 30891, A
c 100	139	6.3	867	3	US-10-321-856-342	Sequence 342, App	173	131	5.9	1132	5	US-10-703-032-2324	Sequence 2324, Ap
c 101	139	6.3	1397	5	US-09-216-393B-343	Sequence 343, App	174	130.5	5.9	625	5	US-10-703-032-71918	Sequence 71918, A
c 102	139	6.3	1397	5	US-09-216-393B-345	Sequence 345, App	175	130.5	5.9	626	5	US-10-703-032-100047	Sequence 100047, A
c 103	139	6.3	1397	5	US-10-321-856-343	Sequence 343, App	176	130.5	5.9	1063	5	US-10-703-032-2890	Sequence 2890, Ap
c 104	139	6.3	1397	5	US-10-321-856-345	Sequence 345, App	177	130.5	5.9	1086	2	US-08-415-751-27	Sequence 27, Appl
c 105	138.5	6.3	3159	3	US-09-437-054A-7	Sequence 7, Appli	c 178	130.5	5.9	1706	2	US-08-415-751-28	Sequence 28, Appl
c 106	138.5	6.3	3183	3	US-08-911-393-1	Sequence 1, Appli	179	130.5	5.9	1706	2	US-09-949-016-2380	Sequence 2380, Ap
c 107	138.5	6.3	3183	3	US-09-955-909-1	Sequence 1, Appli	180	130	5.9	718	5	US-10-703-032-72860	Sequence 72860, Ap
c 108	138.5	6.3	4104	3	US-09-614-221A-44	Sequence 44, Appl	181	130	5.9	888	5	US-10-703-032-2888	Sequence 2888, Ap
c 109	138.5	6.3	4104	3	US-09-487-558B-107	Sequence 107, App	182	130	5.9	1289	5	US-10-703-032-2318	Sequence 2318, Ap
c 110	138.5	6.3	5163	3	US-08-700-651-1	Sequence 1, Appli	183	130	5.9	2418	5	US-10-703-032-2939	Sequence 2939, Ap
c 111	138.5	6.3	5163	3	US-08-928-361B-4	Sequence 4, Appli	184	130	5.9	2418	5	US-10-108-260A-1486	Sequence 1486, Ap
c 112	138.5	6.3	5163	3	US-09-588-995A-4	Sequence 4, Appli	c 185	130	5.9	152132	3	US-09-949-016-13845	Sequence 13845, A
c 113	138.5	6.3	5318	3	US-08-700-651-2	Sequence 2, Appli	c 186	130	5.9	152145	3	US-09-949-016-12371	Sequence 12371, A
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c 115	138.5	6.3	5318	3	US-09-588-995A-3	Sequence 3, Appli	188	129.5	5.9	716	5	US-10-703-032-76015	Sequence 76015, A
c 116	138	6.2	585	5	US-10-703-032-72752	Sequence 72752, A	189	129.5	5.9	716	5	US-10-703-032-76137	Sequence 76137, A
c 117	138	6.2	828	5	US-10-703-032-2946	Sequence 2946, Ap	190	129.5	5.9	812	5	US-10-703-032-76025	Sequence 76025, A
c 118	137	6.2	1038608	5	US-09-201-228B-1	Sequence 1, Appli	191	129.5	5.9	820	5	US-10-703-032-76192	Sequence 76192, A
c 119	136.5	6.2	1512	3	US-09-487-558B-423	Sequence 423, App	192	129.5	5.9	955	5	US-10-703-032-14354	Sequence 14354, A
c 120	136	6.2	1587	5	US-10-703-032-2948	Sequence 2948, Ap	c 193	129.5	5.9	1099	3	US-08-956-171B-825	Sequence 825, App
c 121	136	6.2	1905	5	US-10-455-719-150	Sequence 150, App	c 194	129.5	5.9	1099	3	US-08-781-986A-825	Sequence 825, App
c 122	136	6.2	2150	2	US-08-861-464-13	Sequence 13, Appl	195	129	5.8	756	5	US-10-703-032-103062	Sequence 103062, A
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c 124	136	6.2	2150	3	US-09-323-433A-13	Sequence 13, Appl	197	129	5.8	4725	5	US-10-041-018-147	Sequence 147, App
c 125	136	6.2	2150	3	US-09-826-752-13	Sequence 13, Appl	198	128.5	5.8	698	5	US-10-703-032-72864	Sequence 72864, A
c 126	136	6.2	2188	5	US-10-455-719-25	Sequence 25, Appl	199	128.5	5.8	704	5	US-10-703-032-68202	Sequence 68202, A
c 127	136	6.2	3015	5	US-09-373-658C-37	Sequence 37, Appl	200	128.5	5.8	927	5	US-10-703-032-2956	Sequence 2956, Ap
c 128	136	6.2	134008	3	US-09-949-016-13841	Sequence 13841, A	201	128.5	5.8	1371	5	US-10-703-032-2956	Sequence 427, App
c 129	135.5	6.1	573	5	US-10-703-032-104794	Sequence 104794, A	202	128	5.8	1818	3	US-09-487-558B-427	Sequence 12147, A
c 130	135.5	6.1	878	5	US-10-703-032-8646	Sequence 8646, Ap	203	128	5.8	767677	3	US-09-949-016-12147	Sequence 12147, A
c 131	135.5	6.1	2139	5	US-10-455-719-76	Sequence 76, Appl	204	128	5.8	767677	3	US-09-949-016-17361	Sequence 17361, A
c 132	135.5	6.1	2256646	5	US-10-470-565-1	Sequence 1, Appli	205	128	5.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 133	135	6.1	619	5	US-10-703-032-68308	Sequence 68308, A	206	128	5.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 134	135	6.1	784	5	US-10-703-032-8057	Sequence 8057, Ap	207	127.5	5.8	730	5	US-10-703-032-66048	Sequence 66048, A
c 135	135	6.1	1132	5	US-10-703-032-2923	Sequence 2923, Ap	208	127.5	5.8	750	5	US-10-703-032-76120	Sequence 76120, A
c 136	135	6.1	1140	3	US-09-023-173-4	Sequence 4, Appli	209	127.5	5.8	798	5	US-10-703-032-76198	Sequence 76198, A
c 137	135	6.1	2481	3	US-09-248-796A-3204	Sequence 3204, Ap	210	127.5	5.8	841	5	US-10-703-032-76195	Sequence 76195, A
c 138	134.5	6.1	1923	3	US-09-687-538B-1	Sequence 1, Appli	211	127.5	5.8	849	5	US-10-703-032-66037	Sequence 66037, A
c 139	134.5	6.1	1923	3	US-10-309-437-1	Sequence 1, Appli	212	127.5	5.8	2197	5	US-10-342-887-1153	Sequence 1153, Ap
c 140	134	6.1	630	5	US-10-703-032-71972	Sequence 71972, A	213	127.5	5.8	3969	3	US-09-487-558B-113	Sequence 113, App
c 141	134	6.1	1038	5	US-10-703-032-30847	Sequence 30847, A	214	127.5	5.8	30690	3	US-09-914-286-1	Sequence 1, Appli
c 142	134	6.1	32768	3	US-08-961-527-71	Sequence 71, Appl	215	127	5.7	516	5	US-10-703-032-104621	Sequence 104621, A
c 143	134	6.1	32768	3	US-10-158-844-71	Sequence 71, Appl	216	127	5.7	638	5	US-10-703-032-100898	Sequence 100898, A
c 144	134	6.1	194889	3	US-09-949-016-15654	Sequence 15654, A	217	127	5.7	1404	5	US-10-455-719-79	Sequence 79, Appl
c 145	133.5	6.0	1375	5	US-10-703-032-2316	Sequence 2316, Ap	218	127	5.7	1854	5	US-09-170-496D-217	Sequence 217, App
c 146	133	6.0	640	5	US-10-703-032-77241	Sequence 77241, A	219	127	5.7	3786	5	US-10-455-719-2	Sequence 2, Appli
c 147	133	6.0	725	5	US-10-703-032-72865	Sequence 72865, A	220	127	5.7	7542	3	US-09-734-030-3	Sequence 3, Appli
c 148	133	6.0	1542	3	US-08-685-558A-8	Sequence 8, Appli	221	127	5.7	7542	3	US-10-153-921-3	Sequence 3, Appli
c 149	133	6.0	1542	3	US-09-765-449-8	Sequence 8, Appli	222	127	5.7	7542	3	US-10-669-689-3	Sequence 3, Appli
c 150	133	6.0	1671	3	US-09-614-221A-554	Sequence 554, App	223	126.5	5.7	541	5	US-10-703-032-98533	Sequence 98533, A
c 151	133	6.0	1671	3	US-09-487-558B-425	Sequence 425, App	224	126.5	5.7	610	5	US-10-703-032-76118	Sequence 76118, A
c 152	133	6.0	2398	3	US-09-949-016-4313	Sequence 4313, Ap	225	126.5	5.7	640	5	US-10-703-032-103754	Sequence 103754, A

226	126.5	5.7	671	5	US-10-703-032-72883	Sequence 72883, A	299	124.5	5.6	1425	3	US-09-408-257-2	Sequence 2, Appli
227	126.5	5.7	696	5	US-10-703-032-72750	Sequence 72750, A	300	124.5	5.6	1485	3	US-09-248-796A-2443	Sequence 2443, Ap
228	126.5	5.7	701	5	US-10-703-032-76101	Sequence 76101, A	301	124.5	5.6	2175	3	US-09-605-703B-653	Sequence 653, App
229	126.5	5.7	709	5	US-10-703-032-77228	Sequence 77228, A	302	124.5	5.6	2175	3	US-09-605-703B-655	Sequence 655, App
230	126.5	5.7	729	5	US-10-703-032-76085	Sequence 76085, A	303	124.5	5.6	4116	3	US-09-949-016-2584	Sequence 2584, Ap
231	126.5	5.7	809	5	US-10-703-032-8622	Sequence 8622, Ap	304	124.5	5.6	4116	3	US-09-949-016-2585	Sequence 2585, Ap
232	126.5	5.7	840	5	US-10-703-032-2309	Sequence 2309, Ap	305	124	5.6	416	5	US-10-703-032-98536	Sequence 98536, A
233	126.5	5.7	913	2	US-08-217-327-3	Sequence 3, Appli	306	124	5.6	549	5	US-10-703-032-65470	Sequence 65470, A
234	126.5	5.7	913	2	US-07-885-970A-3	Sequence 3, Appli	307	124	5.6	607	5	US-10-703-032-2869	Sequence 2869, Ap
235	126.5	5.7	913	2	US-08-298-687A-3	Sequence 3, Appli	308	124	5.6	697	5	US-10-703-032-72759	Sequence 72759, A
236	126.5	5.7	913	2	US-08-530-797-2	Sequence 3, Appli	309	124	5.6	698	5	US-10-703-032-72891	Sequence 72891, A
237	126.5	5.7	913	2	US-08-298-829-3	Sequence 3, Appli	310	124	5.6	699	5	US-10-703-032-72817	Sequence 72817, A
238	126.5	5.7	913	2	US-08-787-335-2	Sequence 3, Appli	311	124	5.6	704	5	US-10-703-032-72893	Sequence 72893, A
239	126.5	5.7	1232	5	US-10-703-032-2323	Sequence 2323, Ap	312	124	5.6	710	5	US-10-703-032-71945	Sequence 71945, A
240	126.5	5.7	6699	3	US-09-949-016-1059	Sequence 1059, Ap	313	124	5.6	711	5	US-10-703-032-72762	Sequence 72762, A
241	126.5	5.7	12381	5	US-09-743-162A-1	Sequence 1, Appli	314	124	5.6	736	5	US-10-703-032-85674	Sequence 8574, Ap
242	126	5.7	490	5	US-10-703-032-105236	Sequence 105236, A	315	124	5.6	736	5	US-10-703-032-8660	Sequence 8660, Ap
243	126	5.7	506	5	US-10-703-032-66050	Sequence 66050, A	316	124	5.6	1411	5	US-10-703-032-827	Sequence 827, App
244	126	5.7	673	5	US-10-703-032-77238	Sequence 77238, A	317	124	5.6	2621	3	US-10-104-047-527	Sequence 527, App
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246	126	5.7	708	5	US-10-703-032-74073	Sequence 74073, A	319	124	5.6	580	3	US-09-614-221A-536	Sequence 536, App
247	126	5.7	1021	3	US-09-533-559-745	Sequence 745, App	320	124	5.6	18364	5	US-10-243-243C-7	Sequence 7, Appli
248	126	5.7	1021	3	US-10-653-047-745	Sequence 745, App	321	124	5.6	24459	3	US-09-902-540-5004	Sequence 5004, Ap
249	126	5.7	1059	5	US-09-902-540-7326	Sequence 7326, Ap	322	123.5	5.6	32241	3	US-09-902-540-1247	Sequence 1247, Ap
250	126	5.7	1059	5	US-10-703-032-4477	Sequence 4477, Ap	323	123.5	5.6	1109	5	US-10-703-032-8589	Sequence 8589, Ap
251	126	5.7	1079	3	US-09-145-916-4	Sequence 4, Appli	324	123.5	5.6	2754	2	US-08-270-076A-10	Sequence 10, Appl
252	126	5.7	1079	3	US-10-352-839A-4	Sequence 4, Appli	325	123.5	5.6	99748	3	US-09-949-016-11990	Sequence 11990, A
253	126	5.7	1446	3	US-09-533-559-4423	Sequence 4423, Ap	326	123	5.6	99749	3	US-09-949-016-16518	Sequence 16518, A
254	126	5.7	1446	3	US-10-653-047-4423	Sequence 4423, Ap	327	123	5.6	529	5	US-10-703-032-98703	Sequence 98703, A
255	126	5.7	1824	5	US-10-703-032-8718	Sequence 8718, Ap	328	123	5.6	540	5	US-10-703-032-105245	Sequence 105245, A
256	126	5.7	2093	2	US-08-287-001A-1	Sequence 1, Appli	329	123	5.6	563	5	US-10-703-032-66047	Sequence 66047, A
257	126	5.7	2093	8	PCT-US95-09941-1	Sequence 1, Appli	330	123	5.6	630	5	US-10-703-032-66027	Sequence 66027, A
258	126	5.7	2256	5	US-10-094-749-676	Sequence 676, App	331	123	5.6	631	5	US-10-703-032-102987	Sequence 102987, A
259	126	5.7	3366	5	US-10-455-719-89	Sequence 89, Appl	332	123	5.6	794	5	US-10-703-032-66032	Sequence 66032, A
260	126	5.7	4039	3	US-09-902-540-696	Sequence 696, App	333	123	5.6	844	5	US-10-333-951-5	Sequence 5, Appli
261	126	5.7	7577	3	US-09-637-048C-3	Sequence 3, Appli	334	123	5.6	1614	5	US-10-742-201-1	Sequence 1, Appli
262	126	5.7	7577	3	US-10-435-835-3	Sequence 3, Appli	335	123	5.6	2482	5	US-10-223-081-41	Sequence 41, Appl
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264	126	5.7	7621	3	US-10-435-835-6	Sequence 6, Appli	337	123	5.6	2482	5	US-10-223-084-41	Sequence 41, Appl
265	126	5.7	2256646	5	US-10-470-565-1	Sequence 1, Appli	338	123	5.6	2482	5	US-10-223-084-41	Sequence 41, Appl
266	125.5	5.7	508	5	US-10-703-032-6059	Sequence 6059, A	339	123	5.6	2482	5	US-10-245-913-9	Sequence 9, Appli
267	125.5	5.7	595	5	US-10-703-032-105461	Sequence 105461, A	340	123	5.6	2482	5	US-10-245-752-9	Sequence 9, Appli
268	125.5	5.7	619	5	US-10-703-032-65542	Sequence 65542, A	341	123	5.6	2482	5	US-10-242-652-9	Sequence 9, Appli
269	125.5	5.7	669	5	US-10-703-032-76099	Sequence 76099, A	342	123	5.6	2482	5	US-10-242-652-9	Sequence 9, Appli
270	125.5	5.7	968	5	US-10-703-032-2322	Sequence 2322, Ap	343	123	5.6	2482	5	US-10-223-090-41	Sequence 1, Appli
271	125.5	5.7	1372	5	US-10-703-032-2315	Sequence 2315, Ap	344	123	5.6	2717	2	US-07-723-002C-1	Sequence 1, Appli
272	125.5	5.7	1860	3	US-09-894-844-65	Sequence 65, Appli	345	123	5.6	3069	5	US-10-703-032-14250	Sequence 14250, A
273	125.5	5.7	1917	3	US-09-248-796A-4647	Sequence 4647, Ap	346	123	5.6	38239	3	US-09-949-016-12348	Sequence 12348, A
274	125.5	5.7	2717	5	US-10-451-467A-237	Sequence 237, App	347	123	5.6	38252	3	US-09-949-016-13570	Sequence 13570, A
275	125	5.7	499	5	US-10-703-032-103635	Sequence 103635, A	348	123	5.6	114793	3	US-10-148-806-3	Sequence 3, Appli
276	125	5.7	812	5	US-10-703-032-102939	Sequence 102939, A	349	122.5	5.5	640	5	US-10-703-032-103774	Sequence 103774, A
277	125	5.7	1293	2	US-08-924-440-1	Sequence 1, Appli	350	122.5	5.5	649	5	US-10-703-032-36211	Sequence 36211, A
278	125	5.7	1430	3	US-09-976-594-878	Sequence 878, App	351	122.5	5.5	669	5	US-10-703-032-72854	Sequence 72854, A
279	125	5.7	1463	3	US-09-533-559-11	Sequence 11, Appl	352	122.5	5.5	762	5	US-10-703-032-76086	Sequence 76086, A
280	125	5.7	1463	5	US-10-653-047-11	Sequence 11, Appl	353	122.5	5.5	1042	3	US-09-533-559-5292	Sequence 5292, Ap
281	125	5.7	2142	3	US-09-614-221A-331	Sequence 331, App	354	122.5	5.5	1042	3	US-10-653-047-5292	Sequence 5292, Ap
282	125	5.7	2142	3	US-09-487-558B-407	Sequence 407, App	355	122.5	5.5	1170	5	US-10-703-032-2319	Sequence 2319, Ap
283	125	5.7	2337	5	US-10-333-951-9	Sequence 9, Appli	356	122.5	5.5	2335	5	US-10-104-047-748	Sequence 748, App
284	125	5.7	2835	3	US-09-134-001C-1515	Sequence 1515, Ap	357	122.5	5.5	3004	2	US-08-276-213-6	Sequence 6, Appli
285	125	5.7	3561	3	US-09-134-001C-1685	Sequence 1685, Ap	358	122.5	5.5	3004	3	US-09-373-272-8	Sequence 8, Appli
286	125	5.7	3561	3	US-09-450-965-1309	Sequence 1309, Ap	359	122.5	5.5	3004	3	US-09-981-900B-4	Sequence 4, Appli
287	125	5.7	3561	5	US-10-724-972B-1309	Sequence 1309, Ap	360	122.5	5.5	3306	2	US-08-261-206A-71	Sequence 71, Appl
288	125	5.7	4983	3	US-09-270-767-12587	Sequence 12587, A	361	122.5	5.5	11517	5	US-09-252-691C-4475	Sequence 4475, Ap
289	125	5.7	4998	3	US-09-501-171-5	Sequence 5, Appli	362	122.5	5.5	189268	5	US-10-021-698A-697	Sequence 697, App
290	125	5.7	6414	3	US-09-134-001C-1626	Sequence 1626, Ap	363	122.5	5.5	1082144	4	US-09-531-120-211	Sequence 211, App
291	125	5.7	6414	5	US-09-450-965-1179	Sequence 1179, Ap	364	122.5	5.5	733	5	US-10-703-032-102930	Sequence 102930, A
292	125	5.7	6414	5	US-10-724-972B-1179	Sequence 1179, Ap	365	122	5.5	954	3	US-09-248-796A-3469	Sequence 3469, Ap
293	125	5.7	4403765	3	US-10-103-840A-2	Sequence 2, Appli	366	122	5.5	1150	5	US-10-703-032-2317	Sequence 2317, Ap
294	125	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli	367	122	5.5	1267	3	US-10-703-032-2954	Sequence 2954, Ap
295	124.5	5.6	506	5	US-10-703-032-72742	Sequence 72742, A	368	122	5.5	1347	3	US-09-533-559-5298	Sequence 5298, Ap
296	124.5	5.6	940	5	US-10-703-032-74343	Sequence 74343, A	369	122	5.5	1347	5	US-10-653-047-5298	Sequence 5298, Ap
297	124.5	5.6	1425	2	US-08-578-551-2	Sequence 2, Appli	370	122	5.5	3936	5	US-10-455-719-143	Sequence 143, App
298	124.5	5.6	1425	2	US-09-190-982-2	Sequence 2, Appli	371	122	5.5	5323	3	US-09-799-451-726	Sequence 726, App

372	121.5	5.5	503	5	US-10-703-032-72922	Sequence 72922, A	445	120.5	5.5	1124	2	US-09-190-982-1	Sequence 1, Appli
373	121.5	5.5	548	5	US-10-703-032-72014	Sequence 72014, A	446	120.5	5.5	1124	3	US-09-408-257-1	Sequence 1, Appli
374	121.5	5.5	589	5	US-10-703-032-72737	Sequence 72737, A	447	120.5	5.5	1672	3	US-10-703-032-135	Sequence 135, App
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376	121.5	5.5	1029	5	US-10-031-331C-63	Sequence 63, Appl	449	120.5	5.5	3711	3	US-09-769-787-321	Sequence 321, App
377	121.5	5.5	2164	5	US-10-123-292-151	Sequence 151, App	450	120.5	5.5	5397	5	US-09-619-049-1472	Sequence 1472, Ap
378	121.5	5.5	2164	5	US-10-152-398-151	Sequence 151, App	451	120	5.4	544	5	US-10-703-032-98600	Sequence 98600, A
379	121.5	5.5	2164	5	US-10-123-907-151	Sequence 151, App	452	120	5.4	650	5	US-10-703-032-103871	Sequence 103871,
380	121.5	5.5	2164	5	US-10-147-512-151	Sequence 151, App	453	120	5.4	1823	3	US-09-620-312D-1012	Sequence 1012, Ap
381	121.5	5.5	2164	5	US-10-147-485-151	Sequence 151, App	454	120	5.4	1857	3	US-09-248-796A-5170	Sequence 5170, Ap
382	121.5	5.5	2164	5	US-10-124-814-151	Sequence 151, App	455	120	5.4	2669	5	US-09-983-531A-19	Sequence 19, Appl
383	121.5	5.5	2164	5	US-10-124-822-151	Sequence 151, App	456	120	5.4	3337	5	US-10-617-217A-169	Sequence 169, App
384	121.5	5.5	2164	5	US-10-219-074-227	Sequence 227, App	457	120	5.4	3457	3	US-09-759-451-869	Sequence 869, App
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386	121.5	5.5	2164	5	US-10-131-833A-151	Sequence 151, App	c 459	120	5.4	31422	3	US-09-914-286-2	Sequence 2, Appli
387	121.5	5.5	2164	5	US-10-218-849-227	Sequence 227, App	c 460	120	5.4	35100	5	US-09-782-378A-26	Sequence 26, Appl
388	121.5	5.5	2164	5	US-10-142-419-151	Sequence 151, App	461	120	5.4	145597	5	US-10-624-149A-2	Sequence 2, Appli
389	121.5	5.5	2164	5	US-10-216-168-227	Sequence 227, App	462	119.5	5.4	484	5	US-10-703-032-105467	Sequence 105467,
390	121.5	5.5	2164	5	US-10-152-375-151	Sequence 151, App	463	119.5	5.4	523	5	US-10-703-032-74309	Sequence 74309, A
391	121.5	5.5	2164	5	US-10-131-818A-151	Sequence 151, App	464	119.5	5.4	819	5	US-10-703-032-66014	Sequence 66014, A
392	121.5	5.5	2164	5	US-10-145-873-151	Sequence 151, App	465	119.5	5.4	990	3	US-09-248-796A-6039	Sequence 6039, Ap
393	121.5	5.5	2164	5	US-10-152-395-151	Sequence 151, App	466	119.5	5.4	1149	3	US-09-248-796A-4617	Sequence 4617, Ap
394	121.5	5.5	2164	5	US-10-131-822A-151	Sequence 151, App	c 467	119.5	5.4	1700	3	US-09-533-559-125	Sequence 125, App
395	121.5	5.5	2164	5	US-10-142-763-151	Sequence 151, App	c 468	119.5	5.4	1700	3	US-09-533-559-125	Sequence 125, App
396	121.5	5.5	2164	5	US-10-128-694A-151	Sequence 151, App	469	119.5	5.4	1804	3	US-10-029-517-17	Sequence 17, Appl
397	121.5	5.5	2164	5	US-10-123-213-151	Sequence 151, App	470	119.5	5.4	2017	5	US-10-703-032-17664	Sequence 17664, A
398	121.5	5.5	2164	5	US-10-123-909-151	Sequence 151, App	471	119.5	5.4	2747	3	US-09-620-312D-19	Sequence 19, Appl
399	121.5	5.5	2164	5	US-10-131-826A-151	Sequence 151, App	472	119.5	5.4	3108	5	US-10-210-120-59	Sequence 59, Appl
400	121.5	5.5	2164	5	US-10-147-513-151	Sequence 151, App	473	119.5	5.4	3110	5	US-09-023-655-1072	Sequence 1072, Ap
401	121.5	5.5	2164	5	US-10-121-043-151	Sequence 151, App	474	119.5	5.4	3132	2	US-08-224-482-3	Sequence 3, Appli
402	121.5	5.5	2164	5	US-10-139-980-151	Sequence 151, App	475	119.5	5.4	3132	3	US-09-205-921-1	Sequence 1, Appli
403	121.5	5.5	2901	3	US-09-487-558B-371	Sequence 371, App	476	119.5	5.4	3132	3	US-09-300-958A-32	Sequence 32, Appl
404	121.5	5.5	3401	5	US-10-451-467A-51	Sequence 51, Appl	477	119.5	5.4	3132	3	US-09-702-705-320	Sequence 320, App
405	121.5	5.5	4184	3	US-09-949-016-4495	Sequence 4495, Ap	478	119.5	5.4	3132	3	US-09-736-457-320	Sequence 320, App
406	121.5	5.5	5649	3	US-09-902-540-735	Sequence 735, App	479	119.5	5.4	3132	3	US-09-614-124B-320	Sequence 320, App
407	121.5	5.5	6210	3	US-10-212-962-1	Sequence 1, Appli	480	119.5	5.4	3132	3	US-09-671-325-320	Sequence 320, App
408	121.5	5.5	8201	4	US-09-958-617A-17	Sequence 17, Appl	481	119.5	5.4	3132	3	US-09-589-184-320	Sequence 320, App
409	121.5	5.5	12191	3	US-09-949-016-16237	Sequence 16237, A	482	119.5	5.4	3132	3	US-09-658-824-320	Sequence 320, App
410	121.5	5.5	85692	3	US-10-461-194B-1	Sequence 1, Appli	483	119.5	5.4	3132	3	US-10-017-754-320	Sequence 320, App
411	121	5.5	539	5	US-10-703-032-77283	Sequence 77283, A	484	119.5	5.4	3132	3	US-09-651-563-320	Sequence 320, App
412	121	5.5	551	5	US-10-703-032-77245	Sequence 77245, A	485	119.5	5.4	3132	4	US-09-519-642-320	Sequence 320, App
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414	121	5.5	576	5	US-10-703-032-77257	Sequence 77257, A	487	119.5	5.4	3132	3	US-09-880-107-3721	Sequence 3721, Ap
415	121	5.5	648	5	US-10-703-032-103019	Sequence 103019,	488	119.5	5.4	3137	3	US-09-949-016-5863	Sequence 5863, Ap
416	121	5.5	854	3	US-10-703-032-57737	Sequence 57737, A	489	119.5	5.4	4035	3	US-09-919-039-147	Sequence 147, App
417	121	5.5	1048	3	US-09-533-559-6603	Sequence 6603, Ap	490	119.5	5.4	6340	5	US-10-325-899-9210	Sequence 9210, Ap
418	121	5.5	1048	5	US-10-553-047-6603	Sequence 6603, Ap	491	119.5	5.4	6590	4	US-09-648-389A-4	Sequence 4, Appli
419	121	5.5	1119	5	US-10-333-951-8	Sequence 8, Appli	492	119.5	5.4	6940	4	US-09-880-107-1724	Sequence 1724, Ap
420	121	5.5	1176	5	US-10-703-032-8924	Sequence 8924, Ap	493	119.5	5.4	7825	3	US-09-949-016-17605	Sequence 17605, A
421	121	5.5	1859	3	US-08-894-818B-15	Sequence 15, Appl	494	119.5	5.4	8030	3	US-09-902-540-857	Sequence 857, App
422	121	5.5	1859	3	US-09-841-553-15	Sequence 15, Appl	495	119.5	5.4	57280	3	US-09-949-016-11796	Sequence 11796, A
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424	121	5.5	1985	2	US-08-298-687A-25	Sequence 25, Appl	497	119.5	5.4	57280	3	US-09-949-016-12844	Sequence 12844, A
425	121	5.5	1985	2	US-08-298-829-25	Sequence 25, Appl	498	119.5	5.4	57280	3	US-09-949-016-12846	Sequence 12846, A
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434	121	5.5	6713	3	US-09-949-016-642	Sequence 642, App	507	119.5	5.4	57280	3	US-09-949-016-14637	Sequence 14637, A
435	121	5.5	9700	3	US-09-698-295-9	Sequence 9, Appli	508	119.5	5.4	57280	3	US-09-949-016-14638	Sequence 14638, A
436	121	5.5	9700	5	US-10-754-342-9	Sequence 9, Appli	509	119.5	5.4	57280	3	US-09-949-016-14639	Sequence 14639, A
437	121	5.5	9865	3	US-09-698-295-2	Sequence 2, Appli	510	119.5	5.4	57280	3	US-09-949-016-14640	Sequence 14640, A
438	121	5.5	9865	3	US-10-754-342-2	Sequence 2, Appli	511	119.5	5.4	57280	3	US-09-949-016-12805	Sequence 12805, A
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441	120.5	5.5	807	5	US-10-703-032-102932	Sequence 102932,	514	119	5.4	692	5	US-10-703-032-25255	Sequence 25255, A
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519	119	5.4	1495	3	US-09-902-540-311	Sequence 311, App	592	118	5.3	2436	3	US-10-015-393A-242	Sequence 242, App
520	119	5.4	1495	3	US-09-902-540-6176	Sequence 6176, App	593	118	5.3	2436	3	US-10-011-833A-242	Sequence 242, App
521	119	5.4	1497	5	US-10-124-800B-29	Sequence 29, Appl	594	118	5.3	2436	3	US-10-006-041A-242	Sequence 242, App
522	119	5.4	2183	3	US-10-104-047-1064	Sequence 1064, App	595	118	5.3	2436	3	US-10-012-064A-242	Sequence 242, App
523	119	5.4	2404	5	US-09-983-531A-25	Sequence 25, Appl	596	118	5.3	2436	4	US-10-015-392B-242	Sequence 242, App
524	119	5.4	3531	5	US-10-455-719-163	Sequence 163, App	597	118	5.3	2436	5	US-10-011-795B-242	Sequence 242, App
525	119	5.4	3833	2	US-08-917-320-18	Sequence 18, Appl	598	118	5.3	2436	5	US-10-015-386A-242	Sequence 242, App
526	119	5.4	3833	8	PCT-US95-04611A-18	Sequence 18, Appl	599	118	5.3	2436	5	US-10-012-121A-242	Sequence 242, App
527	119	5.4	4506	5	US-10-124-800B-5	Sequence 5, Appl	600	118	5.3	2436	5	US-10-006-485A-242	Sequence 242, App
528	119	5.4	5931	3	US-08-783-774-1	Sequence 1, Appl	601	118	5.3	2436	5	US-10-006-746A-242	Sequence 242, App
529	119	5.4	5931	3	US-09-556-706B-1	Sequence 1, Appl	602	118	5.3	2436	5	US-10-012-752A-242	Sequence 242, App
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534	118.5	5.4	640	5	US-10-703-032-103753	Sequence 103753, A	607	118	5.3	2436	5	US-10-012-149A-242	Sequence 242, App
535	118.5	5.4	680	5	US-10-703-032-103753	Sequence 72804, A	608	118	5.3	2436	5	US-10-007-194A-242	Sequence 242, App
536	118.5	5.4	715	5	US-10-703-032-72804	Sequence 72863, A	609	118	5.3	2436	5	US-10-013-910A-242	Sequence 242, App
537	118.5	5.4	716	3	US-09-270-767-10097	Sequence 10097, A	610	118	5.3	2436	5	US-10-006-117A-242	Sequence 242, App
538	118.5	5.4	770	5	US-10-703-032-74145	Sequence 74145, A	611	118	5.3	2436	5	US-10-015-480A-242	Sequence 242, App
539	118.5	5.4	774	5	US-10-703-032-102966	Sequence 102966, A	612	118	5.3	2436	5	US-10-006-172A-242	Sequence 242, App
540	118.5	5.4	788	5	US-10-703-032-76129	Sequence 76129, A	613	118	5.3	2436	5	US-10-063-639A-99	Sequence 99, Appl
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543	118.5	5.4	1039	5	US-10-703-032-35528	Sequence 35528, A	616	118	5.3	2436	5	US-10-015-610A-242	Sequence 242, App
544	118.5	5.4	1109	5	US-10-703-032-2898	Sequence 2898, App	617	118	5.3	2436	5	US-10-180-998-309	Sequence 309, App
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546	118.5	5.4	2015	3	US-09-990-444-512	Sequence 512, App	619	118	5.3	2436	5	US-10-006-130A-242	Sequence 242, App
547	118.5	5.4	2015	3	US-09-997-333-512	Sequence 512, App	620	118	5.3	2436	5	US-10-063-638A-99	Sequence 99, Appl
548	118.5	5.4	2015	3	US-09-992-598-512	Sequence 512, App	621	118	5.3	2436	5	US-10-063-510-99	Sequence 99, Appl
549	118.5	5.4	2015	4	US-09-989-735-512	Sequence 512, App	622	118	5.3	2436	5	US-10-063-741-99	Sequence 99, Appl
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551	118.5	5.4	2015	5	US-09-997-514-512	Sequence 512, App	624	118	5.3	2436	5	US-10-174-576-309	Sequence 309, App
552	118.5	5.4	2015	5	US-09-989-728-512	Sequence 512, App	625	118	5.3	2436	5	US-10-174-581-309	Sequence 309, App
553	118.5	5.4	2015	5	US-09-997-349-512	Sequence 512, App	626	118	5.3	2436	5	US-10-006-867-99	Sequence 99, App
554	118.5	5.4	2015	5	US-09-997-653-512	Sequence 512, App	627	118	5.3	2436	5	US-10-063-659-99	Sequence 99, Appl
555	118.5	5.4	2015	5	US-09-989-293A-512	Sequence 512, App	628	118	5.3	2436	5	US-10-015-869A-242	Sequence 242, App
556	118.5	5.4	2015	5	US-09-989-732-512	Sequence 512, App	629	118	5.3	2436	5	US-10-063-742-99	Sequence 99, Appl
557	118.5	5.4	2015	5	US-09-990-441-512	Sequence 512, App	630	118	5.3	2436	5	US-10-063-703-99	Sequence 99, Appl
558	118.5	5.4	2015	5	US-09-989-328-512	Sequence 512, App	631	118	5.3	2436	5	US-10-063-709-99	Sequence 99, Appl
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560	118.5	5.4	2015	5	US-09-989-733-512	Sequence 512, App	633	118	5.3	2436	5	US-10-063-593-99	Sequence 99, Appl
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565	118.5	5.4	2015	5	US-09-997-641-512	Sequence 512, App	638	118	5.3	2436	5	US-10-207-916-309	Sequence 309, App
566	118.5	5.4	2015	5	US-09-997-384-512	Sequence 512, App	639	118	5.3	2436	5	US-10-063-647-99	Sequence 99, Appl
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569	118.5	5.4	2015	5	US-09-997-601-512	Sequence 512, App	642	118	5.3	2436	5	US-10-063-530-99	Sequence 99, Appl
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571	118.5	5.4	2097	3	US-09-620-312D-17	Sequence 17, Appl	644	118	5.3	2436	5	US-10-063-648-99	Sequence 99, Appl
572	118.5	5.4	20721	3	US-09-949-016-16257	Sequence 16257, A	645	118	5.3	2436	5	US-10-063-657-99	Sequence 99, Appl
573	118.5	5.4	39154	3	US-09-949-016-12384	Sequence 12384, A	646	118	5.3	2436	5	US-10-063-702-99	Sequence 99, Appl
574	118.5	5.4	39154	3	US-09-949-016-12801	Sequence 12801, A	647	118	5.3	2436	5	US-10-063-529-99	Sequence 99, Appl
575	118.5	5.4	39443	3	US-09-949-016-14326	Sequence 14326, A	648	118	5.3	2436	5	US-10-063-644-99	Sequence 99, Appl
576	118.5	5.4	39443	3	US-09-949-016-14327	Sequence 14327, A	649	118	5.3	2436	5	US-10-063-585-99	Sequence 99, Appl
577	118.5	5.4	53799	3	US-10-462-665A-3	Sequence 3, Appl	650	118	5.3	2436	5	US-10-063-591A-99	Sequence 99, Appl
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579	118.5	5.4	513509	5	US-09-754-853C-4	Sequence 4, Appl	652	118	5.3	2436	5	US-10-063-532-99	Sequence 99, Appl
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582	118	5.3	900	3	US-09-712-363-88	Sequence 88, Appl	655	118	5.3	2436	5	US-10-063-524-99	Sequence 99, Appl
583	118	5.3	1033	7	US-09-925-065A-718515	Sequence 718515, A	656	118	5.3	2436	5	US-10-972-317-99	Sequence 99, Appl
584	118	5.3	1086	3	US-10-101-464A-451	Sequence 451, App	657	118	5.3	2436	5	US-10-174-583-309	Sequence 309, App
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587	118	5.3	1417	5	US-10-703-032-2940	Sequence 2940, App	660	118	5.3	2436	5	US-10-063-523-99	Sequence 99, Appl
588	118	5.3	2436	3	US-10-012-231A-242	Sequence 242, App	661	118	5.3	2436	5	US-10-063-592A-99	Sequence 99, Appl
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590	118	5.3	2436	3	US-10-006-768A-242	Sequence 242, App	663	118	5.3	2436	5	US-10-063-598-99	Sequence 99, Appl

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665	118	5.3	2436	5	US-10-063-597-99	Sequence 99, Appl	738	117	5.3	5802	3	US-10-152-886-84	Sequence 84, Appl
666	118	5.3	2436	5	US-10-063-600-99	Sequence 99, Appl	c 739	117	5.3	33529	3	US-09-144-085-3	Sequence 3, Appl
667	118	5.3	2436	5	US-10-063-652A-99	Sequence 99, Appl	740	116.5	5.3	624	5	US-10-703-032-66040	Sequence 6040, A
668	118	5.3	2436	5	US-10-063-602-99	Sequence 99, Appl	741	116.5	5.3	650	5	US-10-703-032-103828	Sequence 103828,
669	118	5.3	2436	5	US-10-063-560-99	Sequence 99, Appl	742	116.5	5.3	698	5	US-10-703-032-2314	Sequence 2314, Ap
670	118	5.3	2436	5	US-10-063-517-99	Sequence 99, Appl	743	116.5	5.3	716	5	US-10-703-032-74061	Sequence 74061, A
671	118	5.3	2436	5	US-10-063-548-99	Sequence 99, Appl	744	116.5	5.3	909	3	US-09-248-796A-166	Sequence 166, App
672	118	5.3	2436	5	US-10-063-553-99	Sequence 99, Appl	745	116.5	5.3	1323	5	US-09-248-796A-6068	Sequence 6068, Ap
673	118	5.3	2436	5	US-10-063-653A-99	Sequence 99, Appl	746	116.5	5.3	1393	5	US-09-248-796A-7882	Sequence 7882, Ap
674	118	5.3	2436	5	US-10-063-595-99	Sequence 99, Appl	747	116.5	5.3	1434	3	US-10-228-063-48	Sequence 48, Appl
675	118	5.3	2436	5	US-10-063-587-99	Sequence 99, Appl	748	116.5	5.3	2037	5	US-10-455-719-17	Sequence 17, Appl
676	118	5.3	2436	5	US-10-063-586-99	Sequence 99, Appl	749	116.5	5.3	2138	5	US-09-270-767-13075	Sequence 13075, A
677	118	5.3	2436	5	US-10-187-745-309	Sequence 309, App	750	116.5	5.3	2199	3	US-09-619-049-200	Sequence 200, App
678	118	5.3	2616	3	US-09-220-132-6	Sequence 6, Appl	751	116.5	5.3	2636	5	US-10-104-047-1507	Sequence 1507, Ap
679	118	5.3	2616	5	US-10-007-255-5	Sequence 5, Appl	752	116.5	5.3	2937	3	US-10-231-913-17	Sequence 17, Appl
680	118	5.3	2668	5	US-10-021-698A-4063	Sequence 4063, Ap	753	116.5	5.3	2992	5	US-09-949-016-3897	Sequence 3897, Ap
681	118	5.3	4774	5	US-09-619-049-869	Sequence 869, App	754	116.5	5.3	6586	3	US-09-902-540-1245	Sequence 1245, Ap
682	118	5.3	5017	5	US-09-949-016-4956	Sequence 4956, Ap	c 755	116.5	5.3	23951	3	US-09-949-016-15639	Sequence 15639, A
c 683	118	5.3	10487	5	US-09-619-049-868	Sequence 868, App	756	116.5	5.3	112112	3	US-10-703-032-74123	Sequence 74123, A
684	118	5.3	255679	3	US-09-949-016-17189	Sequence 17189, A	757	116	5.2	556	5	US-10-703-032-74090	Sequence 74090, A
685	117.5	5.3	477	5	US-10-703-032-105246	Sequence 105246,	758	116	5.2	567	5	US-09-370-838-120	Sequence 120, App
686	117.5	5.3	523	5	US-10-703-032-2304	Sequence 2304, Ap	759	116	5.2	603	3	US-09-854-133-120	Sequence 120, App
687	117.5	5.3	601	3	US-09-949-016-180704	Sequence 180704,	760	116	5.2	603	3	US-10-703-032-74070	Sequence 74070, A
688	117.5	5.3	640	5	US-10-703-032-103761	Sequence 103761,	761	116	5.2	659	5	US-08-907-608-3	Sequence 3, Appl
689	117.5	5.3	784	5	US-10-703-032-55605	Sequence 55605, A	762	116	5.2	1155	3	US-08-907-608-5	Sequence 5, Appl
690	117.5	5.3	1191	3	US-09-533-559-5700	Sequence 5700, Ap	763	116	5.2	1155	3	US-09-354-231B-5	Sequence 5, Appl
691	117.5	5.3	1191	5	US-10-653-047-5700	Sequence 5700, Ap	764	116	5.2	1155	3	US-09-128-602B-5	Sequence 5, Appl
692	117.5	5.3	1432	3	US-09-668-097A-9	Sequence 9, Appl	765	116	5.2	1155	3	US-08-482-287-3	Sequence 3, Appl
693	117.5	5.3	1824	3	US-09-248-796A-3178	Sequence 3178, Ap	766	116	5.2	1155	3	US-09-482-287-5	Sequence 5, Appl
c 694	117.5	5.3	2093	3	US-10-104-047-1666	Sequence 1666, Ap	767	116	5.2	1155	3	US-09-966-888-3	Sequence 3, Appl
695	117.5	5.3	2589	2	US-08-325-267A-3	Sequence 3, Appl	768	116	5.2	1155	3	US-09-966-888-5	Sequence 5, Appl
696	117.5	5.3	2685	3	US-08-362-525-21	Sequence 21, Appl	769	116	5.2	1155	3	US-09-995-297-5	Sequence 5, Appl
697	117.5	5.3	2855	2	US-08-776-597A-1	Sequence 1, Appl	770	116	5.2	1155	4	US-09-771-904A-5	Sequence 5, Appl
698	117.5	5.3	2855	2	US-08-693-228-1	Sequence 1, Appl	771	116	5.2	1155	5	US-08-572-027C-5	Sequence 511, App
699	117.5	5.3	4614	2	US-08-325-267A-1	Sequence 1, Appl	772	116	5.2	1155	5	US-10-703-032-511	Sequence 17223, A
700	117.5	5.3	4614	3	US-09-487-558B-103	Sequence 103, App	773	116	5.2	1437	5	US-10-703-032-17223	Sequence 385, App
701	117.5	5.3	4614	5	US-09-936-823A-18	Sequence 18, Appl	774	116	5.2	1875	3	US-09-614-221A-385	Sequence 2, Appl
c 702	117.5	5.3	4824	3	US-09-902-540-9627	Sequence 9627, Ap	775	116	5.2	1977	3	US-08-894-818B-2	Sequence 6, Appl
703	117.5	5.3	5864	5	US-10-324-035-16	Sequence 16, Appl	776	116	5.2	1977	3	US-08-894-818B-6	Sequence 11, Appl
704	117.5	5.3	9046	2	US-08-227-536-1	Sequence 1, Appl	777	116	5.2	1977	3	US-09-445-472-11	Sequence 11, Appl
705	117.5	5.3	9046	8	PCT-US95-04682-1	Sequence 1, Appl	778	116	5.2	1977	3	US-10-090-624-11	Sequence 11, Appl
c 706	117.5	5.3	16187	3	US-09-902-540-1093	Sequence 1093, App	779	116	5.2	1977	3	US-09-841-553-2	Sequence 2, Appl
707	117.5	5.3	26289	3	US-09-902-540-1210	Sequence 1210, Ap	780	116	5.2	1977	3	US-09-841-553-6	Sequence 6, Appl
c 708	117.5	5.3	70770	3	US-09-949-016-16938	Sequence 16938, A	781	116	5.2	1977	5	US-10-888-588-11	Sequence 11, Appl
709	117	5.3	764	5	US-10-703-032-103029	Sequence 103029,	782	116	5.2	1977	3	US-09-310-685-10	Sequence 10, Appl
710	117	5.3	882	3	US-08-818-112-138	Sequence 138, App	783	116	5.2	2883	3	US-08-927-219-3	Sequence 3, Appl
711	117	5.3	882	3	US-08-818-111-133	Sequence 138, App	784	116	5.2	3238	3	US-09-993-777-1	Sequence 1, Appl
712	117	5.3	882	3	US-09-056-556-138	Sequence 138, App	785	116	5.2	13473	4	US-09-994-064-1	Sequence 1, Appl
713	117	5.3	882	3	US-09-072-596-133	Sequence 133, App	786	116	5.2	13473	5	US-10-836-383-1	Sequence 1, Appl
714	117	5.3	882	3	US-09-072-967-138	Sequence 138, App	787	116	5.2	13473	5	PCT-US96-03916-1	Sequence 1, Appl
715	117	5.3	882	3	US-10-193-002-133	Sequence 133, App	788	116	5.2	13473	8	PCT-US96-03916-59	Sequence 59, Appl
716	117	5.3	882	3	US-10-084-843-138	Sequence 138, App	789	116	5.2	18912	3	US-09-993-777-59	Sequence 59, Appl
717	117	5.3	882	5	US-11-082-005-133	Sequence 133, App	790	116	5.2	18913	4	US-09-994-064-59	Sequence 59, Appl
718	117	5.3	882	5	US-11-028-898-138	Sequence 138, App	791	116	5.2	18913	5	US-10-836-383-59	Sequence 59, Appl
c 719	117	5.3	1033	7	US-09-925-065A-718514	Sequence 718514,	792	116	5.2	18913	5	US-10-455-719-19	Sequence 19, Appl
720	117	5.3	1077	5	US-10-703-032-35462	Sequence 35462, A	c 793	116	5.2	37968	5	US-10-703-032-74161	Sequence 74161, A
721	117	5.3	1104	5	US-10-455-719-111	Sequence 111, App	794	115.5	5.2	486	5	US-10-703-032-102336	Sequence 102336,
722	117	5.3	1155	3	US-09-354-231B-7	Sequence 7, Appl	795	115.5	5.2	486	5	US-10-703-032-72774	Sequence 72774, A
723	117	5.3	1155	3	US-09-128-602B-7	Sequence 7, Appl	796	115.5	5.2	490	5	US-10-703-032-97704	Sequence 97704, A
724	117	5.3	1155	3	US-09-995-297-7	Sequence 7, Appl	797	115.5	5.2	568	5	US-10-703-032-77268	Sequence 77268, A
725	117	5.3	1155	4	US-09-771-904A-7	Sequence 7, Appl	798	115.5	5.2	631	5	US-10-703-032-19258	Sequence 19258, A
726	117	5.3	1155	5	US-08-572-027C-7	Sequence 7, Appl	799	115.5	5.2	777	5	US-09-925-065A-71694	Sequence 71694, A
727	117	5.3	1513	2	US-08-314-309A-2	Sequence 2, Appl	c 800	115.5	5.2	1206	7	US-09-925-065A-71695	Sequence 71695, A
728	117	5.3	1546	2	US-08-314-309A-3	Sequence 3, Appl	c 801	115.5	5.2	1206	7	US-10-703-032-28153	Sequence 28153, A
729	117	5.3	1842	3	US-09-170-496D-99	Sequence 99, Appl	802	115.5	5.2	1362	5	US-09-602-787A-211	Sequence 211, App
730	117	5.3	1842	3	US-09-170-496D-215	Sequence 215, App	803	115.5	5.2	1752	3	US-08-468-812-3	Sequence 3, Appl
731	117	5.3	1839	3	US-09-016-434-1112	Sequence 1112, Ap	804	115.5	5.2	1864	2	US-08-590-563-3	Sequence 3, Appl
c 732	117	5.3	2085	5	US-10-703-032-2199	Sequence 2199, Ap	805	115.5	5.2	1864	3	US-09-770-621-3	Sequence 3, Appl
c 733	117	5.3	2479	5	US-10-108-260A-1966	Sequence 1966, Ap	806	115.5	5.2	1864	3	US-09-235-832-3	Sequence 3, Appl
734	117	5.3	2934	3	US-09-248-796A-1476	Sequence 1476, Ap	807	115.5	5.2	1864	3	US-10-195-144-32	Sequence 32, Appl
735	117	5.3	3239	3	US-08-927-219-5	Sequence 5, Appl	808	115.5	5.2	2124	5	US-10-021-698A-2140	Sequence 2140, Ap
736	117	5.3	3808	3	US-09-949-016-1217	Sequence 1217, Ap	809	115.5	5.2	2181	5		

810	115.5	5.2	2235	5	US-09-938-842A-2683	Sequence 2683, Ap	883	114	5.2	2088	3	US-09-310-685-9	Sequence 9, Appli
811	115.5	5.2	2582	4	US-10-094-749-1141	Sequence 1141, Ap	884	114	5.2	2113	3	US-09-533-559-297	Sequence 297, App
812	115.5	5.2	3016	5	US-10-231-913-15	Sequence 15, Appl	885	114	5.2	2113	5	US-10-653-047-297	Sequence 297, App
c 813	115.5	5.2	3337	2	US-08-072-610-1	Sequence 1, Appli	886	114	5.2	2262	5	US-10-455-719-142	Sequence 142, App
c 814	115.5	5.2	3337	2	US-08-719-822B-1	Sequence 1, Appli	887	114	5.2	2508	3	US-08-981-392-1	Sequence 1, Appli
c 815	115.5	5.2	3337	3	US-09-092-45C-1	Sequence 1, Appli	888	114	5.2	2508	3	US-09-908-322-1	Sequence 1, Appli
c 816	115.5	5.2	3337	3	US-08-719-821C-1	Sequence 1, Appli	889	114	5.2	2508	5	US-09-783-931C-1	Sequence 1, Appli
c 817	115.5	5.2	3343	3	US-10-029-517-102	Sequence 102, App	890	114	5.2	2517	2	US-07-906-930B-1	Sequence 1, Appli
c 818	115.5	5.2	12311	3	US-08-750-717-1	Sequence 1, Appli	891	114	5.2	2643	3	US-09-949-002-213	Sequence 213, App
c 819	115.5	5.2	17083	5	US-10-475-970-4	Sequence 4, Appli	892	114	5.2	2883	3	US-08-981-392-3	Sequence 3, Appli
c 820	115.5	5.2	17580	3	US-09-949-016-16055	Sequence 16055, A	893	114	5.2	2883	3	US-09-908-322-3	Sequence 3, Appli
c 821	115.5	5.2	36519	3	US-08-923-137-2	Sequence 2, Appli	894	114	5.2	2883	5	US-09-783-931C-3	Sequence 3, Appli
c 822	115.5	5.2	39154	3	US-09-949-016-12384	Sequence 12384, A	895	114	5.2	3183	5	US-10-108-260A-445	Sequence 445, App
c 823	115.5	5.2	39154	3	US-09-949-016-12384	Sequence 12384, A	896	114	5.2	3238	3	US-08-927-219-1	Sequence 1, Appli
c 824	115.5	5.2	39443	3	US-09-949-016-14326	Sequence 14326, A	897	114	5.2	7541	3	US-09-637-048C-4	Sequence 4, Appli
c 825	115.5	5.2	39443	3	US-09-949-016-14327	Sequence 14327, A	898	114	5.2	7541	3	US-10-435-835-4	Sequence 4, Appli
c 826	115.5	5.2	49377	2	US-08-764-233A-1	Sequence 1, Appli	899	114	5.2	8563	3	US-09-902-540-3318	Sequence 3318, Ap
c 827	115.5	5.2	225724	5	US-10-021-698A-711	Sequence 711, App	900	114	5.2	10838	5	US-11-251-466-31	Sequence 31, Appl
c 828	115.5	5.2	271990	5	US-10-195-144-87	Sequence 87, Appl	901	114	5.2	10838	5	US-11-024-545-57	Sequence 57, Appl
c 829	115.5	5.2	432	5	US-10-703-032-98768	Sequence 98768, A	c 902	114	5.2	15351	3	US-09-902-540-1154	Sequence 1154, Ap
c 830	115.5	5.2	486	5	US-10-703-032-77237	Sequence 77237, A	c 903	114	5.2	53336	3	US-09-949-016-12500	Sequence 12500, A
c 831	115.5	5.2	509	5	US-10-703-032-103636	Sequence 103636, A	c 904	114	5.2	53337	3	US-09-949-016-16092	Sequence 16092, A
c 832	115.5	5.2	568	5	US-10-703-032-77069	Sequence 77069, A	c 905	114	5.2	55216	3	US-09-716-865-23	Sequence 23, Appl
c 833	115.5	5.2	591	5	US-10-703-032-74064	Sequence 74064, A	c 906	113.5	5.1	454	5	US-10-703-032-105329	Sequence 105329, A
c 834	115.5	5.2	639	5	US-10-703-032-77559	Sequence 77559, A	c 907	113.5	5.1	457	5	US-10-703-032-103630	Sequence 103630, A
c 835	115.5	5.2	742	5	US-10-703-032-57852	Sequence 57852, A	c 908	113.5	5.1	459	5	US-10-703-032-98240	Sequence 98240, A
c 836	115.5	5.2	775	5	US-10-703-032-57689	Sequence 57689, A	c 909	113.5	5.1	600	5	US-10-703-032-25137	Sequence 25137, A
c 837	115.5	5.2	804	5	US-10-703-032-57696	Sequence 57696, A	c 910	113.5	5.1	615	5	US-10-703-032-62622	Sequence 62622, A
c 838	115.5	5.2	860	5	US-10-666-642-836	Sequence 836, App	c 911	113.5	5.1	637	5	US-10-703-032-72943	Sequence 72943, A
c 839	115.5	5.2	1197	3	US-09-252-991A-920	Sequence 920, App	c 912	113.5	5.1	645	5	US-09-533-559-5595	Sequence 5595, Ap
c 840	115.5	5.2	1533	3	US-09-248-796A-4410	Sequence 4410, Ap	c 913	113.5	5.1	645	5	US-10-653-037-65985	Sequence 65985, Ap
c 841	115.5	5.2	1608	3	US-09-292-225-20	Sequence 20, Appl	c 914	113.5	5.1	838	5	US-10-703-032-52278	Sequence 52278, A
c 842	115.5	5.2	1608	3	US-09-292-225-22	Sequence 22, Appl	c 915	113.5	5.1	1291	3	US-08-997-897-1	Sequence 1, Appli
c 843	115.5	5.2	1608	3	US-09-662-293-20	Sequence 20, Appl	c 916	113.5	5.1	1291	3	US-09-156-836B-1	Sequence 1, Appli
c 844	115.5	5.2	1608	3	US-09-662-293-22	Sequence 22, Appl	c 917	113.5	5.1	1380	3	US-09-620-312D-59	Sequence 59, Appl
c 845	115.5	5.2	1644	3	US-10-703-032-8673	Sequence 8673, Ap	c 918	113.5	5.1	2328	3	US-09-252-991A-5729	Sequence 5729, Ap
c 846	115.5	5.2	1662	3	US-09-949-016-2911	Sequence 2911, Ap	c 919	113.5	5.1	4015	5	US-10-426-776-45	Sequence 45, Appl
c 847	115.5	5.2	1665	3	US-09-292-225-17	Sequence 17, Appl	c 920	113.5	5.1	4230	3	US-09-252-991A-5711	Sequence 5711, Ap
c 848	115.5	5.2	1665	3	US-09-292-225-19	Sequence 19, Appl	c 921	113.5	5.1	4941	3	US-09-252-991A-5741	Sequence 5741, Ap
c 849	115.5	5.2	1665	5	US-09-662-293-17	Sequence 17, Appl	c 922	113.5	5.1	8147	3	US-09-514-247A-9	Sequence 9, Appli
c 850	115.5	5.2	1665	5	US-09-662-293-19	Sequence 19, Appl	c 923	113.5	5.1	8147	5	US-10-109-886-9	Sequence 9, Appli
c 851	115.5	5.2	1752	3	US-09-292-225-14	Sequence 14, Appl	c 924	113.5	5.1	42000	5	US-10-159-257C-1	Sequence 1, Appli
c 852	115.5	5.2	1752	3	US-09-292-225-16	Sequence 16, Appl	c 925	113.5	5.1	63158	3	US-10-292-198-1	Sequence 1, Appli
c 853	115.5	5.2	1752	5	US-09-662-293-14	Sequence 14, Appl	c 926	113.5	5.1	77536	3	US-09-410-551B-1	Sequence 1, Appli
c 854	115.5	5.2	1752	5	US-09-662-293-16	Sequence 16, Appl	c 927	113.5	5.1	77536	3	US-09-940-316B-1	Sequence 1, Appli
c 855	115.5	5.2	2262	3	US-09-252-991A-1041	Sequence 1041, Ap	c 928	113	5.1	557	5	US-10-703-032-68218	Sequence 68218, A
c 856	115.5	5.2	2288	3	US-09-023-655-1151	Sequence 1151, Ap	c 929	113	5.1	571	5	US-10-703-032-25053	Sequence 25053, A
c 857	115.5	5.2	2622	3	US-10-132-350-3	Sequence 3, Appli	c 930	113	5.1	615	3	US-09-248-796A-7881	Sequence 7881, Ap
c 858	115.5	5.2	2912	3	US-10-132-350-1	Sequence 1, Appli	c 931	113	5.1	648	3	US-09-248-796A-2888	Sequence 2888, Ap
c 859	115.5	5.2	6040	3	US-09-949-016-14653	Sequence 14653, A	c 932	113	5.1	722	5	US-10-703-032-66256	Sequence 66256, A
c 860	115.5	5.2	6320	3	US-09-949-016-14122	Sequence 14122, A	c 933	113	5.1	769	5	US-10-703-032-76037	Sequence 76037, A
c 861	115.5	5.2	7202	3	US-09-949-016-14385	Sequence 14385, A	c 934	113	5.1	1107	2	US-08-991-300-1	Sequence 1, Appli
c 862	114.5	5.2	630	5	US-10-703-032-72851	Sequence 72851, A	c 935	113	5.1	1129	5	US-10-703-032-14216	Sequence 14216, A
c 863	114.5	5.2	763	5	US-10-703-032-103024	Sequence 103024, A	c 936	113	5.1	1226	5	US-10-703-032-6475	Sequence 6475, Ap
c 864	114.5	5.2	777	5	US-10-703-032-15782	Sequence 15782, A	c 937	113	5.1	1347	3	US-09-350-756-6	Sequence 6, Appli
c 865	114.5	5.2	1194	5	US-10-703-032-35822	Sequence 35822, A	c 938	113	5.1	1386	3	US-09-248-796A-3124	Sequence 3124, Ap
c 866	114.5	5.2	1206	7	US-09-925-065A-71696	Sequence 71696, A	c 939	113	5.1	1492	5	US-10-703-032-29214	Sequence 29214, A
c 867	114.5	5.2	1245	5	US-10-703-032-20888	Sequence 20888, A	c 940	113	5.1	1503	3	US-09-797-039-3	Sequence 3, Appli
c 868	114.5	5.2	1378	5	US-10-703-032-28186	Sequence 28186, A	c 941	113	5.1	1503	5	US-10-170-789-3	Sequence 3, Appli
c 869	114.5	5.2	1575	3	US-09-605-703B-1467	Sequence 1467, Ap	c 942	113	5.1	1721	3	US-10-029-517-3	Sequence 3, Appli
c 870	114.5	5.2	1839	3	US-09-248-796A-3174	Sequence 3174, Ap	c 943	113	5.1	1721	3	US-10-171-311-155	Sequence 155, App
c 871	114.5	5.2	2489	3	US-09-141-047-7	Sequence 7, Appli	c 944	113	5.1	1721	5	US-10-342-887-775	Sequence 775, App
c 872	114.5	5.2	2943	5	US-10-475-970-1	Sequence 1, Appli	c 945	113	5.1	1840	3	US-09-016-434-1367	Sequence 1367, App
c 873	114.5	5.2	4375	5	US-10-475-970-27	Sequence 27, Appl	c 946	113	5.1	2070	3	US-09-949-016-5494	Sequence 5494, Ap
c 874	114.5	5.2	4375	5	US-10-475-970-27	Sequence 27, Appl	c 947	113	5.1	2070	3	US-09-949-016-5495	Sequence 5495, Ap
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c 878	114	5.2	636	5	US-10-703-032-74119	Sequence 74119, A	c 951	113	5.1	2179	7	US-09-925-065A-683197	Sequence 683197, A
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c 880	114	5.2	763	5	US-10-703-032-57846	Sequence 57846, A	c 953	113	5.1	2297	3	US-09-797-039-1	Sequence 1, Appli
c 881	114	5.2	863	5	US-10-703-032-24597	Sequence 24597, A	c 954	113	5.1	2297	5	US-10-170-789-1	Sequence 1, Appli
c 882	114	5.2	951	3	US-09-248-796A-12352	Sequence 12352, A	c 955	113	5.1	2409	3	US-09-533-559-282	Sequence 282, App
c 883	114	5.2	1007	5	US-10-703-032-2313	Sequence 2313, Ap							

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c 958	113	5.1	2780	5	US-10-653-047-44	Sequence 44, Appl	c1031	111.5	5.0	392	5	US-09-702-705-1217	Sequence 1217, Ap
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995	112.5	5.1	8194	5	US-11-024-545-56	Sequence 56, Appl	1068	111.5	5.0	1281	5	US-09-997-641-415	Sequence 415, App
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1021	112	5.1	3834	3	US-09-614-221A-353	Sequence 353, App	1094	111.5	5.0	1551	3	US-09-248-796A-5414	Sequence 5414, App
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1024	112	5.1	6407	2	US-08-599-654-7	Sequence 7, Appli	1097	111.5	5.0	1809	3	US-10-015-389A-71	Sequence 71, Appl
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1105	111.5	5.0	1809	5	US-10-011-795B-71	Sequence 71, Appl	1178	111	5.0	6231	3	US-09-854-856-45	Sequence 45, Appl
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1108	111.5	5.0	1809	5	US-10-006-485A-71	Sequence 71, Appl	1181	111	5.0	6279	3	US-10-010-720-9	Sequence 29, Appl
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1115	111.5	5.0	1809	5	US-10-012-149A-71	Sequence 71, Appl	1188	111	5.0	6474	3	US-09-854-856-51	Sequence 51, Appl
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1121	111.5	5.0	1809	5	US-10-015-395A-71	Sequence 71, Appl	1194	111	5.0	6606	3	US-09-854-856-23	Sequence 23, Appl
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1135	111.5	5.0	3057	3	US-09-949-016-3892	Sequence 3892, Ap	1208	111	5.0	7149	3	US-09-854-856-1	Sequence 1, Appl
1136	111.5	5.0	3265	3	US-09-832-129-13	Sequence 13, Appl	1209	111	5.0	7149	3	US-10-010-720-1	Sequence 1, Appl
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1138	111.5	5.0	5956	5	US-10-342-887-5	Sequence 5, Appl	1211	111	5.0	8442	3	US-09-272-032-6	Sequence 6, Appl
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1145	111	5.0	704	5	US-10-703-032-1887	Sequence 1887, Ap	1218	110.5	5.0	521	5	US-10-703-032-96886	Sequence 96886, A
1146	111	5.0	813	3	US-09-134-000C-148	Sequence 148, App	1219	110.5	5.0	688	5	US-08-998-416-915	Sequence 915, App
1147	111	5.0	897	5	US-10-703-032-3982	Sequence 3982, Ap	1220	110.5	5.0	738	5	US-10-703-032-58771	Sequence 58771, A
1148	111	5.0	1017	3	US-09-614-212A-127	Sequence 127, App	1221	110.5	5.0	843	5	US-09-938-842A-1864	Sequence 1864, Ap
1149	111	5.0	1305	5	US-10-455-719-85	Sequence 85, Appl	1222	110.5	5.0	843	5	US-10-703-032-102957	Sequence 102957, A
1150	111	5.0	1326	3	US-09-248-796A-1833	Sequence 1833, Ap	1223	110.5	5.0	985	5	US-10-703-032-20351	Sequence 20351, A
1151	111	5.0	1430	2	US-08-276-452A-25	Sequence 25, Appl	1224	110.5	5.0	1043	5	US-10-703-032-15754	Sequence 15754, A
1152	111	5.0	1430	2	US-08-798-744-25	Sequence 25, Appl	1225	110.5	5.0	1838	5	US-09-938-842A-4653	Sequence 4653, Ap
1153	111	5.0	1461	3	US-09-716-865-5	Sequence 5, Appl	1226	110.5	5.0	2814	5	US-10-455-719-116	Sequence 116, App
1154	111	5.0	1722	5	US-10-703-032-8717	Sequence 8717, Ap	1227	110.5	5.0	2839	8	PCT-US94-07297-38	Sequence 38, Appl
1155	111	5.0	1965	3	US-09-178-252-26	Sequence 26, Appl	1228	110.5	5.0	3000	5	US-10-455-719-26	Sequence 26, Appl
1156	111	5.0	1965	3	US-09-826-660-26	Sequence 26, Appl	1229	110.5	5.0	4914	5	US-10-021-698A-2830	Sequence 2830, Ap
1157	111	5.0	2691	3	US-09-605-703B-2759	Sequence 2759, Ap	1230	110.5	5.0	23847	3	US-09-902-540-11777	Sequence 1177, Ap
1158	111	5.0	3465	3	US-09-023-655-1136	Sequence 1136, Ap	1231	110.5	5.0	28783	3	US-09-902-540-1242	Sequence 1242, Ap
1159	111	5.0	3687	5	US-09-917-383-2	Sequence 2, Appl	1232	110	5.0	488	5	US-10-703-032-98671	Sequence 98671, A
1160	111	5.0	3831	2	US-08-993-228-18	Sequence 18, Appl	1233	110	5.0	621	5	US-10-703-032-2894	Sequence 2894, Ap
1161	111	5.0	5736	3	US-09-854-856-63	Sequence 63, Appl	1234	110	5.0	1095	5	US-10-332-231A-13	Sequence 13, Appl
1162	111	5.0	5736	3	US-10-010-720-63	Sequence 63, Appl	1235	110	5.0	1110	3	US-09-342-143-1	Sequence 1, Appl
1163	111	5.0	5785	5	US-10-021-698A-3606	Sequence 3606, Ap	1236	110	5.0	1110	3	US-09-924-439-1	Sequence 1, Appl
1164	111	5.0	5820	3	US-09-854-856-47	Sequence 47, Appl	1237	110	5.0	1110	3	US-09-999-170-3	Sequence 3, Appl
1165	111	5.0	5820	3	US-10-010-720-47	Sequence 47, Appl	1238	110	5.0	1155	3	US-08-907-608-1	Sequence 1, Appl
1166	111	5.0	5916	3	US-09-854-856-31	Sequence 31, Appl	1239	110	5.0	1155	3	US-09-354-231B-1	Sequence 1, Appl
1167	111	5.0	5916	3	US-10-010-720-31	Sequence 31, Appl	1240	110	5.0	1155	3	US-09-128-602B-1	Sequence 1, Appl
1168	111	5.0	6000	3	US-09-854-856-15	Sequence 15, Appl	1241	110	5.0	1155	3	US-09-482-287-1	Sequence 1, Appl
1169	111	5.0	6000	3	US-10-010-720-15	Sequence 15, Appl	1242	110	5.0	1155	3	US-09-966-888-1	Sequence 1, Appl
1170	111	5.0	6015	3	US-09-854-856-57	Sequence 57, Appl	1243	110	5.0	1155	4	US-09-995-297-1	Sequence 1, Appl
1171	111	5.0	6015	3	US-10-010-720-57	Sequence 57, Appl	1244	110	5.0	1155	4	US-09-771-904A-1	Sequence 1, Appl
1172	111	5.0	6099	3	US-09-854-856-41	Sequence 41, Appl	1245	110	5.0	1155	5	US-08-572-027C-1	Sequence 1, Appl
1173	111	5.0	6099	3	US-10-010-720-41	Sequence 41, Appl	1246	110	5.0	1170	5	US-10-332-231A-5	Sequence 5, Appl
1174	111	5.0	6147	3	US-09-854-856-61	Sequence 61, Appl	1247	110	5.0	1170	5	US-10-332-231A-32	Sequence 32, Appl

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1249	110	5.0	1254	5	US-10-703-032-4095	Sequence 4095, Ap	1322	109	4.9	2163	5	US-10-147-485-127	Sequence 127, App
1250	110	5.0	1269	2	US-08-265-429A-4	Sequence 4, Appli	1323	109	4.9	2163	5	US-10-124-814-127	Sequence 127, App
1251	110	5.0	1269	8	PCT-US95-09069-4	Sequence 4, Appli	1324	109	4.9	2163	5	US-10-124-822-127	Sequence 127, App
1252	110	5.0	1332	2	US-08-481-814A-3	Sequence 3, Appli	1325	109	4.9	2163	5	US-10-131-833A-127	Sequence 127, App
1253	110	5.0	1336	3	US-09-949-016-3800	Sequence 3800, Ap	1326	109	4.9	2163	5	US-10-142-419-127	Sequence 127, App
1254	110	5.0	1489	3	US-08-836-582-1	Sequence 1, Appli	1327	109	4.9	2163	5	US-10-152-375-127	Sequence 127, App
1255	110	5.0	1489	3	US-09-265-566-1	Sequence 1, Appli	1328	109	4.9	2163	5	US-10-131-818A-127	Sequence 127, App
1256	110	5.0	1489	3	US-09-242-737-3	Sequence 3, Appli	1329	109	4.9	2163	5	US-10-145-873-127	Sequence 127, App
1257	110	5.0	1489	3	US-09-023-655-871	Sequence 871, App	1330	109	4.9	2163	5	US-10-152-395-127	Sequence 127, App
1258	110	5.0	1746	5	US-10-225-066A-271	Sequence 271, App	1331	109	4.9	2163	5	US-10-131-822A-127	Sequence 127, App
1259	110	5.0	2613	5	US-09-252-691C-485	Sequence 485, App	1332	109	4.9	2163	5	US-10-142-763-127	Sequence 127, App
1260	110	5.0	2910	3	US-09-949-016-4412	Sequence 4412, App	1333	109	4.9	2163	5	US-10-128-694A-127	Sequence 127, App
1261	110	5.0	2939	2	US-07-906-930E-3	Sequence 3, Appli	1334	109	4.9	2163	5	US-10-123-213-127	Sequence 127, App
1262	110	5.0	3404	2	US-08-265-429A-1	Sequence 1, Appli	1335	109	4.9	2163	5	US-10-123-909-127	Sequence 127, App
1263	110	5.0	3404	8	PCT-US95-09069-1	Sequence 1, Appli	1336	109	4.9	2163	5	US-10-131-826A-127	Sequence 127, App
1264	110	5.0	6158	3	US-09-799-451-897	Sequence 897, App	1337	109	4.9	2163	5	US-10-147-513-127	Sequence 127, App
1265	110	5.0	6429	3	US-10-144-198-3	Sequence 3, Appli	1338	109	4.9	2163	5	US-10-121-043-127	Sequence 127, App
1266	110	5.0	6726	3	US-10-144-198-1	Sequence 1, Appli	1339	109	4.9	2163	5	US-10-139-980-127	Sequence 127, App
1267	110	5.0	11907	3	US-08-061-376-4	Sequence 4, Appli	1340	109	4.9	2446	3	US-09-345-236B-1	Sequence 1, Appli
1268	110	5.0	14101	3	US-09-902-540-1080	Sequence 1080, Ap	c1341	109	4.9	2446	3	US-09-925-065A-695249	Sequence 4, Appli
1269	110	5.0	14255	2	US-08-320-559-1	Sequence 1, Appli	1342	109	4.9	2566	7	US-09-925-065A-695250	Sequence 695250,
1270	110	5.0	14255	2	US-08-327-392-1	Sequence 1, Appli	1343	109	4.9	2566	7	US-09-925-065A-695251	Sequence 695251,
1271	110	5.0	14255	2	US-08-306-691B-55	Sequence 55, Appli	1344	109	4.9	3232	4	US-10-094-749-1013	Sequence 1013, Ap
1272	110	5.0	14255	3	US-08-545-860D-1	Sequence 1, Appli	1345	109	4.9	3232	4	US-09-620-312D-1020	Sequence 1020, Ap
1273	110	5.0	14255	8	PCT-US94-04496-1	Sequence 1, Appli	1346	109	4.9	3303	3	US-09-373-272-2	Sequence 2, Appli
1274	109.5	5.0	565	5	US-10-703-032-68298	Sequence 68298, A	1347	109	4.9	3303	3	US-10-455-719-152	Sequence 152, App
c1275	109.5	5.0	601	3	US-09-949-016-165983	Sequence 165983,	1348	109	4.9	4044	5	US-10-455-719-6	Sequence 6, Appli
1276	109.5	5.0	652	5	US-10-703-032-72773	Sequence 72773, A	1349	109	4.9	4723	5	US-09-902-540-1136	Sequence 1136, Ap
1277	109.5	5.0	1209	3	US-09-533-559-6340	Sequence 6340, Ap	c1350	109	4.9	16047	3	US-09-949-016-14319	Sequence 14319, A
1278	109.5	5.0	1209	5	US-10-653-047-6340	Sequence 6340, Ap	c1351	109	4.9	31391	3	US-09-949-016-12565	Sequence 12565, A
1279	109.5	5.0	1426	3	US-09-133-962A-3	Sequence 3, Appli	1352	109	4.9	136058	3	US-09-949-016-17064	Sequence 17064, A
1280	109.5	5.0	1426	3	US-09-697-379-3	Sequence 3, Appli	1353	109	4.9	136480	3	US-09-270-767-1305	Sequence 1305, Ap
1281	109.5	5.0	1426	3	US-10-116-212A-3	Sequence 3, Appli	1354	108.5	4.9	532	3	US-09-270-767-16587	Sequence 16587, A
1282	109.5	5.0	1426	5	US-10-108-795A-3	Sequence 3, Appli	1355	108.5	4.9	532	3	US-10-703-032-98772	Sequence 98772, A
1283	109.5	5.0	1452	3	US-10-061-943A-5	Sequence 5, Appli	1356	108.5	4.9	566	5	US-10-703-032-53315	Sequence 53315, A
1284	109.5	5.0	1452	5	US-09-944-049-13	Sequence 13, Appli	1357	108.5	4.9	738	5	US-10-703-032-58718	Sequence 58718, A
1285	109.5	5.0	1464	5	US-09-643-579A-1	Sequence 1, Appli	1358	108.5	4.9	790	5	US-09-925-065A-208	Sequence 208, App
1286	109.5	5.0	1539	5	US-10-703-032-2245	Sequence 2245, Ap	c1359	108.5	4.9	906	5	US-10-666-642-838	Sequence 838, App
1287	109.5	5.0	1671	3	US-09-248-796A-8235	Sequence 8235, Ap	c1360	108.5	4.9	970	2	US-08-148-910-3	Sequence 3, Appli
1288	109.5	5.0	2490	2	US-07-847-743B-23	Sequence 23, Appli	1361	108.5	4.9	970	2	US-08-448-937A-3	Sequence 3, Appli
1289	109.5	5.0	2490	2	US-08-456-201-23	Sequence 23, Appli	1362	108.5	4.9	1028	5	US-10-703-032-36520	Sequence 36520, A
1290	109.5	5.0	2490	2	US-08-456-241-23	Sequence 23, Appli	1363	108.5	4.9	1089	3	US-09-248-796A-7664	Sequence 7664, Ap
1291	109.5	5.0	2490	5	US-10-453-183A-6	Sequence 6, Appli	1364	108.5	4.9	1149	3	US-09-248-796A-3173	Sequence 3173, Ap
1292	109.5	5.0	2490	8	PCT-US92-04295A-23	Sequence 23, Appli	1365	108.5	4.9	1344	3	US-09-902-540-7395	Sequence 7395, Ap
c1293	109.5	5.0	2728	3	US-09-270-767-10233	Sequence 10233, A	1366	108.5	4.9	1474	3	US-09-270-767-12852	Sequence 12852, A
1294	109.5	5.0	4108	3	US-08-981-729-8	Sequence 8, Appli	1367	108.5	4.9	1697	3	US-09-533-559-7099	Sequence 7099, Ap
1295	109.5	5.0	4108	3	US-08-981-446B-1	Sequence 1, Appli	1368	108.5	4.9	1846	5	US-10-653-047-7099	Sequence 7099, Ap
1296	109.5	5.0	4619	4	US-10-094-749-1094	Sequence 1094, Ap	1369	108.5	4.9	2033	2	US-10-130-323A-11	Sequence 11, Appli
1297	109.5	5.0	6003	5	US-10-455-719-200	Sequence 200, App	1370	108.5	4.9	2033	2	US-08-148-910-14	Sequence 14, Appli
1298	109.5	5.0	8186	3	US-10-029-517-19	Sequence 19, Appli	1371	108.5	4.9	2036	4	US-08-448-937A-14	Sequence 14, Appli
1300	109.5	5.0	11707	3	US-09-136-574A-1	Sequence 1, Appli	1372	108.5	4.9	2036	4	US-09-880-107-1612	Sequence 1612, Ap
c1301	109.5	5.0	77536	3	US-09-410-551B-1	Sequence 1, Appli	1373	108.5	4.9	2157	5	US-10-130-323A-2	Sequence 2, Appli
c1302	109.5	5.0	77536	3	US-09-940-316B-1	Sequence 1, Appli	1374	108.5	4.9	2464	3	US-09-620-312D-448	Sequence 448, App
1303	109	4.9	463	5	US-10-703-032-98725	Sequence 98725, A	1375	108.5	4.9	2511	5	US-10-130-323A-1	Sequence 1, Appli
1304	109	4.9	465	5	US-10-703-032-98312	Sequence 98312, A	1376	108.5	4.9	2537	3	US-09-949-016-4397	Sequence 4397, Ap
1305	109	4.9	914	5	US-10-703-032-2868	Sequence 2868, Ap	1377	108.5	4.9	2584	3	US-08-758-662-8	Sequence 8, Appli
1306	109	4.9	1017	3	US-09-605-703B-229	Sequence 229, App	1378	108.5	4.9	2584	3	US-09-949-016-393	Sequence 393, App
1307	109	4.9	1173	5	US-10-703-032-8683	Sequence 8683, Ap	1379	108.5	4.9	2721	3	US-09-252-991A-14887	Sequence 14887, A
1308	109	4.9	1413	3	US-09-875-076-9	Sequence 9, Appli	c1380	108.5	4.9	2781	3	US-09-252-991A-14882	Sequence 14882, A
1309	109	4.9	1413	5	US-10-393-807-9	Sequence 9, Appli	1381	108.5	4.9	3285	5	US-10-228-063-46	Sequence 46, Appli
1310	109	4.9	1554	5	US-10-455-719-123	Sequence 123, App	1382	108.5	4.9	4464	2	US-08-400-159-7	Sequence 7, Appli
1311	109	4.9	1623	5	US-10-230-026-9	Sequence 9, Appli	1383	108.5	4.9	4483	3	US-08-611-729A-7	Sequence 7, Appli
1312	109	4.9	1706	3	US-09-774-528-383	Sequence 383, App	1384	108.5	4.9	4483	3	US-09-195-524-7	Sequence 5, Appli
1313	109	4.9	1706	3	US-10-120-988-383	Sequence 383, App	1385	108.5	4.9	4483	3	US-09-310-685-5	Sequence 5, Appli
1314	109	4.9	1710	3	US-09-248-796A-2594	Sequence 2594, Ap	1386	108.5	4.9	4702	4	US-09-880-107-1545	Sequence 1545, Ap
1315	109	4.9	1924	5	US-10-703-032-28203	Sequence 28203, A	1387	108.5	4.9	4702	4	US-09-880-107-1545	Sequence 9, Appli
1316	109	4.9	2131	3	US-08-234-784B-91	Sequence 91, Appli	1388	108.5	4.9	6360	3	US-09-171-699-9	Sequence 64, Appli
1317	109	4.9	2131	5	US-08-816-454B-91	Sequence 91, Appli	c1389	108.5	4.9	229354	3	US-09-705-400-64	Sequence 64, Appli
1318	109	4.9	2163	5	US-10-123-292-127	Sequence 127, App	1390	108	4.9	519	5	US-10-703-032-105520	Sequence 105520,
1319	109	4.9	2163	5	US-10-152-398-127	Sequence 127, App	1391	108	4.9	580	5	US-10-703-032-98747	Sequence 98747, A
1320	109	4.9	2163	5	US-10-123-907-127	Sequence 127, App	1392	108	4.9	677	5	US-10-703-032-72846	Sequence 72846, A
							1393	108	4.9	787	5	US-10-703-032-9996	Sequence 9996, Ap

1394	108	4.9	829	5	US-10-703-032-8627	Sequence 8627, Ap	1467	107.5	4.9	3306	3	US-09-700-354A-10	Sequence 10, Appl
1395	108	4.9	897	3	US-09-248-796A-12659	Sequence 12659, A	1468	107.5	4.9	4312	3	US-10-104-047-468	Sequence 468, App
1396	108	4.9	995	3	US-09-540-014-10	Sequence 10, Appl	1469	107.5	4.9	4466	3	US-09-410-551B-20	Sequence 20, Appl
1397	108	4.9	995	3	US-09-540-014-23	Sequence 23, Appl	1470	107.5	4.9	4466	3	US-09-940-316B-20	Sequence 20, Appl
1398	108	4.9	995	3	US-10-091-841A-10	Sequence 10, Appl	1471	107.5	4.9	4478	3	US-09-410-551B-16	Sequence 16, Appl
1399	108	4.9	995	3	US-10-091-841A-23	Sequence 23, Appl	1472	107.5	4.9	4478	3	US-09-940-316B-16	Sequence 16, Appl
1400	108	4.9	1155	2	US-08-675-650B-1	Sequence 1, Appl	1473	107.5	4.9	4547	3	US-09-410-551B-22	Sequence 22, Appl
1401	108	4.9	1173	3	US-09-602-787A-257	Sequence 257, App	1474	107.5	4.9	4547	3	US-09-940-316B-22	Sequence 22, Appl
1402	108	4.9	1224	3	US-09-252-991A-8171	Sequence 8171, Ap	1475	107.5	4.9	4571	3	US-09-410-551B-18	Sequence 18, Appl
1403	108	4.9	1380	3	US-09-252-991A-7981	Sequence 7981, Ap	1476	107.5	4.9	4571	3	US-09-940-316B-18	Sequence 18, Appl
1404	108	4.9	1383	3	US-09-399-646-3	Sequence 3, Appl	1477	107.5	4.9	6463	3	US-09-332-063-1	Sequence 1, Appl
1405	108	4.9	1791	2	US-08-399-646-3	Sequence 3, Appl	1478	107.5	4.9	6897	5	US-10-455-719-8	Sequence 8, Appl
1406	108	4.9	1791	2	US-08-607-321-3	Sequence 3, Appl	1479	107.5	4.9	10096	3	US-09-902-540-935	Sequence 935, App
1407	108	4.9	1791	2	US-08-961-240-3	Sequence 3, Appl	1480	107.5	4.9	12173	3	US-09-902-540-1022	Sequence 1022, Ap
1408	108	4.9	1791	2	US-08-605-501-3	Sequence 3, Appl	1481	107.5	4.9	16423	3	US-09-902-540-1120	Sequence 1120, Ap
1409	108	4.9	2056	2	US-08-399-646-13	Sequence 13, Appl	1482	107.5	4.9	36535	5	US-10-494-364A-9	Sequence 9, Appl
1410	108	4.9	2056	2	US-08-607-321-13	Sequence 13, Appl	1483	107.5	4.9	60785	3	US-09-949-016-12774	Sequence 12774, A
1411	108	4.9	2056	2	US-08-961-240-13	Sequence 13, Appl	1484	107.5	4.9	60785	3	US-09-949-016-15665	Sequence 15665, A
1412	108	4.9	2056	2	US-08-605-501-13	Sequence 13, Appl	1485	107.5	4.9	83617	3	US-09-949-016-12254	Sequence 12254, A
1413	108	4.9	2115	3	US-08-388-852B-1	Sequence 1, Appl	1486	107	4.8	650	5	US-10-703-032-103837	Sequence 103837, A
1414	108	4.9	2130	3	US-09-056-105-1	Sequence 1, Appl	1487	107	4.8	665	5	US-10-703-032-74149	Sequence 74149, A
1415	108	4.9	2130	3	US-09-862-260A-1	Sequence 1, Appl	1488	107	4.8	702	5	US-10-703-032-76154	Sequence 76154, A
1416	108	4.9	2172	2	US-08-417-174-26	Sequence 26, Appl	1489	107	4.8	768	5	US-09-938-842A-812	Sequence 812, App
1417	108	4.9	2172	2	US-08-231-565A-26	Sequence 26, Appl	1490	107	4.8	900	3	US-10-101-464A-282	Sequence 282, App
1418	108	4.9	2172	2	US-09-007-961-26	Sequence 26, Appl	1491	107	4.8	965	5	US-10-666-642-1435	Sequence 1435, Ap
1419	108	4.9	2172	3	US-09-267-439-26	Sequence 26, Appl	1492	107	4.8	985	5	US-10-225-066A-1085	Sequence 1085, Ap
1420	108	4.9	2172	3	US-09-073-138-26	Sequence 26, Appl	1493	107	4.8	1119	5	US-10-630-880-11	Sequence 11, Appl
1421	108	4.9	2172	4	US-09-898-860-26	Sequence 26, Appl	1494	107	4.8	1155	3	US-09-354-231B-9	Sequence 9, Appl
1422	108	4.9	2172	5	US-10-685-977-26	Sequence 26, Appl	1495	107	4.8	1155	3	US-09-354-231B-11	Sequence 11, Appl
1423	108	4.9	2172	3	US-08-910-925-2	Sequence 2, Appl	1496	107	4.8	1155	3	US-09-128-602B-9	Sequence 9, Appl
1424	108	4.9	3411	4	US-09-880-107-1711	Sequence 1711, Ap	1497	107	4.8	1155	3	US-09-128-602B-11	Sequence 11, Appl
1425	108	4.9	3479	5	US-10-021-698A-3640	Sequence 3640, Ap	1498	107	4.8	1155	3	US-09-995-297-11	Sequence 11, Appl
1426	108	4.9	4053	3	US-09-620-312D-156	Sequence 156, App	1499	107	4.8	1155	3	US-09-995-297-11	Sequence 11, Appl
1427	108	4.9	4699	3	US-09-949-016-5277	Sequence 5277, Ap	1500	107	4.8	1155	4	US-09-771-904A-9	Sequence 9, Appl
1428	108	4.9	4699	3	US-09-949-016-5278	Sequence 5278, Ap							
1429	108	4.9	4699	3	US-09-949-016-5279	Sequence 5279, Ap							
1430	108	4.9	4699	3	US-09-949-016-5280	Sequence 5280, Ap							
1431	108	4.9	5022	2	US-09-289-368-1	Sequence 1, Appl							
1432	108	4.9	5688	3	US-09-221-017B-865	Sequence 865, App							
1433	108	4.9	9126	2	US-08-580-038-26	Sequence 26, Appl							
1434	108	4.9	9126	2	US-08-639-857-3	Sequence 3, Appl							
1435	108	4.9	9879	3	US-09-949-016-13270	Sequence 13270, A							
1436	108	4.9	14896	5	US-09-750-972-6	Sequence 6, Appl							
1437	108	4.9	14896	5	US-09-625-137B-6	Sequence 6, Appl							
1438	108	4.9	15225	2	US-08-892-403A-2	Sequence 2, Appl							
1439	108	4.9	15225	3	US-09-291-894-2	Sequence 2, Appl							
1440	108	4.9	15225	3	US-09-827-688-10	Sequence 10, Appl							
1441	107.5	4.9	378	5	US-10-703-032-105237	Sequence 105237, A							
1442	107.5	4.9	407	5	US-10-703-032-98663	Sequence 98663, A							
1443	107.5	4.9	535	5	US-10-703-032-98701	Sequence 98701, A							
1444	107.5	4.9	606	5	US-10-703-032-6099	Sequence 6099, Ap							
1445	107.5	4.9	706	5	US-10-703-032-8670	Sequence 8670, Ap							
1446	107.5	4.9	783	5	US-10-703-032-15760	Sequence 15760, A							
1447	107.5	4.9	1239	3	US-09-902-540-8805	Sequence 8805, Ap							
1448	107.5	4.9	1266	5	US-10-214-446-17	Sequence 17, Appl							
1449	107.5	4.9	1279	3	US-09-686-583B-7	Sequence 7, Appl							
1450	107.5	4.9	1279	3	US-09-686-583B-8	Sequence 8, Appl							
1451	107.5	4.9	1279	5	US-10-401-324A-7	Sequence 7, Appl							
1452	107.5	4.9	1279	5	US-10-401-324A-8	Sequence 8, Appl							
1453	107.5	4.9	1359	3	US-09-686-583B-14	Sequence 14, Appl							
1454	107.5	4.9	1359	3	US-09-686-583B-15	Sequence 15, Appl							
1455	107.5	4.9	1359	5	US-10-401-324A-14	Sequence 14, Appl							
1456	107.5	4.9	1359	5	US-10-401-324A-15	Sequence 15, Appl							
1457	107.5	4.9	1360	5	US-10-703-032-20818	Sequence 20818, A							
1458	107.5	4.9	1465	3	US-09-686-583B-11	Sequence 11, Appl							
1459	107.5	4.9	1465	3	US-09-686-583B-13	Sequence 13, Appl							
1460	107.5	4.9	1465	5	US-10-401-324A-11	Sequence 11, Appl							
1461	107.5	4.9	1465	5	US-10-401-324A-13	Sequence 13, Appl							
1462	107.5	4.9	1828	3	US-09-902-540-3724	Sequence 3724, Ap							
1463	107.5	4.9	2477	3	US-09-902-540-1971	Sequence 1971, Ap							
1464	107.5	4.9	3306	3	US-09-081-385-10	Sequence 10, Appl							
1465	107.5	4.9	3306	3	US-09-752-639-10	Sequence 10, Appl							
1466	107.5	4.9	3306	3	US-09-712-813-10	Sequence 10, Appl							

ALIGNMENTS

RESULT 1

US-09-866-028-82
; Sequence 82, Application US/098666028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Batson, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior Application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-866-028-82
Alignment Scores:

Pred. No.: 1,82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-944-929-83 (1-431) x US-09-866-028-82 (1-2284)

QY 1 MetPheGlyGlyGluGlySerLeuThrThrLeuValIleleCysPheLeuThr 20
DB 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnGlnCysLeuLysSerLeuGluaspValIleleAsp 40
DB 286 CTAAGGCTGCTGCTAGTCAGAAATTCCTCAAAAAGAGTCTAGAGCATGTTGTCAATGAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
DB 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGATATATACTTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCATTATTTCTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTATAC 465
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrlleuPhePheCys 100
DB 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCAACTGCTACCTATTTTCTGT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrllele 120
DB 526 CCCAACGAGAGCCCTGCTCATTTGAACACAGCAAAAGGACTTATGATGTTACAGGATAAT 585
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 586 ACAGATTTTCCATCTTTGACCAAAATTTGCCAAGCCAAAGATTACCCAGAGAGTTCT 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyrl 160
DB 646 CTCCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACACAGATTAT 705
QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 706 TCAAAAGCCACCGATATCTCATGGAGACACACTTTTCTCAGAAGTTTGGATCTCCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrlLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCTTCTCTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla 240
DB 886 GAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 946 ACTCCAAAGCCCGCCACCTTCTTACCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
DB 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGATACCACTGCTACTTCTCAGCTCCACG 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB 1066 ACCCTCATTTCTACAGTTTTTACCGGCTCGGCTTACACTCCAAAGCAATGGCTACAACA 1125
QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB 1126 GCAGTTCTTACTACCACTTCTTACGGGACCTTACGGACTTCGAAAGGAGCTTAGAAACATA 1185

RESULT 2

US-09-944-457-82
; Sequence 82, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017

QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1366 TTGTGAAAATAGCTCTTATTCGGTCCCTGCTCTTTGGTGTCTCTGTCTGGTGATAGGC 1425
QY 401 LeuValLeuGluValArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
Db 1426 CTCGTCCTCTCGGTAGATCTCTTCGGATCACTCCGAGGAAAGCTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GATTATTTTCATCAATGGGATCTATGTGGACATC 1518

RESULT 3

US-09-945-584-82
; Sequence 82, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296

; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-945-584-82
Alignment Scores:
Pred. No.: 1.82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-09-944-929-83 (1-431) x US-09-945-584-82 (1-2284)
QY 1 MetPhePheGlyGlyGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
Db 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
Db 286 CTAAAGGCTGCTGCTAGTCAAGATTCCTCAAAAGAGCTTAGAAGATGTTGCTCATTGAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
Db 346 ATCCAGTCACTCTCTTCTTAAGGGAATCAGAGCAATGAGCCGTATATACCTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 406 GAAGACTGCATTAATTTCTTGTGTTCAACAAAAAACATATCAGGGGGACAAAGCATGTAAAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaargGlnProAsnCysTyrIleuPhePheCys 100
DB 466 TTGATGATCTTCGACACTCGAAACACGTAGAACCCAACTGCTACTATTTTTCGT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
DB 526 CCCACAGGAGGAGCTGCTCAATTGAAACAGCAAGAGCTTATGAGTTACAGGATATT 585
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 586 ACAGATTTTCCATCTTTCACAGAAATTTGCCAAGCCAAAGAGTTACCCAGGAGATTCT 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB 646 CTCCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
QY 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 706 TCAAGGCCACCGATATCTCATGGAGAGACACATTTCTCAGAAGTTTGGATCCTCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGGATGAGCAAGTGGCCAGCTCTCTGCTTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATCTCAGAGTTCAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB 886 GAAATGTGAGTGGCTCCCACTACGTGAGTGGAGTGTCTTCCACATACCACTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 946 ACTCCAAAGCCGCGCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGACTTCC 1005
QY 261 GlnProGlnLeuAlaThrAlaProProValThrValThrValThrSerGlnProProThr 280
DB 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTAAACCACTGTCACTTCTCAGCCTCCACG 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB 1066 ACCCTCATTTCTACAGTTTTTACAGGGCTGGGCTACACTCCAAGCAATGGCTACAACA 1125
QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB 1126 GCAGTTCTGACTACCACCTTTCCAGGCACCTACGGACTCGAAAGCGCAGCTTGAACCATA 1185
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
DB 1186 CCGTTTACAGAAATCTCAACTTAATTTGAACACAGGAAATGTATTAACCTTACTGCA 1245
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
DB 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTAATAATAAACTGCTTCTCTGGGAAGTAGG 1305
QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB 1306 GAGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCAGAAATAATCAGTACGGCCTTCCA 1365
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
DB 1366 TTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGTGTATGAGC 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
DB 1426 CTCGCTCTCTGGGTAGAAATCTTTTCGGAATCACTCCGCGAGGAAGCTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB 1486 GATTATTTGATCAATGGGATCTTATGGGACATC 1518

RESULT 4

US-09-991-181-514
; Sequence 514, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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 ; PRIOR FILING DATE: 1998-07-09

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US-09-944-929-83 (1-431) x US-09-991-181-514 (1-2284)

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Db 346 ATCCAGTCATCTCTTTCTAAGGAATCAGAGCAATGAGCCCGTATATATCTCACTCAACTCA 405
Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 406 GAAGACTGCATTAATCTTGCTGTTCCACAAAACATATACAGGGACAAAGCATGTAAAC 465
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Db 646 CTCCTACATGGCCAAATTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
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Db 706 TCAAGCCCAACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
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Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GATTATTTGATCAATGGATCTATGTGCACATC 1518

RESULT 5

US-09-944-944-82
; Sequence 82, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
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; PRIOR FILING DATE: December 18, 1997
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; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999

; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

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 Query Match: 100.0% Indels: 0
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 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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 Db 766 CACTGGAGAACTATTTAAGATGGATGAAGCAAGTCCCGCAGCTCTTCTGTATTAAGAA 825
 QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
 Db 826 AAAGGCCATTTCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAAATAGCTCATCTGTGCT 885
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
 Db 886 GAAAAATGTGAGTGGCTCCCGAGTACGGTGGCGAGTTGCTTCTCCACATACCACTCGGCT 945
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
 Db 946 ACTCCAAAGCCCGCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
 Db 1006 CAGCCACAGCTGGCCACCAACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCCACG 1065
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
 Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGGGCTACACTCCAAGCAATGGCTACACA 1125
 QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
 Db 1126 GCAGTTCTGACTACCACTTCTCAGGCACCTACGAGCTCGAAAGGAGCTTAGAAACCAATA 1185
 QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340
 Db 1186 CCGTTTACAGAAATCTCCAATTAACCTTGAACACAGGAAATGTATAAACCTACTGCA 1245
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerThrGluGlyArg 360
 Db 1246 CTTTCTATGTCAATGTGAGTCTTCCACTATGATAAAACTGCTTCTCTGGGAGGAGTAGG 1305
 QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAenGlnThrGlyLeuPro 380
 Db 1306 GAGGCCAGTCCAGGCAGTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA 1365
 QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTGTCTCTGCTGATAGGC 1425
 QY 401 LeuValLeuLeuGlyArgIleLeuSerGlnSerLeuArgArgLysArgThrSerArgLeu 420

Db 1426 CTCGCTCTCTGGGTAGAATCCTTTCCGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485
 Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
 Db 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 7

US-09-945-587-82
 ; Sequence 82, Application US/09945587
 ; Patent No. 6936254
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Batton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerlitsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/945,587
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067,411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,278
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,425
 ; PRIOR FILING DATE: December 12, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,696
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,694
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216,021
 ; PRIOR FILING DATE: December 15, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. 6936254ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. 6936254ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: March 2, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: December 1, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: February 28, 2001
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 82
 ; LENGTH: 2284
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-945-587-82

Alignment Scores:
 Pred. No.: 1,82e-216 Length: 2284
 Score: 2211.00 Matches: 431
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-09-944-929-83 (1-431) x US-09-945-587-82 (1-2284)

Qy 1 MetPhePheGlyGlyGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
 Db 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTGGTAATAATTGCTTCTGACA 285
 Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
 Db 286 CTAAGGCTGTCTGCTAGTCAGAAATTCCTCAAAAGAGCTAGAGATGTTCATTGAC 345
 Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
 Db 346 ATCCAGTCATCTCTTCTAAGGGAATCAGAGGCAATCAGCCCGTATATATCTCACTCAA 405
 Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
 Db 406 GAAGACTGCATTAAATTTCTGCTTTCACCAAAAAACATATCAGGGGACAAAGCATGTAAC 465
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
 Db 466 TTGATGATCTTCGACACATGAAAAACAGCTAGACAAACCCAGCTACCTATTTTCTGT 525
 Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120

Db 526 CCACAGGAGGAGCCTGCTCCATTTGAAACCAAGAGACTTATGAGTTACAGGATAAT 585
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCAAGAGATTACCCAGGAAGATTCT 645
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
Db 646 CTCCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
Qy 161 SerLysProThrAspLeuSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 706 TCRAAGCCCAACGATATCTCATGGAGAGACACACTTCTCAGAAGTTTGGATCCTCAGAT 765
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCTTCTGCTTATAAGGAA 825
Qy 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluLeuAlaHisLeuLeuPro 220
Db 826 AAAGGCCATTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCT 945
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 946 ACTCCAAAGCCGCCACCTTCTACCCCAATGCTTCAGTGACACTTCTGGGACTTCC 1005
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrValThrSerGlnProProThr 280
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCACG 1065
Qy 281 ThrLeuLeuSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Db 1066 ACCCTCATTTTACAGTTTTTACACGGGCTCGGCTACACTCCAAAGCAATGGCTACAACA 1125
Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db 1126 GCAGTTCTCAGTACCACTTTCAGGCACCTTACGGACTCGAAGGCAGCTTAGNAACATA 1185
Qy 321 ProPheThrGluLeuSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
Db 1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGTAGG 1305
Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1306 GAGGCCAGTCCAGGAGTCTCTCCAGGGCAGTGTTCAGAAATCAGTACGGCCCTTCCA 1365
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheValIleGly 400
Db 1366 TTTGAAAAATGGCTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGGTGATAGGC 1425
Qy 401 LeuValLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
Db 1426 CTCGCTCTCTGGGTAGATCTTTTCGAATCACTCCGAGGAACGTTACTCAAGACTG 1485
Qy 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431
Db 1486 GATTATTTCATCAATGGATCTATGTGGACATC 1518

RESULT 8

US-09-997-333-514
; Sequence 514, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167

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2	PRIOR APPLICATION NUMBER: 60/088202	
3	PRIOR FILING DATE: 1998-06-05	
4	PRIOR APPLICATION NUMBER: 60/088212	
5	PRIOR FILING DATE: 1998-06-05	
6	PRIOR APPLICATION NUMBER: 60/088217	
7	PRIOR FILING DATE: 1998-06-05	
8	PRIOR APPLICATION NUMBER: 60/088655	
9	PRIOR FILING DATE: 1998-06-09	
10	PRIOR APPLICATION NUMBER: 60/088734	
11	PRIOR FILING DATE: 1998-06-10	
12	PRIOR APPLICATION NUMBER: 60/088738	
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14	PRIOR APPLICATION NUMBER: 60/088742	
15	PRIOR FILING DATE: 1998-06-10	
16	PRIOR APPLICATION NUMBER: 60/088810	
17	PRIOR FILING DATE: 1998-06-10	
18	PRIOR APPLICATION NUMBER: 60/088824	
19	PRIOR FILING DATE: 1998-06-10	
20	PRIOR APPLICATION NUMBER: 60/088826	
21	PRIOR FILING DATE: 1998-06-10	
22	PRIOR APPLICATION NUMBER: 60/088858	
23	PRIOR FILING DATE: 1998-06-11	
24	PRIOR APPLICATION NUMBER: 60/088861	
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32	PRIOR APPLICATION NUMBER: 60/089512	
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35	PRIOR FILING DATE: 1998-06-16	
36	PRIOR APPLICATION NUMBER: 60/089532	
37	PRIOR FILING DATE: 1998-06-17	
38	PRIOR APPLICATION NUMBER: 60/089538	
39	PRIOR FILING DATE: 1998-06-17	
40	PRIOR APPLICATION NUMBER: 60/089598	
41	PRIOR FILING DATE: 1998-06-17	
42	PRIOR APPLICATION NUMBER: 60/089599	
43	PRIOR FILING DATE: 1998-06-17	
44	PRIOR APPLICATION NUMBER: 60/089600	
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46	PRIOR APPLICATION NUMBER: 60/089653	
47	PRIOR FILING DATE: 1998-06-17	
48	PRIOR APPLICATION NUMBER: 60/089801	
49	PRIOR FILING DATE: 1998-06-18	
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51	PRIOR FILING DATE: 1998-06-18	
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53	PRIOR FILING DATE: 1998-06-19	
54	PRIOR APPLICATION NUMBER: 60/089952	
55	PRIOR FILING DATE: 1998-06-19	
56	PRIOR APPLICATION NUMBER: 60/090246	
57	PRIOR FILING DATE: 1998-06-22	
58	PRIOR APPLICATION NUMBER: 60/090252	
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61	PRIOR FILING DATE: 1998-06-22	
62	PRIOR APPLICATION NUMBER: 60/090349	
63	PRIOR FILING DATE: 1998-06-23	
64	PRIOR APPLICATION NUMBER: 60/090355	
65	PRIOR FILING DATE: 1998-06-23	
66	PRIOR APPLICATION NUMBER: 60/090429	
67	PRIOR FILING DATE: 1998-06-24	
68	PRIOR APPLICATION NUMBER: 60/090431	
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70	PRIOR APPLICATION NUMBER: 60/090431	

?	PRIOR APPLICATION NUMBER:	60/090435
?	PRIOR FILING DATE:	1998-06-24
?	PRIOR APPLICATION NUMBER:	60/090444
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?	PRIOR FILING DATE:	1998-07-02
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?	PRIOR FILING DATE:	1998-07-02
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?	PRIOR FILING DATE:	1998-07-02
?	PRIOR APPLICATION NUMBER:	60/091978
?	PRIOR FILING DATE:	1998-07-07
?	PRIOR APPLICATION NUMBER:	60/091982
?	PRIOR FILING DATE:	1998-07-07
?	PRIOR APPLICATION NUMBER:	60/092182
?	PRIOR FILING DATE:	1998-07-09

Alignment Scores:	
Pred. NO.:	1.82e-216
Score:	2211.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	3
Length:	2284
Matches:	431
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-944-929-83 (1-431) X US-09-997-333-514 (1-2284)

Qy	1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr	20
Db	226	ATGTTCTTCGGGGGAGAAGGAGCTTGACTTTACACTTTGGTAAATAATTTGCTTCCTGACA	285
Qy	21	LeuArgLeuSerAlaSerGlnAnnCysLeuIysSerLeuGluAspValValIleAsp	40
Db	286	CTAAGGCTGTCTCTAGTTCAGAAATTCCTCAAAAGAGCTAGAGAAGTTGTCATTGAC	345
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGAAATCAGAGGCAATGAGCCGTATATATCTTCAACTCAA	405

QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAan 80
DB 406 GAAGACTGATTAATTCCTGCTGTGTTCAACAAACAAATATACAGGGACAAAGATGTAAC 465
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
DB 466 TTGATGATCTTCGACACTCGAAACACAGCTAGACAAACCACTGCTACCTATTTTCTCT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
DB 526 CCCAACGAGGAGCGCTGCTCATTTGAACACAGCAAAAGGACTTATGATGTTTACAGGATAAT 585
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCT 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB 646 CTCCTACATGGCCATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACACAGATTAT 705
QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 706 TCAAAAGCCACCGATATCTCATGGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTCTTATAGGAA 825
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATTTCTCAGAGTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB 886 GAAATGTGAGTGCGCTCCAGCTAGCGTGCGAGTGCTTCTCCACATACCACCTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 946 ACTCCAAAGCCGCCACCTTACCCACCAATGCTTCAGTCACACCTTCTGGGACTTCC 1005
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrValThrSerGlnProProThr 280
DB 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCC 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB 1066 ACCCTCATTTCTACAGTTTTCACAGGCTGCGGCTACACTCAAGCAATGGCTACAACA 1125
QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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DB 1486 GATTATTTGATCATCGGATCATATGTCGATC 1518
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; Sequence 514, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCES: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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; Sequence 514, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-06-16
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61	PRIOR APPLICATION NUMBER: 60/091982
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64	PRIOR FILING DATE: 1998-07-09

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Length:      2284
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Conservative: 0

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Qy	281	ThrIleLysSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
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Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1126	GCAGTTCTGTACCATCTTTCAGGCACCTTACGGACTTCGAAAGGCGACTTAGAAACCAT	1185
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RESULT 11

US-09-989-726-514
; Sequence 514, Application US/09989726

FACE NO. 101011
: GENERAL INFORMATION:

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, APPLICANT: Ashkenazi, Avi J.
, APPLICANT: Baker, Kevin P.
, APPLICANT: Botstein, David
, APPLICANT: Desnoyers, Luc
, APPLICANT: Eaton, Dan L.
, APPLICANT: Ferrara, Napoleone
, APPLICANT: Fong, Sherman
, APPLICANT: Gerber, Hanspeter
, APPLICANT: Gerritsen, Mary E.
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Grimaldi, J. Christopher
, APPLICANT: Gurney, Austin L.
, APPLICANT: Kljavin, Ivar J.
, APPLICANT: Napier, Mary A.
, APPLICANT: Pan, James
, APPLICANT: Paoni, Nicholas F.
, APPLICANT: Roy, Margaret Ann
, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tumas, Daniel
, APPLICANT: Watanabe, Colin K.
, APPLICANT: Williams, P. Wickey
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: Secreted and Transmembrane P
, FILE OF INVENTION: Acids Encoding the Same
, FILE REFERENCE: P2730P1C60
, CURRENT APPLICATION NUMBER: US/09/989,726
, CURRENT FILING DATE: 2001-11-19
, PRIOR APPLICATION NUMBER: 60/049787
, PRIOR FILING DATE: 1997-06-16
, PRIOR APPLICATION NUMBER: 60/062250
, PRIOR FILING DATE: 1997-10-17
, PRIOR APPLICATION NUMBER: 60/065186
, PRIOR FILING DATE: 1997-11-12
, PRIOR APPLICATION NUMBER: 60/065311
, PRIOR FILING DATE: 1997-11-13
, PRIOR APPLICATION NUMBER: 60/066770
, PRIOR FILING DATE: 1997-11-24
, PRIOR APPLICATION NUMBER: 60/075945
, PRIOR FILING DATE: 1998-02-25
, PRIOR APPLICATION NUMBER: 60/078910
, PRIOR FILING DATE: 1998-03-20
, PRIOR APPLICATION NUMBER: 60/083322
, PRIOR FILING DATE: 1998-04-28
, PRIOR APPLICATION NUMBER: 60/084600
, PRIOR FILING DATE: 1998-05-07

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, , PRIOR FILING DATE: 1998-06-17
, , PRIOR APPLICATION NUMBER: 60/089801
, , PRIOR FILING DATE: 1998-06-18
, , PRIOR APPLICATION NUMBER: 60/089907
, , PRIOR FILING DATE: 1998-06-18
, , PRIOR APPLICATION NUMBER: 60/089908
, , PRIOR FILING DATE: 1998-06-18
, , PRIOR APPLICATION NUMBER: 60/089947
, , PRIOR FILING DATE: 1998-06-19
, , PRIOR APPLICATION NUMBER: 60/089948
, , PRIOR FILING DATE: 1998-06-19
, , PRIOR APPLICATION NUMBER: 60/089952
, , PRIOR FILING DATE: 1998-06-19
, , PRIOR APPLICATION NUMBER: 60/090254
, , PRIOR FILING DATE: 1998-06-22
, , PRIOR APPLICATION NUMBER: 60/090349
, , PRIOR FILING DATE: 1998-06-23
, , PRIOR APPLICATION NUMBER: 60/090355
, , PRIOR FILING DATE: 1998-06-23
, , PRIOR APPLICATION NUMBER: 60/090429
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, , PRIOR APPLICATION NUMBER: 60/090431
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, , PRIOR APPLICATION NUMBER: 60/090445
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, , PRIOR APPLICATION NUMBER: 60/090863
, , PRIOR FILING DATE: 1998-06-26
, , PRIOR APPLICATION NUMBER: 60/091360
, , PRIOR FILING DATE: 1998-07-01
, , PRIOR APPLICATION NUMBER: 60/091478
, , PRIOR FILING DATE: 1998-07-02
, , PRIOR APPLICATION NUMBER: 60/091626
, , PRIOR FILING DATE: 1998-07-02
, , PRIOR APPLICATION NUMBER: 60/091633
, , PRIOR FILING DATE: 1998-07-02
, , PRIOR APPLICATION NUMBER: 60/091978
, , PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1,82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-989-726-514 (1-2284)

QY 1 MetPheGlyGlyGlySerLeuThrThrLeuValIlelleCysPheLeuThr 20
DB 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACATTTGGTAATATTTGCTTCCTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIlelleAsp 40
DB 286 CTAGGCTGCTCTTCTTAAGGGAATCGAGCAATGAGCCGATATATCTTCAACTCAA 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
DB 346 ATCCAGTCATCTCTTCTTAAGGGAATCGAGCAATGAGCCGATATATCTTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCTAATTTCTTGCTGTTTCAACAAAACATATCAGGGCAACAGATGTAAC 465
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
DB 466 TTGATGATCTTCGACACTCGAAAACAGCTAGACAAACCACTGCTACCTATTTTCTCT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIlelle 120
DB 526 CCCAACGAGGAGCCCTGCTCATTTGAACACAGCAAGAGCTTATGAGTTACAGGATAAT 585
QY 121 ThrAspPheProSerLeuThrArgLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCAAGCAAGAGTTACCCAGGAAGATTC 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB 646 CTCATTACATGGCAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 706 TCAAAAGCCACCGATATCTCATGGAGAGACACACTTCTCAGAAAGTTTGGATCCTCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTCTTATAAGGAA 825
QY 201 LysGlyHisSerGlnPheSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATCTCAGATTCAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 946 ACTCCAAAAGCCGCCACCTTCTTACCACCAATGCTTCAGTGACACTTCTGGGACTTC 1005
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
DB 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTAACCACTGTCACTTCTCAGCCTCCACG 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300

DB 1066 ACCTCATTTCTACAGTTTTTACACGGGCTGGCTACACTCCAAGCAATGGCTACAACA 1125
QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB 1126 GCAGTTCTGACTACCACTTTTACGGCACCTTACGGACTCGAAAGGCGAGCTTAGAAACCAT 1185
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
DB 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
DB 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGTAGG 1305
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB 1306 GAGGCCAGTCCAGGCAGTTCTCCAGGCGAGTGTTCAGAAAATCAGTACGGCTTCCA 1365
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
DB 1366 TTTGAAAAATGGCTTCTTATTCGGGTCCCTGCTCTTTGGTGTCTTCTGCTGATAGGC 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
DB 1426 CTGTCCTCTCTGGGTAGAATCTTTCGAAATCACTCCGAGGAACGTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB 1486 GATTATTTGATCAATGGATCTATGTGGACATC 1518

RESULT 12

US-09-944-884-82
; Sequence 82, Application US/09944884
; Patent No. 7018837

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Garritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,884
; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82

; LENGTH: 2284
; TYPE: DNA

; ORGANISM: Homo Sapien
US-09-944-884-82

Alignment Scores:

Pred. No.: 1,82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-944-884-82 (1-2284)

QY 1 MetPhePheGlyGlyGlySerLeuThrThrLeuValIleIleCysPheLeuThr 20
 Db 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAAATAATTTGCTTCCTGACA 285
 QY 21 LeuArgLeuSerAlaSerGlnAsnGlnCysLeuValSerLeuGluAspValValIleAsp 40
 Db 286 CTAAGGCTGCTGCTAGTGCAGATTGCTTCAAAAAGAGTCTAGAGATGTTGTTCATTGAC 345
 QY 41 IleGlnSerSerLeuSerIleArgGlyAsnGluProValThrThrSerThrGln 60
 Db 346 ATCCAGTCATCTCTTTCAAGGGAATCAGAGCAATGAGCCCGTATATATCTCAACTCAA 405
 QY 61 GluAspCysIleAsnSerCysCysSerThrIleAsnIleSerGlyAspIleCysAsn 80
 Db 406 GAAGAGTCGATTAATTTCTGCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465
 QY 81 LeuMetIlePheAspThrArgIleThrAlaArgGlnProAsnGlyIlePhePheCys 100
 Db 466 TTGATGATCTTCGACATCGAAAAACAGCTGACAAACCCAACTGCTTACCTATTTTCTGT 525
 QY 101 ProAsnGluGluAlaCysProLeuIleCysProAlaIleGlyLeuMetSerIleArgIleIle 120
 Db 526 CCCAAGGAGAGCCCTGCTCATTTGAACCAAGCAAGAGCTTATGAGTTACAGGATAAT 585
 QY 121 ThrAspPheProSerIleThrArgAsnLeuProSerGlnGluLeuProGlnIleAspSer 140
 Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCAAGAGTTATCCCCAGGAAGATTCT 645
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisIleThrAspThr 160
 Db 646 CTCCTACATGGGCAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705
 QY 161 SerIleProThrAspIleSerIleArgAspThrLeuSerGlnIlePheGlySerSerAsp 180
 Db 706 TCAAGGCCCAAGATATCTCATGGAGAGACACATTTCTCAGAAGTTTGGATCCTCAGAT 765
 QY 181 HisLeuGluIleLeuPheIleMetAspGluAlaSerAlaGlnLeuLeuAlaIleValGlu 200
 Db 766 CACCTGGAGAACTATTTAAGATGATGATGAGCAAGTCCAGCTCTTCTGCTTATAAGGA 825
 QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
 Db 826 AAAGGCCATCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
 Db 886 GAAAATGTGAGTCCGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCT 945
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
 Db 946 ACTCCAAAGCCGCAACCTTCTACCCCAATGCTTCAAGTACACCTTCTGGGACTTCC 1005
 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
 Db 1006 CAGCCACACCTGGCCACACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCACG 1065
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
 Db 1066 ACCCTCATTTCTACAGTTTTTACCGGGCTGGGGCTACACTCCAGCAATGGCTACAACA 1125
 QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerIleGlySerLeuGluThrIle 320
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 QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340
 Db 1186 CCGTTTACAGAATCTCCAACTTAATTTGAACACAGGGAATGTGTATACCTTACTGCA 1245
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnIleThrAlaSerTrpGluIleArg 360
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RESULT 13

US-09-997-514-514
 ; Sequence 514, Application US/09997514
 ; Patent No. 7019116
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC46
 ; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
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 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02

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/	PRIOR	FILING DATE:	1998-06-18	/
/	PRIOR	APPLICATION NUMBER:	60/089908	/
/	PRIOR	FILING DATE:	1998-06-18	/
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/	PRIOR	FILING DATE:	1998-07-07	/
/	PRIOR	APPLICATION NUMBER:	60/091982	/
/	PRIOR	FILING DATE:	1998-07-07	/
/	PRIOR	APPLICATION NUMBER:	60/092182	/
/	PRIOR	FILING DATE:	1998-07-09	/

Alignment Scores:

Pred. No.: 1.82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-997-514-514 (1-2284)

QY 1 MetPheGlyGlyGluGlySerLeuThrThrLeuValIleileCysPheLeuThr 20
DB 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAAATTTGCTTCCTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleLeuAsp 40
DB 286 CTAAGGCTGCTGCTAGTACAGAAATTCCTCAAAAGAGAGCTAGAGAGATGTTGTCATTGAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrSerThrGln 60
DB 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGCAATGAGCCGATATATATCTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCATTAATTTCTTGCTGTTCAACAAAAACATATCAGGGGCAAAAGCATGTAAAC 465
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysFyrLeuPheCys 100
DB 466 TTGATGATCTTCGACACTCGAAAACAGTAGACAAACCACTGCTACTATTTTCTGT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
DB 526 CCAACAGGAGGAGCTGCTCCATTGAAACAGCAAAAGGACTTATGAGTTACAGGATAATT 585
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAGAGTTACCCAGGAAGATTCT 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB 646 CTCCTACATGGCCAAATTTTCAACAGCTGCTCCCTAGCCCATCATCACACAGATTAT 705
QY 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 706 TCBAAGCCACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGGCCAGCTCTCTGCTTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATCTTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCC 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB 886 GAAATGTAGTGCCTCCAGCTACGTGGGAGATGCTTCTCCACATACCACTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrValThrSerGlnProProThr 280
DB 1006 CAGCCACAGCTGGCCACACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACG 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB 1066 ACCCTCATTTCTACAGTTTTTACCGGGCTGGCTACACTCAAGCAATGGCTTACAA 1125
QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320

DB 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTTACGGACTCGAAAGGACAGCTTTAGAAACCAT 1185
QY 321 PropheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
DB 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360
DB 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGAAGGTAGG 1305
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DB 1306 GAGGCAGTCCAGGCACTTCTCCAGGCGAGTTCAGGAAATCAGTACGGCCTTCCA 1365
QY 381 PheGluLysTyrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
DB 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGG 1425
QY 401 LeuValLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420
DB 1426 CTCGTCTCTCGGTAGAATCTTTCGGAATCACTCCGCAAGAAACGTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB 1486 GATTATTGATCAATCGGATCTATGTGACATC 1518

RESULT 14

US-09-989-728-514
; Sequence 514, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC72
; CURRENT APPLICATION NUMBER: US/09/989, 728
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1,826-216 Length: 2284
 Score: 2211.00 Matches: 431
 Percent Similarity: 100.0% Conservatives: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-989-728-514 (1-2284)

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 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
 DB 286 CTAAGGCTGTCTGCTAGTACAGAAATTCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
 DB 346 ATCCAGTCACTCTTCTTAAGGGAATCAGAGCAATGAGCCGTAATATTAATCACTCAA 405
 QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
 DB 406 GAAGACTGCATTAAATCTTCTGCTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
 DB 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCACTGCTACCTATTTTCTGT 525
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
 DB 526 CCCAAGAGGAGGCTGCTCATTTGAAGAACAGCAAAAGGACTTATGAGTTACAGGATAAT 585
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
 DB 586 ACAGATTTTCCATCTTGACCAAGAAATTTGCCAAGCAAGAGTTACCCAGGAGATTCT 645
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
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 QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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 DB 766 CACCTGGAGAACTATTTAAGATGATGATGAGCAAGTCCAGCTCTCTCTATTAAGGAA 825
 QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
 DB 826 AAAGGCCATTTCTCAGATTTCACAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
 DB 886 GAAAAATGTGAGTGCCTCCAGCTAGCTGGTGGAGGATGCTTCTCCACATACCACTCGGCT 945
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
 DB 946 ACTCAAGCCCGCCACCTCTTACCCCAATGCTTCAGTACACCTTCTGGACTTCC 1005
 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280

DB 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTACCACTGTCACTTCTCAACCTCCACG 1065
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300
 DB 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTCGGCTACACTCCCAAGCAATGGCTACACA 1125
 QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
 DB 1126 GCAGTTCTGACTACCACCTTTTCAGGCACCTCAGGACTCGAAAGGAGCTTTAGAACCA 1185
 QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
 DB 1186 CCGTTTACAGAAATCTCCAACTTAACCTTGAACACACAGGATGTGTATAACCTACTGCA 1245
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
 DB 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGTAGG 1305
 QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
 DB 1306 GAGGCCAGTCCAGGCAGTTCTCCAGGCGAGTGTCCAGAAAAATCAGTACGGCTTCCA 1365
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 DB 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGTTGTTCTCTGTTGATAGGC 1425
 QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420
 DB 1426 CTGCTCTCTCGGTAGAACTCTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485
 QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
 DB 1486 GATTAATTGATCAATGGATCTATGTGACATC 1518

RESULT 15

US-09-997-349-514
 ; Sequence 514, Application US/09997349
 ; Patent No. 7034106

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P27301C37
 ; CURRENT APPLICATION NUMBER: US/09/997,349
 ; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17

[illegible]

; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1.82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-997-349-514 (1-2284)

QY 1 MetPheGlyGlyGluSerLeuThrThrLeuValIleCysPheLeuThr 20
DB 226 ATGTTCTTCGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
DB 286 CTAAGGCTGCTGCTAGTCAGAAATTCCTCAAAAGAGGCTAGAGATGTTGTCATGAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrGln 60
DB 346 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGCAATGAGCCCGTATATACTTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCATTAATTCCTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465
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QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
DB 526 CCCAAGGAGAGCTGTCATTTGAACCCAGGAAAGGACTTATGATGTTACAGGATAT 585
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QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 766 CACCTGGAGAACTATTTAAGATGATGAAGCAAGTCCAGCTCTTCTGCTTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 826 AAAGGCCATCTCTCAGAGTTCAAAATTTCTCTGTGATCAAGAAATAGCTCATCTGCTGCT 885

QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValaSerProHisThrThrSerAla 240
DB 886 GAAATGTGAGTGGCTCCAGCTAGCGTGGCAGTTGCTTCTCCACATACACCTCGCT 945
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QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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DB 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGAAAGGTAGG 1305
QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB 1306 GAGGCCAGTCCAGGCAGTTCCTCCAGGCGAGTGTCCAGAAATCAGTACGGCTTCCA 1365
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
DB 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTCTGCTGTATAGGC 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
DB 1426 CTCGTCTCTCGGTAGAAATCTTTCGGAATCACTCCGCGAGGAAACGTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

Search completed: September 20, 2007, 05:11:10

Job time : 4766 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 20, 2007, 01:46:47 ; Search time 4565 Seconds
(without alignments)
2240.550 Million cell updates/sec

Perfect score: 2211

Sequence: 1 MFPGEGSLTYTLVILCLT.....LRRKYSRLDLINGIYVDI 431

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 31364175 seqs, 1186555624 residues

Total number of hits satisfying chosen parameters: 62727632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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44	2211	100.0	2284	3	US-09-997-428-514	Sequence 514, App
94	2211	100.0	2284	8	US-10-429-667-82	Sequence 82, Appl
96	2211	100.0	2284	9	US-10-677-471-82	Sequence 82, Appl
97	2211	100.0	2284	9	US-10-677-663-82	Sequence 82, Appl
98	2211	100.0	2284	10	US-10-735-014-82	Sequence 82, Appl
99	2211	100.0	2284	10	US-10-854-947-82	Sequence 82, Appl
100	2211	100.0	2284	10	US-10-858-993-82	Sequence 82, Appl
101	2211	100.0	2284	10	US-10-901-400-82	Sequence 82, Appl
102	2211	100.0	2284	10	US-10-858-981-82	Sequence 82, Appl
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106	2211	100.0	2284	11	US-11-296-092-82	Sequence 82, Appl
107	2211	100.0	2284	21	US-11-296-155-82	Sequence 82, Appl
108	2211	100.0	2297	16	US-10-917-503-17949	Sequence 17949, A
109	2211	100.0	2297	21	US-11-266-748A-30338	Sequence 30338, A
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116	2210	98.5	1695	21	US-11-266-748A-187628	Sequence 187628,
117	2072	93.7	2015	3	US-09-374-046A-39	Sequence 39, Appl
118	2072	93.7	2015	9	US-10-616-263-39	Sequence 39, Appl
119	2072	93.7	2015	22	US-11-395-249-39	Sequence 39, Appl
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130	1573.5	71.2	175023	20	US-11-121-086-18	Sequence 18, Appl
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156	204.5	9.2	2058	14	US-10-527-469-103	Sequence 103, App

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164	197	8.9	10615	23	US-11-033-056A-38342	Sequence 38342, A	687	160.5	7.3	2753	18	US-11-097-143-40007	Sequence 40007, A
165	196.5	8.9	1826	8	US-10-120-988-230	Sequence 230, App	688	160.5	7.3	22622	18	US-10-956-157-4662	Sequence 4662, Ap
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181	188	8.5	1661	14	US-10-964-241-223	Sequence 223, App	704	160	7.2	9812	26	US-11-443-428A-304852	Sequence 304852, A
182	188	8.5	1661	21	US-11-280-153-223	Sequence 223, App	705	160	7.2	10174	7	US-10-171-311-82	Sequence 82, Appl
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c 232	186.5	8.4	2081	21	US-11-266-748A-127192	Sequence 127192, A	755	160	7.2	10361	14	US-10-540-898-629	Sequence 629, App
c 233	186.5	8.4	2081	21	US-11-266-748A-127192	Sequence 127192, A							

C 899	141	6.4	3953	8	US-10-029-386-20602	Sequence 20602, A	972	137.5	6.2	73764	6	US-09-815-264-63352	Sequence 63352, A
C 900	141	6.4	21959	23	US-11-491-125A-38503	Sequence 38503, A	973	137.5	6.2	73764	27	US-11-595-983-63352	Sequence 63352, A
C 901	141	6.4	32539	6	US-09-815-264-77728	Sequence 77728, A	974	137.5	6.2	193636	23	US-11-417-450-36	Sequence 36, Appl
C 902	141	6.4	32539	23	US-11-491-125A-6919	Sequence 6919, Ap	975	137.5	6.2	247939	23	US-11-033-056A-36594	Sequence 36594, A
C 903	141	6.4	32539	27	US-11-595-983-77728	Sequence 77728, A	976	137.5	6.2	247939	23	US-11-033-056A-36594	Sequence 36594, A
C 904	141	6.4	79344	6	US-09-815-264-79860	Sequence 79860, A	C 977	137.5	6.2	315341	15	US-10-915-727-12206	Sequence 12206, A
C 905	141	6.4	79344	27	US-11-595-983-79860	Sequence 79860, A	C 978	137	6.2	1303	8	US-10-029-386-25315	Sequence 25315, A
C 906	140.5	6.4	1490	16	US-10-703-032-8641	Sequence 8641, Ap	979	137	6.2	2106	10	US-10-425-115-119533	Sequence 119533, A
C 907	140.5	6.4	2032	18	US-11-097-143-5312	Sequence 5312, Ap	980	137	6.2	5664	8	US-10-074-024-439	Sequence 439, App
C 908	140.5	6.4	2070	8	US-10-156-761-8	Sequence 8, Appli	981	137	6.2	5943	18	US-11-097-143-10882	Sequence 10882, A
C 909	140.5	6.4	4282	22	US-11-056-355B-79587	Sequence 79587, A	982	137	6.2	67446	23	US-11-033-056A-37003	Sequence 37003, A
C 910	140.5	6.4	4282	10	US-10-472-928-3657	Sequence 3657, Ap	983	137	6.2	67446	23	US-11-033-056A-37003	Sequence 37003, A
C 911	140.5	6.4	13152	10	US-10-472-928-3657	Sequence 3657, Ap	984	137	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
C 912	140.5	6.4	14328	14	US-10-552-156-73	Sequence 73, Appl	985	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
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C 914	140.5	6.4	14328	14	US-10-552-156-73	Sequence 73, Appl	987	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
C 915	140.5	6.4	24935	6	US-09-815-264-60478	Sequence 60478, A	988	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
C 916	140.5	6.4	24935	23	US-11-491-125A-3636	Sequence 3636, Ap	989	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
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C 918	140.5	6.4	2162598	10	US-10-472-928-4979	Sequence 4979, Ap	991	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
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C 921	140	6.3	8429	18	US-11-097-143-7999	Sequence 7999, Ap	994	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
C 922	139.5	6.3	1467	26	US-11-443-428A-481352	Sequence 481352, A	995	136.5	6.2	1038608	22	US-11-366-965-1	Sequence 1, Appli
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C 930	139.5	6.3	172569	7	US-10-087-192-1366	Sequence 1366, Ap	1003	136	6.2	1412	9	US-10-437-963-31328	Sequence 31328, A
C 931	139	6.3	657	16	US-10-703-032-35646	Sequence 35646, A	1004	136	6.2	1547	25	US-11-503-243A-385180	Sequence 385180, A
C 932	139	6.3	867	3	US-09-216-393-340	Sequence 340, App	1005	136	6.2	1587	16	US-10-703-032-2948	Sequence 2948, Ap
C 933	139	6.3	867	3	US-09-216-393-342	Sequence 342, App	1006	136	6.2	1740	26	US-11-443-428A-75839	Sequence 75839, A
C 934	139	6.3	867	8	US-10-321-856-340	Sequence 340, App	1007	136	6.2	1808	12	US-10-517-696-77	Sequence 77, Appl
C 935	139	6.3	867	8	US-10-321-856-342	Sequence 342, App	1008	136	6.2	2150	3	US-09-826-752-13	Sequence 13, Appl
C 936	139	6.3	867	21	US-11-321-421-340	Sequence 340, App	1009	136	6.2	2150	10	US-10-912-434-13	Sequence 13, Appl
C 937	139	6.3	867	21	US-11-321-421-342	Sequence 342, App	1010	136	6.2	3015	3	US-09-373-658-37	Sequence 37, Appl
C 938	139	6.3	1014	18	US-11-097-143-39134	Sequence 39134, A	1011	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 939	139	6.3	1397	3	US-09-216-393-343	Sequence 343, A	1012	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 940	139	6.3	1397	3	US-09-216-393-345	Sequence 345, App	1013	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 941	139	6.3	1397	8	US-10-321-856-343	Sequence 343, App	1014	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 942	139	6.3	1397	8	US-10-321-856-345	Sequence 345, App	1015	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 943	139	6.3	1397	21	US-11-321-421-343	Sequence 343, App	1016	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
C 944	139	6.3	1397	21	US-11-321-421-345	Sequence 345, App	1017	136	6.2	3015	3	US-09-989-687-37	Sequence 37, Appl
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C 949	138.5	6.3	3183	3	US-09-955-909-1	Sequence 1, Appli	1022	135.5	6.1	573	16	US-10-703-032-104794	Sequence 104794, A
C 950	138.5	6.3	3183	10	US-10-798-625-1	Sequence 1, Appli	1023	135.5	6.1	889	22	US-11-216-545-6283	Sequence 6283, Ap
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C 952	138.5	6.3	4104	10	US-10-793-639-44	Sequence 44, Appl	1025	135.5	6.1	889	22	US-10-424-599-809	Sequence 809, App
C 953	138.5	6.3	4104	14	US-10-309-407-107	Sequence 107, App	1026	135.5	6.1	1718	13	US-10-449-902-406	Sequence 406, App
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C 955	138.5	6.3	5735	3	US-09-728-952-44	Sequence 44, Appl	1028	135.5	6.1	1718	13	US-10-449-902-406	Sequence 406, App
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C 964	138	6.2	91096	10	US-10-612-869-8	Sequence 8, Appli	1037	135	6.1	1718	13	US-10-449-902-406	Sequence 406, App
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C 967	137.5	6.2	4518	9	US-10-467-490-1	Sequence 4, Appli	1040	135	6.1	1718	13	US-10-449-902-406	Sequence 406, App
C 968	137.5	6.2	4519	9	US-10-467-490-1	Sequence 4, Appli	1041	135	6.1	1718	13	US-10-449-902-406	Sequence 406, App
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C 970	137.5	6.2	6828	15	US-10-859-198-40	Sequence 40, Appl	1043	135	6.1	1718	13	US-10-449-902-406	Sequence 406, App
C 971	137.5	6.2	17674	23	US-11-491-125A-66761	Sequence 66761, A	1044	135	6.1	1718	13	US-10-449-902-406	Sequence 406, App

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1049	134.5	6.1	1446	11	US-10-985-109-15	Sequence 15, Appl	1122	133	6.0	2636	9	US-10-152-319A-2142	Sequence 2142, Ap
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1060	134.5	6.1	2075	9	US-10-767-701-14561	Sequence 14561, A	1133	133	6.0	3228	12	US-10-309-407-109	Sequence 109, App
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1066	134.5	6.1	9931	22	US-11-314-987-4	Sequence 4, Appl	c1139	132.5	6.0	792	16	US-10-703-032-2920	Sequence 2920, Ap
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1080	134	6.1	1671	9	US-10-424-599-69411	Sequence 69411, A	1153	132.5	6.0	3530	26	US-11-443-428A-379731	Sequence 379731, A
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1083	134	6.1	2075	13	US-10-449-902-14131	Sequence 14131, A	1156	132.5	6.0	3671	26	US-11-443-428A-379724	Sequence 379724, A
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1085	134	6.1	4287	18	US-11-097-143-37922	Sequence 37922, A	c1158	132.5	6.0	3908	23	US-11-491-125A-58693	Sequence 58693, A
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1093	133.5	6.0	911	23	US-11-241-607-59318	Sequence 59318, A	1166	132.5	6.0	6813	13	US-10-471-571A-3947	Sequence 3947, Ap
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1095	133.5	6.0	1098	11	US-10-663-497-22	Sequence 22, Appl	1168	132.5	6.0	6816	15	US-10-859-198-42	Sequence 42, Appl
1096	133.5	6.0	1098	20	US-11-087-177-38	Sequence 28, Appl	1169	132.5	6.0	6852	8	US-10-172-502-3	Sequence 3, Appl
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1102	133.5	6.0	5699	17	US-10-873-426-127	Sequence 127, App	1175	132.5	6.0	24387	15	US-10-105-299-8953	Sequence 8953, Ap
c1103	133.5	6.0	28847	23	US-10-033-056A-37359	Sequence 37359, A	1176	132.5	6.0	24387	16	US-10-868-184-6802	Sequence 6802, Ap
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1106	133	6.0	1542	3	US-09-765-449-8	Sequence 8, Appl	c1179	132	6.0	576	3	US-09-864-761-20529	Sequence 20529, A
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1117	133	6.0	2353	26	US-11-443-428A-383987	Sequence 383987, A	1190	132	6.0	2562	16	US-10-990-328-1360	Sequence 1360, Ap

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1196	132	6.0	4892	26	US-11-443-428A-732423	Sequence 732423, A	1269	131	5.9	784328	15	US-10-915-727-12217	Sequence 12217, A
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1206	131.5	5.9	1068	21	US-10-425-115-104248	Sequence 104248, A	1279	130.5	5.9	1542	25	US-11-433-832-43454	Sequence 43454, A
1207	131.5	5.9	1425	21	US-11-096-568A-19566	Sequence 19566, A	1280	130.5	5.9	1551	8	US-10-156-761-96	Sequence 96, Appl
1208	131.5	5.9	1425	22	US-11-056-355B-5840	Sequence 5840, Ap	1281	130.5	5.9	1706	7	US-10-087-192-1175	Sequence 1175, Ap
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1216	131	5.9	993	16	US-10-703-032-30891	Sequence 30891, A	1289	130.5	5.9	2404	26	US-11-443-428A-8278	Sequence 8278, Ap
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1219	131	5.9	1295	21	US-11-266-748A-188416	Sequence 188416, A	1292	130.5	5.9	3559	26	US-11-443-428A-497871	Sequence 497871, A
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1227	131	5.9	2303	22	US-11-218-305-17345	Sequence 17345, A	1300	130.5	5.9	14016	8	US-10-315-515-127	Sequence 127, App
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1232	131	5.9	6557	26	US-11-443-428A-467022	Sequence 467022, A	cl305	130.5	5.9	718	16	US-10-703-032-72860	Sequence 72860, A
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1238	131	5.9	10221	26	US-11-443-428A-467013	Sequence 467013, A	1311	130	5.9	1289	16	US-10-703-032-2318	Sequence 2318, Ap
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1342	5.9	10359	26	US-11-443-428A-467015	Sequence 467015, A	1415	129	5.8	3711	26	US-11-443-428A-595030	Sequence 595030, A	
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1344	5.9	152132	16	US-10-940-774-13845	Sequence 13845, A	1417	129	5.8	3862	26	US-11-443-428A-532394	Sequence 532394, A	
1345	5.9	152145	16	US-10-940-774-12371	Sequence 12371, A	1418	129	5.8	3862	26	US-11-443-428A-595027	Sequence 595027, A	
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1362	129.5	5.9	2381	26	US-11-443-428A-383999	Sequence 383999, A	1435	129	5.8	6817	16	US-10-270-333-187	Sequence 187, App
1363	129.5	5.9	2770	13	US-10-449-902-12819	Sequence 12819, A	1436	129	5.8	11847	7	US-11-097-143-41404	Sequence 41404, A
1364	129.5	5.9	2922	11	US-10-450-763-8483	Sequence 8483, App	1437	129	5.8	11847	18	US-09-815-264-71648	Sequence 71648, A
1365	129.5	5.9	3767	18	US-11-097-143-40630	Sequence 40630, A	1438	129	5.8	14542	27	US-11-595-983-81786	Sequence 81786, A
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1494	128	5.8	2010	23	US-11-416-261-16	Sequence 16, Appl
1495	128	5.8	2062	26	US-11-443-428A-586414	Sequence 586414,
1496	128	5.8	2115	23	US-11-416-261-18	Sequence 18, Appl
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1498	128	5.8	3345	11	US-10-840-512-60	Sequence 60, Appl
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Searched: 1726171 seqs, 177918795 residues

Total number of hits satisfying chosen parameters: 3452336

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	148	6.7	43816	8	US-11-699-229-58 Sequence 58, Appl
2	140.5	6.4	2544	8	US-11-713-768-79587 Sequence 79587, A
3	136.5	6.2	1061	8	US-11-514-704-5545 Sequence 5545, Ap
4	136.5	6.2	1923	8	US-11-544-679-14 Sequence 14, Appl
5	136.5	6.2	3637	8	US-11-544-679-13 Sequence 13, Appl
6	131.5	5.9	1425	8	US-11-713-768-5840 Sequence 5840, Ap
7	131	5.9	2903	8	US-11-514-704-17345 Sequence 17345, A
8	130	5.9	2443	8	US-11-514-704-13576 Sequence 13576, A
9	129.5	5.9	1297	8	US-11-713-768-9744 Sequence 9744, Ap
10	128.5	5.8	705	8	US-11-561-363-119 Sequence 119, App

11	128.5	5.8	1153	8	US-11-514-704-20175 Sequence 20175, A
12	127.5	5.8	1644	8	US-11-514-704-2455 Sequence 2455, Ap
13	127.5	5.8	2085	8	US-11-713-768-72372 Sequence 72372, A
14	127.5	5.8	2154	8	US-11-713-768-71163 Sequence 71163, A
15	127	5.7	1348	8	US-11-514-704-14352 Sequence 14352, A
16	126.5	5.7	1785	1	US-10-438-246-12882 Sequence 12882, A
17	126.5	5.7	2180	1	US-10-438-246-22240 Sequence 22240, A
18	126.5	5.7	3379	8	US-11-514-704-62220 Sequence 6220, Ap
19	125.5	5.7	1541	8	US-11-649-663A-5299 Sequence 5299, Ap
c	125	5.7	2818	1	US-10-562-377-156 Sequence 156, App
21	125	5.7	2964	1	US-10-438-246-12791 Sequence 12791, A
22	125	5.7	2964	1	US-10-438-246-22220 Sequence 22220, A
23	125	5.7	46030	8	US-11-257-477-1 Sequence 1, Appli
24	124.5	5.6	1209	8	US-11-649-663A-1609 Sequence 1609, Ap
25	124.5	5.6	1209	8	US-11-713-768-81597 Sequence 81597, A
26	124.5	5.6	3117	1	US-10-567-764-14 Sequence 14, Appl
27	124	5.6	2252	8	US-11-514-704-21629 Sequence 21629, A
28	123.5	5.6	4441	8	US-11-514-704-19034 Sequence 19034, A
29	123.5	5.6	117750	8	US-11-257-477-169 Sequence 169, App
30	123	5.6	2482	8	US-11-234-694-9 Sequence 9, Appli
31	123	5.6	2946	1	US-10-567-764-6 Sequence 6, Appli
32	123	5.6	2969	8	US-11-257-477-2 Sequence 2, Appli
33	123	5.6	8049	1	US-10-567-764-5 Sequence 5, Appli
34	122.5	5.5	857	1	US-10-438-246-47 Sequence 47, Appl
c	122.5	5.5	1348	8	US-11-649-663A-2881 Sequence 2881, Ap
36	122.5	5.5	3004	8	US-11-489-234-4 Sequence 4, Appli
37	122	5.5	4839	1	US-10-533-069-1679 Sequence 1679, Ap
38	121.5	5.5	2164	8	US-11-552-437-227 Sequence 227, App
39	121.5	5.5	2374	8	US-11-514-704-7147 Sequence 7147, Ap
40	121.5	5.5	3210	1	US-10-567-764-18 Sequence 18, Appl
41	121.5	5.5	3271	8	US-10-567-764-5311 Sequence 5311, Ap
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46	120	5.4	1328	8	US-11-713-768-61011 Sequence 61011, A
47	120	5.4	2410	8	US-10-567-764-22 Sequence 22, Appl
48	120	5.4	3303	1	US-11-713-768-71358 Sequence 71358, A
49	120	5.4	4443	8	US-10-565-068-95 Sequence 95, Appl
c	120	5.4	9645	1	US-10-438-246-27134 Sequence 27134, A
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53	119.5	5.4	3329	8	US-11-514-704-4838 Sequence 4838, Ap
54	119.5	5.4	1556	1	US-10-567-764-6219 Sequence 6219, Ap
55	119	5.4	3024	1	US-10-567-764-10 Sequence 10, Appl
56	119	5.4	3024	1	US-11-524-253-1 Sequence 1, Appli
57	119	5.4	5931	8	US-11-514-704-18123 Sequence 18123, A
58	118.5	5.4	2160	8	US-11-561-363-59 Sequence 59, Appl
59	118.5	5.4	2724	8	US-10-438-246-12713 Sequence 12713, A
c	118.5	5.4	5373	1	US-11-713-768-12766 Sequence 12766, A
61	118	5.3	1161	8	US-10-438-246-11631 Sequence 11631, A
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63	117.5	5.3	795	8	US-10-438-246-3982 Sequence 3982, Ap
64	117.5	5.3	2251	1	US-11-514-704-8575 Sequence 8575, Ap
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67	117	5.3	1480	8	US-11-514-704-4869 Sequence 4869, Ap
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c	117	5.3	1922	8	US-11-649-663A-4329 Sequence 4329, Ap
70	117	5.3	3788	8	US-11-713-768-81415 Sequence 81415, A
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72	116.5	5.3	1191	8	US-11-713-768-81492 Sequence 81492, A
c	116.5	5.3	1789	8	US-11-649-663A-4267 Sequence 4267, Ap
74	116.5	5.3	8041	8	US-11-514-704-14588 Sequence 14588, A
75	116	5.2	1106	8	US-11-713-768-64806 Sequence 64806, A
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79	116	5.2	4473	8	US-11-514-704-733 Sequence 733, App
80	116	5.2	4829	8	US-11-514-704-97 Sequence 97, Appl
81	116	5.2	4829	8	US-11-514-704-20177 Sequence 20177, A
82	115.5	5.2	999	8	US-11-713-768-62162 Sequence 62162, A
83	115.5	5.2	1525	8	US-11-713-768-62162 Sequence 62162, A

84	115.5	5.2	2444	8	US-11-713-768-91589	Sequence 91589, A	157	111	5.0	1269	8	US-11-713-768-57665	Sequence 57665, A
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86	115	5.2	1080	1	US-10-438-246-12618	Sequence 12618, A	159	111	5.0	1900	8	US-11-514-704-6528	Sequence 6528, Ap
87	115	5.2	1308	8	US-11-514-704-11332	Sequence 11332, A	160	111	5.0	1993	8	US-11-514-704-7577	Sequence 7577, Ap
88	115	5.2	1330	8	US-11-713-768-62336	Sequence 62336, A	161	111	5.0	2263	8	US-11-713-768-44936	Sequence 44936, A
89	115	5.2	1360	8	US-11-649-663A-3535	Sequence 3535, Ap	162	111	5.0	2263	8	US-11-713-768-46082	Sequence 46082, A
90	115	5.2	1336	8	US-11-514-704-20552	Sequence 20552, A	163	111	5.0	2263	8	Sequence 49157, A	Sequence 49157, A
91	115	5.2	2283	8	US-11-713-768-47906	Sequence 47906, A	164	111	5.0	2699	8	Sequence 16608, A	Sequence 16608, A
92	115	5.2	2632	1	US-11-514-704-3724	Sequence 3724, Ap	165	111	5.0	3885	1	Sequence 22018, A	Sequence 22018, A
93	115	5.2	10722	1	US-10-438-246-5243	Sequence 5243, Ap	166	111	5.0	5382	8	Sequence 22337, A	Sequence 22337, A
94	114.5	5.2	1069	8	US-11-514-704-20232	Sequence 20232, A	167	111	5.0	10291	8	Sequence 500, App	Sequence 500, App
95	114.5	5.2	1444	8	US-11-713-768-20180	Sequence 20180, A	168	110.5	5.0	893	8	Sequence 3779, Ap	Sequence 3779, Ap
96	114.5	5.2	1457	1	US-10-438-246-21254	Sequence 21254, A	169	110.5	5.0	939	8	Sequence 6552, Ap	Sequence 6552, Ap
97	114.5	5.2	2200	8	US-10-438-246-3973	Sequence 3973, Ap	170	110.5	5.0	979	8	Sequence 18500, A	Sequence 18500, A
98	114.5	5.2	2819	8	US-11-514-704-20884	Sequence 20884, A	171	110.5	5.0	1074	1	Sequence 13172, A	Sequence 13172, A
99	114	5.2	936	8	US-11-713-768-51047	Sequence 51047, A	172	110.5	5.0	1249	8	Sequence 57833, A	Sequence 57833, A
100	114	5.2	1160	8	US-11-514-704-23346	Sequence 23346, A	173	110.5	5.0	1307	8	Sequence 4163, Ap	Sequence 4163, Ap
101	114	5.2	2329	8	US-11-713-768-97016	Sequence 97016, A	174	110.5	5.0	1478	1	Sequence 23517, A	Sequence 23517, A
102	114	5.2	2330	8	US-11-713-768-30481	Sequence 30481, A	175	110.5	5.0	1818	8	Sequence 1559, Ap	Sequence 1559, Ap
103	114	5.2	2330	8	US-11-713-768-34071	Sequence 34071, A	176	110.5	5.0	1983	1	Sequence 931, App	Sequence 931, App
104	114	5.2	2681	8	US-11-514-704-996	Sequence 996, App	177	110.5	5.0	2158	8	Sequence 20955, A	Sequence 20955, A
105	114	5.2	3073	8	US-11-514-704-21517	Sequence 21517, A	178	110.5	5.0	2410	8	Sequence 3823, Ap	Sequence 3823, Ap
106	114	5.2	10838	8	US-11-717-800-31	Sequence 31, Appl	179	110.5	5.0	2440	8	Sequence 23345, A	Sequence 23345, A
107	113.5	5.1	1490	8	US-11-713-768-62765	Sequence 62765, A	180	110.5	5.0	12649	8	Sequence 12, Appl	Sequence 12, Appl
108	113.5	5.1	1629	1	US-10-594-266-45	Sequence 45, Appl	181	110	5.0	1437	8	Sequence 21627, A	Sequence 21627, A
109	113.5	5.1	1658	8	US-11-713-768-8284	Sequence 8284, Ap	182	110	5.0	1455	1	Sequence 13051, A	Sequence 13051, A
110	113.5	5.1	1757	8	US-11-514-704-17840	Sequence 17840, A	183	110	5.0	1746	8	Sequence 271, App	Sequence 271, App
111	113.5	5.1	1920	1	US-10-438-246-11132	Sequence 11132, A	184	110	5.0	1776	8	Sequence 45411, A	Sequence 45411, A
112	113.5	5.1	4227	8	US-11-514-704-13683	Sequence 13683, A	185	110	5.0	1776	8	Sequence 49806, A	Sequence 49806, A
113	113.5	5.1	5372	8	US-11-514-704-15923	Sequence 15923, A	186	110	5.0	1855	8	Sequence 5306, Ap	Sequence 5306, Ap
114	113	5.1	1663	8	US-11-713-768-105811	Sequence 105811, A	187	110	5.0	2631	1	Sequence 13632, A	Sequence 13632, A
115	113	5.1	1665	8	US-11-713-768-30064	Sequence 30064, A	188	110	5.0	5759	8	Sequence 9343, Ap	Sequence 9343, Ap
116	113	5.1	1665	8	US-11-713-768-33654	Sequence 33654, A	189	109.5	5.0	1077	8	Sequence 3601, Ap	Sequence 3601, Ap
117	113	5.1	2046	8	US-11-713-768-73756	Sequence 73756, A	190	109.5	5.0	1191	8	Sequence 20639, A	Sequence 20639, A
118	113	5.1	2481	8	US-11-514-704-23281	Sequence 23281, A	191	109.5	5.0	1255	1	Sequence 28517, A	Sequence 28517, A
119	113	5.1	3200	1	US-10-533-069-301	Sequence 301, App	192	109.5	5.0	1305	8	Sequence 79864, A	Sequence 79864, A
120	113	5.1	9781	1	US-11-514-704-7075	Sequence 7075, App	193	109.5	5.0	1367	8	Sequence 2793, Ap	Sequence 2793, Ap
121	112.5	5.1	891	1	US-10-438-246-11605	Sequence 11605, A	194	109.5	5.0	1437	8	Sequence 23884, A	Sequence 23884, A
122	112.5	5.1	984	8	US-11-713-768-82958	Sequence 82958, A	195	109.5	5.0	1606	8	Sequence 18897, A	Sequence 18897, A
123	112.5	5.1	1094	8	US-11-649-663A-1355	Sequence 1355, Ap	196	109.5	5.0	1685	1	Sequence 4699, Ap	Sequence 4699, Ap
124	112.5	5.1	1094	8	US-11-713-768-77112	Sequence 77112, A	197	109.5	5.0	3072	8	Sequence 8, Appl	Sequence 8, Appl
125	112.5	5.1	1335	1	US-10-438-246-3917	Sequence 3917, Ap	198	109	4.9	988	8	Sequence 21790, A	Sequence 21790, A
126	112.5	5.1	1796	8	US-11-713-768-8531	Sequence 8531, Ap	199	109	4.9	1062	8	Sequence 58035, A	Sequence 58035, A
127	112.5	5.1	2582	1	US-10-438-246-3194	Sequence 3194, Ap	200	109	4.9	1335	8	Sequence 56708, A	Sequence 56708, A
128	112.5	5.1	2708	8	US-11-514-704-10383	Sequence 10383, A	201	109	4.9	1363	8	Sequence 7349, Ap	Sequence 7349, Ap
129	112.5	5.1	2856	8	US-11-514-704-15052	Sequence 15052, A	202	109	4.9	1450	8	Sequence 5224, Ap	Sequence 5224, Ap
130	112.5	5.1	3153	8	US-11-514-704-3852	Sequence 3852, Ap	203	109	4.9	1585	8	Sequence 3359, Ap	Sequence 3359, Ap
131	112.5	5.1	3550	8	US-11-713-768-5508	Sequence 5508, Ap	204	109	4.9	1632	8	Sequence 3735, Ap	Sequence 3735, Ap
132	112.5	5.1	4375	8	US-11-514-704-24808	Sequence 24808, A	205	109	4.9	1636	8	Sequence 334, App	Sequence 334, App
133	112.5	5.1	5169	8	US-11-514-704-231	Sequence 231, App	206	109	4.9	1763	8	Sequence 13351, A	Sequence 13351, A
134	112.5	5.1	6065	8	US-11-625-795-12	Sequence 12, Appl	207	109	4.9	1831	8	Sequence 3899, Ap	Sequence 3899, Ap
135	112.5	5.1	8194	8	US-11-717-800-30	Sequence 30, Appl	208	109	4.9	1856	8	Sequence 5101, Ap	Sequence 5101, Ap
136	112	5.1	994	8	US-11-514-704-11355	Sequence 11355, A	209	109	4.9	1908	8	Sequence 12934, A	Sequence 12934, A
137	112	5.1	1482	8	US-11-649-663A-4961	Sequence 4961, Ap	210	109	4.9	2131	8	Sequence 9713, Ap	Sequence 9713, Ap
138	112	5.1	1486	8	US-11-713-768-110682	Sequence 110682, A	211	109	4.9	2372	8	Sequence 14237, A	Sequence 14237, A
139	112	5.1	2165	8	US-11-713-768-4605	Sequence 4605, Ap	212	109	4.9	2380	1	Sequence 15533, A	Sequence 15533, A
140	112	5.1	2885	8	US-11-514-704-4839	Sequence 4839, Ap	213	109	4.9	2530	1	Sequence 23426, A	Sequence 23426, A
141	112	5.1	3487	8	US-11-514-704-3720	Sequence 3720, Ap	214	109	4.9	2530	1	Sequence 10391, A	Sequence 10391, A
142	111.5	5.0	924	8	US-11-514-704-20886	Sequence 20886, A	215	109	4.9	2978	8	Sequence 15232, A	Sequence 15232, A
143	111.5	5.0	958	8	US-11-514-704-11966	Sequence 11966, A	216	109	4.9	3684	1	Sequence 12046, A	Sequence 12046, A
144	111.5	5.0	1122	1	US-10-438-246-13475	Sequence 13475, A	217	109	4.9	3981	1	Sequence 21630, A	Sequence 21630, A
145	111.5	5.0	1184	8	US-11-713-768-67723	Sequence 67723, A	218	109	4.9	5468	1	Sequence 18823, A	Sequence 18823, A
146	111.5	5.0	1392	8	US-11-713-768-67361	Sequence 67361, A	219	109	4.9	5468	1	Sequence 22992, A	Sequence 22992, A
147	111.5	5.0	1759	1	US-10-438-246-786	Sequence 786, App	220	108.5	4.9	894	8	Sequence 1891, Ap	Sequence 1891, Ap
148	111.5	5.0	2367	1	US-10-567-763-1	Sequence 1, Appl	221	108.5	4.9	894	8	Sequence 88758, A	Sequence 88758, A
149	111.5	5.0	2539	8	US-11-514-704-11792	Sequence 11792, A	222	108.5	4.9	894	8	Sequence 92514, A	Sequence 92514, A
150	111.5	5.0	3085	8	US-11-407-888-63	Sequence 63, Appl	223	108.5	4.9	957	8	Sequence 1975, Ap	Sequence 1975, Ap
151	111.5	5.0	3114	1	US-10-438-246-11254	Sequence 11254, A	224	108.5	4.9	957	8	Sequence 91210, A	Sequence 91210, A
152	111.5	5.0	49175	8	US-11-257-477-4	Sequence 4, Appl	225	108.5	4.9	957	8	Sequence 94966, A	Sequence 94966, A
153	111	5.0	797	8	US-11-713-768-55845	Sequence 55845, A	226	108.5	4.9	1062	8	Sequence 7227, Ap	Sequence 7227, Ap
154	111	5.0	918	1	US-10-438-246-27137	Sequence 27137, A	227	108.5	4.9	1076	8	Sequence 56136, A	Sequence 56136, A
155	111	5.0	1071	8	US-11-514-704-997	Sequence 997, App	228	108.5	4.9	1284	1	Sequence 11720, A	Sequence 11720, A
156	111	5.0	1255	8	US-11-713-768-47047	Sequence 47047, A	229	108.5	4.9	1318	1	Sequence 21299, A	Sequence 21299, A

C 230	108.5	4.9	1418	8	US-11-713-768-25846	Sequence 25846, A	303	106	4.8	2271	8	US-11-713-768-89080	Sequence 89080, A
C 231	108.5	4.9	1418	8	US-11-713-768-3032	Sequence 3032, A	304	106	4.8	2271	8	US-11-713-768-92836	Sequence 92836, A
C 232	108.5	4.9	1977	1	US-10-438-246-29387	Sequence 29387, A	305	106	4.8	2275	8	US-11-514-704-4071	Sequence 4071, Ap
C 233	108.5	4.9	4625	1	US-10-533-069-1028	Sequence 1028, Ap	306	106	4.8	2418	8	US-11-713-768-50710	Sequence 50710, A
C 234	108.5	4.9	6131	8	US-11-514-704-3190	Sequence 3190, Ap	307	106	4.8	2604	8	US-11-514-704-13361	Sequence 13361, A
C 235	108.5	4.9	6408	1	US-10-438-246-11810	Sequence 11810, A	308	106	4.8	3318	1	US-10-438-246-11282	Sequence 11282, A
C 236	108.5	4.9	6408	1	US-10-438-246-21380	Sequence 21380, A	309	106	4.8	3318	8	US-11-514-704-1842	Sequence 1842, Ap
C 237	108	4.9	742	8	US-11-514-704-22761	Sequence 22761, A	310	106	4.8	3372	1	US-10-438-246-21032	Sequence 21032, A
C 238	108	4.9	1911	8	US-11-514-704-1000	Sequence 1000, Ap	311	106	4.8	3516	8	US-11-365-630-9	Sequence 9, Appli
C 239	108	4.9	2142	1	US-10-438-246-12114	Sequence 12114, A	312	106	4.8	4102	1	US-10-562-377-138	Sequence 138, App
C 240	108	4.9	2142	1	US-10-438-246-21659	Sequence 21659, A	313	106	4.8	4240	8	US-11-514-704-22510	Sequence 22510, A
C 241	108	4.9	2293	1	US-11-514-704-3387	Sequence 3387, Ap	314	106	4.8	4561	8	US-11-514-704-23219	Sequence 23219, A
C 242	108	4.9	2853	8	US-11-514-704-9222	Sequence 9222, Ap	315	105.5	4.8	1068	1	US-10-438-246-13271	Sequence 13271, A
C 243	108	4.9	5091	1	US-10-438-246-12692	Sequence 12692, A	316	105.5	4.8	1280	8	US-11-514-704-23105	Sequence 23105, A
C 244	108	4.9	5091	1	US-10-438-246-22105	Sequence 22105, A	317	105.5	4.8	1312	1	US-10-438-246-953	Sequence 953, App
C 245	108	4.9	7598	8	US-11-514-704-10960	Sequence 10960, A	318	105.5	4.8	1388	8	US-11-514-704-9682	Sequence 9682, Ap
C 246	107.5	4.9	840	8	US-11-514-704-5518	Sequence 5518, Ap	319	105.5	4.8	1479	1	US-10-438-246-22489	Sequence 22489, A
C 247	107.5	4.9	878	8	US-11-514-704-6221	Sequence 6221, Ap	320	105.5	4.8	1498	8	US-11-514-704-6465	Sequence 6465, Ap
C 248	107.5	4.9	1060	8	US-11-713-768-107178	Sequence 107178, A	321	105.5	4.8	1605	8	US-11-713-768-22766	Sequence 22766, A
C 249	107.5	4.9	1065	8	US-11-713-768-63805	Sequence 63805, A	322	105.5	4.8	1605	8	US-11-713-768-8207	Sequence 8207, Ap
C 250	107.5	4.9	1113	1	US-10-438-246-13458	Sequence 13458, A	323	105.5	4.8	1958	8	US-11-713-768-15424	Sequence 15424, A
C 251	107.5	4.9	1338	8	US-11-713-768-60538	Sequence 60538, A	324	105.5	4.8	1958	8	US-11-514-704-24905	Sequence 24905, A
C 252	107.5	4.9	1470	1	US-10-438-246-4378	Sequence 4378, Ap	325	105.5	4.8	2963	8	US-11-514-704-2264	Sequence 2264, Ap
C 253	107.5	4.9	1507	1	US-10-438-246-23587	Sequence 23587, A	326	105	4.7	3459	8	US-11-514-704-6243	Sequence 6243, Ap
C 254	107.5	4.9	1660	8	US-11-649-663A-2925	Sequence 2925, Ap	327	105	4.7	959	8	US-11-514-704-22421	Sequence 22421, A
C 255	107.5	4.9	1854	1	US-10-438-246-508	Sequence 508, App	328	105	4.7	1082	8	US-11-514-704-22241	Sequence 22241, A
C 256	107.5	4.9	2297	8	US-11-514-704-18728	Sequence 18728, A	329	105	4.7	1163	8	US-11-713-768-103696	Sequence 103696, A
C 257	107.5	4.9	2379	8	US-11-514-704-21485	Sequence 21485, A	330	105	4.7	1191	8	US-11-649-663A-2165	Sequence 2165, Ap
C 258	107.5	4.9	2742	8	US-11-514-704-11612	Sequence 11612, A	331	105	4.7	1191	8	US-11-713-768-4665	Sequence 4665, Ap
C 259	107.5	4.9	2837	8	US-11-257-477-5	Sequence 5, Appli	332	105	4.7	1233	8	US-11-713-768-26301	Sequence 26301, A
C 260	107.5	4.9	2961	8	US-11-514-704-11394	Sequence 11394, A	333	105	4.7	1360	8	US-11-713-768-53291	Sequence 53291, A
C 261	107.5	4.9	3469	8	US-11-514-704-20883	Sequence 20883, A	334	105	4.7	1407	1	US-10-547-956-751	Sequence 751, App
C 262	107.5	4.9	3737	8	US-11-514-704-15165	Sequence 15165, A	335	105	4.7	1561	8	US-11-713-768-6855	Sequence 6855, Ap
C 263	107	4.8	965	8	US-11-728-567-1085	Sequence 1085, Ap	336	105	4.7	1636	1	US-10-438-246-4009	Sequence 4009, Ap
C 264	107	4.8	1029	8	US-11-649-663A-1923	Sequence 1923, Ap	337	105	4.7	1636	1	US-11-713-768-62310	Sequence 62310, A
C 265	107	4.8	1029	8	US-11-713-768-89547	Sequence 89547, A	338	105	4.7	1651	8	US-10-438-246-3075	Sequence 3075, Ap
C 266	107	4.8	1029	8	US-11-713-768-93303	Sequence 93303, A	339	105	4.7	1678	8	US-11-713-768-17674	Sequence 17674, A
C 267	107	4.8	1387	8	US-11-514-704-12043	Sequence 12043, A	340	105	4.7	1797	8	US-11-514-704-12581	Sequence 12581, A
C 268	107	4.8	1562	8	US-11-713-768-98870	Sequence 98870, A	341	105	4.7	1916	8	US-11-514-704-17843	Sequence 17843, A
C 269	107	4.8	1566	8	US-11-713-768-26022	Sequence 26022, A	342	105	4.7	1982	8	US-11-514-704-869	Sequence 869, App
C 270	107	4.8	1622	8	US-11-514-704-22799	Sequence 22799, A	343	105	4.7	2030	8	US-11-649-663A-3681	Sequence 3681, App
C 271	107	4.8	1809	8	US-11-713-768-96499	Sequence 96499, A	344	105	4.7	2085	8	US-11-514-704-16725	Sequence 16725, A
C 272	107	4.8	1943	1	US-10-438-246-654	Sequence 654, App	345	105	4.7	2271	8	US-11-713-768-903	Sequence 903, App
C 273	107	4.8	1948	8	US-11-514-704-13087	Sequence 13087, A	346	105	4.7	2320	8	US-11-713-768-107648	Sequence 107648, A
C 274	107	4.8	2011	8	US-11-713-768-64205	Sequence 64205, A	347	105	4.7	3178	1	US-10-565-068-79	Sequence 79, Appli
C 275	107	4.8	2286	8	US-11-514-704-18779	Sequence 18779, A	348	105	4.7	3476	8	US-11-234-694-51	Sequence 51, Appli
C 276	107	4.8	3015	8	US-11-514-704-735	Sequence 735, App	349	105	4.7	3552	8	US-11-395-197-136	Sequence 136, App
C 277	107	4.8	3232	8	US-11-514-704-3625	Sequence 3625, Ap	350	105	4.7	3552	8	US-11-396-216-136	Sequence 136, App
C 278	107	4.8	3791	8	US-11-514-704-7761	Sequence 7761, Ap	351	105	4.7	5003	8	US-11-514-704-2758	Sequence 2758, App
C 279	106.5	4.8	846	8	US-11-514-704-20178	Sequence 20178, A	352	105	4.7	5350	1	US-10-533-069-2297	Sequence 2297, Ap
C 280	106.5	4.8	846	8	US-11-514-704-20178	Sequence 20178, A	353	105	4.7	5350	1	US-10-438-246-23229	Sequence 23229, Ap
C 281	106.5	4.8	962	1	US-10-438-246-29760	Sequence 29760, A	354	104.5	4.7	6813	1	US-11-514-704-21055	Sequence 21055, A
C 282	106.5	4.8	1085	8	US-11-514-704-20179	Sequence 20179, A	355	104.5	4.7	916	8	US-11-514-704-11356	Sequence 11356, A
C 283	106.5	4.8	1150	8	US-11-713-768-59072	Sequence 59072, A	356	104.5	4.7	1075	8	US-11-649-663A-1629	Sequence 1629, Ap
C 284	106.5	4.8	1176	1	US-10-438-246-364	Sequence 364, App	357	104.5	4.7	1077	8	US-11-713-768-82114	Sequence 82114, A
C 285	106.5	4.8	1191	1	US-10-438-246-12627	Sequence 12627, A	358	104.5	4.7	1138	8	US-11-713-768-57597	Sequence 57597, A
C 286	106.5	4.8	1367	8	US-11-649-663A-4343	Sequence 4343, Ap	359	104.5	4.7	1172	1	US-10-438-246-4376	Sequence 4376, Ap
C 287	106.5	4.8	1594	8	US-11-713-768-60242	Sequence 60242, A	360	104.5	4.7	1266	8	US-11-713-768-2604	Sequence 2604, Ap
C 288	106.5	4.8	1726	1	US-10-438-246-4312	Sequence 4312, Ap	361	104.5	4.7	1484	8	US-11-713-768-43445	Sequence 43445, A
C 289	106.5	4.8	2207	8	US-11-514-704-1147	Sequence 1147, Ap	362	104.5	4.7	1599	8	US-11-713-768-65334	Sequence 65334, A
C 290	106.5	4.8	2235	1	US-10-438-246-13260	Sequence 13260, A	363	104.5	4.7	1819	8	US-11-514-704-16932	Sequence 16932, A
C 291	106.5	4.8	2997	8	US-11-514-704-13844	Sequence 13844, A	364	104.5	4.7	2008	8	US-11-514-704-2759	Sequence 2759, Ap
C 292	106.5	4.8	3152	8	US-11-514-704-24322	Sequence 24322, A	365	104.5	4.7	2334	8	US-11-713-768-86895	Sequence 86895, A
C 293	106.5	4.8	5788	8	US-11-514-704-20794	Sequence 20794, A	366	104.5	4.7	2669	8	US-11-514-704-15173	Sequence 15173, A
C 294	106	4.8	921	8	US-11-514-704-11535	Sequence 11535, A	367	104.5	4.7	2934	8	US-11-713-768-100661	Sequence 100661, A
C 295	106	4.8	1339	8	US-11-713-768-58905	Sequence 58905, A	368	104.5	4.7	3057	8	US-11-514-704-12933	Sequence 12933, A
C 296	106	4.8	1397	8	US-11-713-768-16362	Sequence 16362, A	369	104.5	4.7	3323	8	US-11-514-704-21248	Sequence 21248, A
C 297	106	4.8	1450	8	US-11-514-704-12852	Sequence 12852, A	370	104.5	4.7	3732	8	US-11-514-704-2717	Sequence 2717, Ap
C 298	106	4.8	1566	8	US-11-514-704-10390	Sequence 10390, A	371	104.5	4.7	4314	1	US-11-514-704-22823	Sequence 22823, A
C 299	106	4.8	1798	8	US-11-514-704-17670	Sequence 17670, A	372	104.5	4.7	4437	1	US-10-438-246-12694	Sequence 12694, A
C 300	106	4.8	1876	8	US-11-514-704-22505	Sequence 22505, A	373	104.5	4.7	4845	1	US-10-438-246-22103	Sequence 22103, A
C 301	106	4.8	2105	8	US-11-560-738A-125	Sequence 125, App	374	104.5	4.7	5550	8	US-11-514-704-11712	Sequence 11712, A
C 302	106	4.8	2106	8	US-11-560-738A-1	Sequence 1, Appli	375	104.5	4.7	5826	1	US-10-565-068-94	Sequence 94, Appli

376	104	4.7	870	8	US-11-713-768-110056	Sequence 110056,	449	102.5	4.6	1366	8	US-11-713-768-49416	Sequence 49416, A
377	104	4.7	1188	1	US-10-438-246-13289	Sequence 13289, A	450	102.5	4.6	2079	1	US-10-438-246-11126	Sequence 11126, A
c 378	104	4.7	1188	1	US-10-438-246-22508	Sequence 22508, A	451	102.5	4.6	2161	8	US-11-713-768-7401	Sequence 7401, Ap
379	104	4.7	1245	8	US-11-514-704-2794	Sequence 2794, Ap	452	102.5	4.6	2161	8	US-11-713-768-19207	Sequence 19207, A
380	104	4.7	1252	8	US-11-514-704-20636	Sequence 20636, A	453	102.5	4.6	2166	1	US-10-438-246-13948	Sequence 13948, A
381	104	4.7	1500	8	US-11-713-768-59255	Sequence 59255, A	454	102.5	4.6	2235	8	US-11-514-704-11995	Sequence 11995, A
c 382	104	4.7	1710	1	US-10-438-246-21272	Sequence 21272, A	455	102.5	4.6	2257	8	US-11-514-704-15475	Sequence 15475, A
383	104	4.7	2365	8	US-11-514-704-1693	Sequence 1693, Ap	c 456	102.5	4.6	2798	8	US-11-514-704-15624	Sequence 15624, A
384	104	4.7	2674	8	US-11-514-704-6550	Sequence 6550, Ap	457	102.5	4.6	2964	8	US-11-234-694-109	Sequence 109, App
c 385	104	4.7	3104	8	US-11-342-364-10	Sequence 10, Appl	458	102.5	4.6	3303	8	US-11-514-704-15308	Sequence 15308, A
386	104	4.7	4263	8	US-11-514-704-15281	Sequence 15281, A	459	102.5	4.6	5160	1	US-10-438-246-13812	Sequence 13812, A
c 387	104	4.7	6019	1	US-10-438-246-20856	Sequence 20856, A	c 460	102.5	4.6	6131	8	US-11-514-704-3190	Sequence 3190, Ap
388	104	4.7	6820	1	US-10-572-442B-1	Sequence 1, Appli	461	102.5	4.6	7080	8	US-11-514-704-6741	Sequence 6741, Ap
c 389	103.5	4.7	726	1	US-10-438-246-11675	Sequence 11675, A	462	102.5	4.6	7657	8	US-11-514-704-9986	Sequence 9986, Ap
c 390	103.5	4.7	955	8	US-11-713-768-87041	Sequence 87041, A	c 463	102.5	4.6	8799	1	US-10-438-246-11638	Sequence 11638, A
391	103.5	4.7	957	1	US-10-438-246-11236	Sequence 11236, A	464	102.5	4.6	10188	1	US-10-438-246-15176	Sequence 15176, A
392	103.5	4.7	957	1	US-10-438-246-20977	Sequence 20977, A	465	102.5	4.6	10484	8	US-11-514-704-11456	Sequence 11456, A
393	103.5	4.7	1017	8	US-11-713-768-2776	Sequence 2776, Ap	c 466	102	4.6	967	8	US-11-713-768-6112	Sequence 6112, Ap
394	103.5	4.7	1017	8	US-11-713-768-7297	Sequence 7297, Ap	467	102	4.6	938	8	US-11-713-768-1268	Sequence 1268, Ap
c 395	103.5	4.7	1040	8	US-11-514-704-23546	Sequence 23546, A	c 468	102	4.6	1192	8	US-11-649-663A-393	Sequence 393, App
396	103.5	4.7	1365	8	US-11-713-768-11734	Sequence 11734, A	c 469	102	4.6	1192	8	US-11-649-663A-1831	Sequence 1831, Ap
397	103.5	4.7	1409	8	US-11-713-768-58104	Sequence 58104, A	c 470	102	4.6	1192	8	US-11-713-768-43620	Sequence 43620, A
398	103.5	4.7	1610	1	US-10-533-069-640	Sequence 640, App	c 471	102	4.6	1192	8	US-11-713-768-87108	Sequence 87108, A
399	103.5	4.7	1625	8	US-11-514-704-18105	Sequence 18105, A	472	102	4.6	1198	8	US-11-514-704-22765	Sequence 22765, A
c 400	103.5	4.7	1956	8	US-11-713-768-91425	Sequence 91425, A	473	102	4.6	1251	8	US-11-713-768-64978	Sequence 64978, A
c 401	103.5	4.7	1956	8	US-11-713-768-95181	Sequence 95181, A	474	102	4.6	1296	8	US-11-713-768-8023	Sequence 8023, Ap
402	103.5	4.7	2000	8	US-11-514-704-1108	Sequence 1108, Ap	c 475	102	4.6	1312	1	US-10-438-246-953	Sequence 953, App
403	103.5	4.7	2022	8	US-11-551-744-162	Sequence 162, App	c 476	102	4.6	1398	8	US-11-713-768-5511	Sequence 5511, Ap
404	103.5	4.7	2040	8	US-11-514-704-17668	Sequence 17668, A	c 477	102	4.6	1444	8	US-11-514-704-9534	Sequence 9534, Ap
405	103.5	4.7	2074	8	US-11-713-768-68448	Sequence 68448, A	c 478	102	4.6	1496	8	US-11-728-567-447	Sequence 447, App
406	103.5	4.7	2157	8	US-11-713-768-88392	Sequence 88392, A	479	102	4.6	1580	8	US-11-713-768-65089	Sequence 65089, A
407	103.5	4.7	2157	8	US-11-713-768-92148	Sequence 92148, A	480	102	4.6	1653	8	US-11-514-704-7418	Sequence 7418, Ap
408	103.5	4.7	2321	8	US-11-514-704-20815	Sequence 20815, A	481	102	4.6	1847	1	US-10-438-246-29099	Sequence 29099, Ap
c 409	103.5	4.7	2414	8	US-11-514-704-22108	Sequence 22108, A	482	102	4.6	1928	8	US-11-514-704-11549	Sequence 11549, A
c 410	103.5	4.7	2662	8	US-11-514-704-12334	Sequence 12334, A	483	102	4.6	2024	8	US-11-514-704-4060	Sequence 4060, Ap
c 411	103.5	4.7	3458	8	US-11-514-704-24822	Sequence 24822, A	484	102	4.6	2213	8	US-11-713-768-64244	Sequence 64244, A
412	103.5	4.7	4064	8	US-11-585-666-38	Sequence 38, Appl	c 485	102	4.6	2274	8	US-11-514-704-1888	Sequence 1888, Ap
413	103.5	4.7	5311	8	US-11-514-704-14475	Sequence 14475, A	c 486	102	4.6	2298	8	US-11-514-704-16325	Sequence 16325, Ap
414	103	4.7	748	8	US-11-713-768-61851	Sequence 61851, A	487	102	4.6	3069	8	US-11-514-704-7529	Sequence 7529, Ap
415	103	4.7	843	8	US-11-713-768-111368	Sequence 111368, A	488	102	4.6	3536	8	US-11-514-704-7948	Sequence 7948, Ap
416	103	4.7	992	8	US-11-713-768-59888	Sequence 59888, A	489	102	4.6	4091	8	US-11-514-704-20973	Sequence 20973, A
417	103	4.7	1098	8	US-11-514-704-11968	Sequence 11968, A	490	102	4.6	4179	8	US-11-514-704-7880	Sequence 7880, Ap
c 418	103	4.7	1146	8	US-11-713-768-98263	Sequence 98263, A	491	102	4.6	4693	8	US-11-407-888-62	Sequence 62, Appl
419	103	4.7	1450	8	US-11-713-768-8563	Sequence 8563, Ap	492	102	4.6	4693	8	US-11-585-666-27	Sequence 27, Appl
420	103	4.7	1679	8	US-11-514-704-20980	Sequence 20980, A	493	102	4.6	4764	8	US-11-514-704-4025	Sequence 4025, Ap
421	103	4.7	1681	8	US-11-649-663A-5165	Sequence 5165, Ap	494	102	4.6	4850	8	US-11-514-704-11132	Sequence 11132, A
422	103	4.7	1758	8	US-11-514-704-22345	Sequence 22345, A	495	102	4.6	5376	1	US-10-438-246-14325	Sequence 14325, A
423	103	4.7	1775	8	US-11-713-768-66577	Sequence 66577, A	496	102	4.6	5376	1	US-10-438-246-23166	Sequence 23166, A
424	103	4.7	1950	8	US-11-713-768-69413	Sequence 69413, A	497	102	4.6	6704	8	US-11-572-508-3	Sequence 3, Appli
425	103	4.7	2125	8	US-11-514-704-14285	Sequence 14285, A	c 498	102	4.6	7696	8	US-11-514-704-9539	Sequence 9539, Ap
426	103	4.7	3178	1	US-10-533-069-541	Sequence 541, App	499	102	4.6	7986	8	US-11-407-888-66	Sequence 66, Appl
c 427	103	4.7	3381	1	US-10-533-069-311	Sequence 311, App	500	102	4.6	8937	1	US-10-438-246-14551	Sequence 14551, A
c 428	103	4.7	4000	8	US-11-514-704-3274	Sequence 3274, Ap	c 501	101.5	4.6	982	8	US-11-713-768-35933	Sequence 35933, A
429	103	4.7	4382	8	US-11-514-704-3302	Sequence 3302, Ap	502	101.5	4.6	1034	8	US-11-713-768-22074	Sequence 22074, A
c 430	103	4.7	5095	1	US-10-438-246-12647	Sequence 12647, A	503	101.5	4.6	1129	8	US-11-713-768-68468	Sequence 68468, A
c 431	103	4.7	5334	1	US-10-438-246-13648	Sequence 12648, A	504	101.5	4.6	1194	1	US-10-554-789-8	Sequence 8, Appli
432	103	4.7	5478	1	US-10-438-246-15196	Sequence 15196, A	505	101.5	4.6	1203	8	US-11-514-704-3902	Sequence 3902, Ap
433	103	4.7	5620	1	US-10-438-246-22076	Sequence 22076, A	506	101.5	4.6	1337	8	US-11-514-704-13247	Sequence 13247, A
434	103	4.7	7059	8	US-11-514-704-20979	Sequence 20979, A	507	101.5	4.6	1533	8	US-11-514-704-17669	Sequence 17669, A
c 435	103	4.7	7581	8	US-11-514-704-20599	Sequence 20599, A	508	101.5	4.6	1635	8	US-11-713-768-11387	Sequence 11387, A
c 436	102.5	4.6	761	1	US-10-438-246-291	Sequence 291, App	509	101.5	4.6	1677	8	US-11-649-663A-3229	Sequence 3229, Ap
437	102.5	4.6	959	1	US-10-438-246-29759	Sequence 29759, A	c 510	101.5	4.6	1771	8	US-11-713-768-39258	Sequence 39258, A
c 438	102.5	4.6	1143	8	US-11-514-704-22239	Sequence 22239, A	c 511	101.5	4.6	1771	8	US-11-713-768-48325	Sequence 48325, A
439	102.5	4.6	1162	8	US-11-713-768-104447	Sequence 104447, A	c 512	101.5	4.6	2082	8	US-11-514-704-24716	Sequence 24716, A
440	102.5	4.6	1263	8	US-11-713-768-40592	Sequence 40592, A	513	101.5	4.6	2229	8	US-11-514-704-732	Sequence 732, App
c 441	102.5	4.6	1263	8	US-11-713-768-62735	Sequence 62735, A	514	101.5	4.6	2237	8	US-11-514-704-17841	Sequence 17841, A
442	102.5	4.6	1522	8	US-11-713-768-16761	Sequence 16761, A	c 515	101.5	4.6	2258	8	US-11-514-704-19871	Sequence 19871, A
443	102.5	4.6	1529	8	US-11-713-768-17637	Sequence 17637, A	516	101.5	4.6	2656	1	US-10-438-246-1104	Sequence 1104, Ap
c 444	102.5	4.6	1854	1	US-10-547-956-119	Sequence 119, App	517	101.5	4.6	2656	1	US-10-438-246-1104	Sequence 1104, Ap
445	102.5	4.6	1863	8	US-11-544-679-11	Sequence 11, Appl	518	101.5	4.6	2658	8	US-11-514-704-6846	Sequence 6846, Ap
446	102.5	4.6	1966	8	US-11-713-768-45864	Sequence 45864, A	519	101.5	4.6	2773	8	US-11-649-663A-1465	Sequence 1465, Ap
447	102.5	4.6	1966	8	US-11-713-768-49029	Sequence 49029, A	520	101.5	4.6	2773	8	US-11-713-768-49006	Sequence 49006, A
448	102.5	4.6	1966	8	US-11-713-768-49275	Sequence 49275, A	521	101.5	4.6	2791	8	US-11-649-663A-2825	Sequence 2825, Ap

522	101.5	4.6	2791	8	US-11-713-768-45476	Sequence 45476, A	c 595	100.5	4.5	2771	8	US-11-514-704-4743	Sequence 4743, Ap
523	101.5	4.6	2844	1	US-10-438-246-4385	Sequence 4385, Ap	596	100.5	4.5	2895	1	US-10-438-246-13842	Sequence 13842, A
524	101.5	4.6	2987	8	US-11-514-704-15556	Sequence 15556, A	597	100.5	4.5	3446	8	US-11-514-704-7610	Sequence 7610, Ap
525	101.5	4.6	3112	8	US-11-514-704-2688	Sequence 2688, Ap	598	100.5	4.5	4227	1	US-10-438-246-13300	Sequence 13300, A
526	101.5	4.6	3188	8	US-11-514-704-13552	Sequence 13552, A	599	100.5	4.5	4674	1	US-10-438-246-23020	Sequence 23020, A
c 527	101.5	4.6	3237	8	US-11-514-704-3798	Sequence 3798, Ap	600	100.5	4.5	12738	1	US-10-438-246-12914	Sequence 12914, A
528	101.5	4.6	3742	8	US-11-514-704-1615	Sequence 1615, Ap	601	100.5	4.5	12922	1	US-10-438-246-22255	Sequence 22255, A
529	101.5	4.6	4172	8	US-11-514-704-18845	Sequence 18845, A	c 602	100	4.5	1013	8	US-11-514-704-16670	Sequence 16670, A
c 530	101.5	4.6	4522	8	US-11-514-704-11120	Sequence 11120, A	603	100	4.5	1195	8	US-11-713-768-45080	Sequence 45080, A
531	101.5	4.6	6901	8	US-11-514-704-14826	Sequence 14826, A	604	100	4.5	1226	8	US-11-713-768-2231	Sequence 2231, Ap
c 532	101.5	4.6	7685	1	US-11-514-704-24334	Sequence 24334, A	605	100	4.5	1357	8	US-11-713-768-68401	Sequence 68401, A
533	101	4.6	779	1	US-10-438-246-5382	Sequence 5382, Ap	606	100	4.5	1341	8	US-11-713-768-68496	Sequence 68496, A
534	101	4.6	795	1	US-10-438-246-62830	Sequence 62830, A	c 607	100	4.5	1412	8	US-11-713-768-85206	Sequence 85206, A
535	101	4.6	889	8	US-11-514-704-6265	Sequence 6265, Ap	608	100	4.5	1452	8	US-11-514-704-2302	Sequence 2302, Ap
536	101	4.6	1051	8	US-11-713-768-99665	Sequence 99665, A	609	100	4.5	1452	8	US-11-514-704-23665	Sequence 23665, A
537	101	4.6	1077	8	US-11-514-704-23074	Sequence 23074, A	610	100	4.5	1488	8	US-11-713-768-8719	Sequence 8719, Ap
538	101	4.6	1206	8	US-11-514-704-5482	Sequence 5482, Ap	611	100	4.5	1536	8	US-11-713-768-4733	Sequence 4733, Ap
539	101	4.6	1385	8	US-11-713-768-55732	Sequence 55732, A	c 612	100	4.5	1622	8	US-11-514-704-20545	Sequence 20545, A
540	101	4.6	1549	8	US-11-713-768-13432	Sequence 13432, A	613	100	4.5	1683	8	US-11-395-197-65	Sequence 65, Appl
541	101	4.6	1588	8	US-11-713-768-98665	Sequence 98665, A	614	100	4.5	1683	8	US-11-396-216-65	Sequence 65, Appl
542	101	4.6	1589	8	US-11-713-768-28814	Sequence 28814, A	c 615	100	4.5	1731	8	US-11-514-704-11014	Sequence 11014, A
543	101	4.6	1589	8	US-11-713-768-32404	Sequence 32404, A	616	100	4.5	1734	8	US-11-514-704-2689	Sequence 2689, Ap
544	101	4.6	1684	8	US-11-514-704-12577	Sequence 12577, A	617	100	4.5	1751	8	US-11-713-768-3422	Sequence 3422, Ap
545	101	4.6	1814	8	US-11-514-704-19334	Sequence 19334, A	c 618	100	4.5	1954	8	US-11-713-768-9709	Sequence 9709, Ap
546	101	4.6	1825	8	US-11-514-704-21735	Sequence 21735, A	619	100	4.5	1997	8	US-11-649-663A-5507	Sequence 5507, Ap
547	101	4.6	1895	8	US-11-514-704-19889	Sequence 19889, A	620	100	4.5	2018	8	US-11-649-663A-4303	Sequence 4303, Ap
548	101	4.6	1904	8	US-11-713-768-6833	Sequence 6833, Ap	621	100	4.5	2149	8	US-11-514-704-3855	Sequence 3855, Ap
549	101	4.6	1913	1	US-10-438-246-26761	Sequence 26761, A	c 622	100	4.5	2197	8	US-11-713-768-45830	Sequence 45830, A
550	101	4.6	2027	8	US-11-514-704-9201	Sequence 9201, Ap	623	100	4.5	2228	8	US-11-713-768-98343	Sequence 98343, A
551	101	4.6	2146	8	US-11-514-704-2674	Sequence 2674, Ap	c 624	100	4.5	2232	1	US-11-713-768-48737	Sequence 48737, A
552	101	4.6	2172	8	US-11-514-704-4078	Sequence 4078, Ap	625	100	4.5	2367	1	US-10-567-763-26	Sequence 26, Appl
c 553	101	4.6	2188	8	US-11-713-768-12298	Sequence 12298, Ap	626	100	4.5	2395	8	US-11-514-704-8378	Sequence 8378, Ap
554	101	4.6	2197	1	US-10-438-246-386	Sequence 386, Ap	627	100	4.5	2563	8	US-11-514-704-14903	Sequence 14903, A
555	101	4.6	2397	1	US-10-438-246-12039	Sequence 12039, A	c 628	100	4.5	2782	8	US-11-649-663A-721	Sequence 721, App
556	101	4.6	2489	8	US-11-514-704-5677	Sequence 5677, Ap	c 629	100	4.5	2782	8	US-11-713-768-19015	Sequence 19015, A
c 557	101	4.6	2661	8	US-11-514-704-22481	Sequence 22481, A	630	100	4.5	3043	8	US-11-514-704-9281	Sequence 9281, Ap
c 558	101	4.6	2712	8	US-11-514-704-12998	Sequence 12998, Ap	631	100	4.5	3316	8	US-11-234-694-53	Sequence 53, Appl
c 559	101	4.6	2896	8	US-11-713-768-78378	Sequence 78378, A	632	100	4.5	3327	8	US-11-395-216-76	Sequence 76, Appl
560	101	4.6	3138	8	US-11-514-704-17750	Sequence 17750, A	633	100	4.5	3327	8	US-11-395-216-76	Sequence 76, Appl
561	101	4.6	3231	8	US-11-514-704-12648	Sequence 12648, A	c 634	100	4.5	3480	8	US-11-514-704-539	Sequence 539, App
562	101	4.6	3327	8	US-11-514-704-3371	Sequence 3371, Ap	c 635	100	4.5	3492	8	US-11-514-704-11548	Sequence 11548, A
563	101	4.6	3553	8	US-11-514-704-16982	Sequence 16982, A	636	100	4.5	4135	8	US-11-514-704-11198	Sequence 11198, A
c 564	101	4.6	3845	8	US-11-514-704-22951	Sequence 22951, A	637	100	4.5	4175	8	US-11-514-704-9523	Sequence 9523, Ap
565	101	4.6	5446	1	US-10-438-246-13825	Sequence 13825, A	638	100	4.5	4526	8	US-11-514-704-12767	Sequence 12767, A
566	101	4.6	5449	1	US-10-438-246-13882	Sequence 13882, A	639	100	4.5	4716	1	US-10-438-246-13782	Sequence 13782, A
567	101	4.6	5450	1	US-10-438-246-29888	Sequence 29888, A	640	100	4.5	4716	1	US-10-438-246-22984	Sequence 22984, A
568	101	4.6	6576	8	US-11-514-704-192	Sequence 192, App	641	100	4.5	5187	1	US-10-438-246-14206	Sequence 14206, A
c 569	100.5	4.5	960	8	US-11-713-768-9977	Sequence 9977, Ap	642	100	4.5	5284	8	US-11-514-704-10672	Sequence 10672, A
c 570	100.5	4.5	1081	8	US-11-649-663A-307	Sequence 307, App	643	100	4.5	5418	1	US-10-438-246-23123	Sequence 23123, A
c 571	100.5	4.5	1081	8	US-11-713-768-25379	Sequence 25379, A	644	100	4.5	5616	8	US-11-514-704-4461	Sequence 4461, Ap
c 572	100.5	4.5	1081	8	US-11-713-768-25513	Sequence 25513, A	645	100	4.5	7981	8	US-11-407-888-42	Sequence 42, Appl
573	100.5	4.5	1101	1	US-10-547-956-89	Sequence 89, Appl	c 646	99.5	4.5	760	8	US-11-514-704-21057	Sequence 21057, A
574	100.5	4.5	1124	8	US-11-713-768-41940	Sequence 41940, A	647	99.5	4.5	940	8	US-11-514-704-22763	Sequence 22763, A
c 575	100.5	4.5	1278	1	US-10-438-246-3826	Sequence 3826, Ap	648	99.5	4.5	1001	8	US-11-725-235-189	Sequence 189, App
c 576	100.5	4.5	1278	1	US-11-514-704-24105	Sequence 24105, A	649	99.5	4.5	1023	1	US-10-438-246-13116	Sequence 13116, A
577	100.5	4.5	1314	8	US-11-713-768-7381	Sequence 7381, Ap	c 650	99.5	4.5	1042	8	US-11-713-768-6043	Sequence 6043, Ap
578	100.5	4.5	1443	8	US-11-514-704-16040	Sequence 16040, A	651	99.5	4.5	1114	8	US-11-713-768-64077	Sequence 64077, A
c 579	100.5	4.5	1479	8	US-11-514-704-9983	Sequence 9983, Ap	652	99.5	4.5	1132	8	US-11-713-768-57492	Sequence 57492, A
580	100.5	4.5	1527	1	US-10-438-246-914	Sequence 914, App	c 653	99.5	4.5	1231	8	US-11-514-704-24906	Sequence 24906, A
581	100.5	4.5	1592	8	US-11-514-704-22493	Sequence 22493, A	654	99.5	4.5	1294	8	US-11-514-704-13363	Sequence 13363, A
582	100.5	4.5	1689	8	US-11-514-704-4886	Sequence 4886, Ap	c 655	99.5	4.5	1307	8	US-11-514-704-4250	Sequence 4250, Ap
c 583	100.5	4.5	1736	8	US-11-713-768-41745	Sequence 41745, A	656	99.5	4.5	1395	8	US-11-514-704-4225	Sequence 4225, Ap
584	100.5	4.5	1807	1	US-10-533-069-2309	Sequence 2309, Ap	657	99.5	4.5	1422	8	US-11-713-768-7448	Sequence 7448, Ap
c 585	100.5	4.5	1895	8	US-11-514-704-19618	Sequence 19618, A	658	99.5	4.5	1617	1	US-10-438-246-3173	Sequence 3173, Ap
c 586	100.5	4.5	1940	8	US-11-514-704-1617	Sequence 1617, Ap	659	99.5	4.5	1720	8	US-11-514-704-6940	Sequence 6940, Ap
c 587	100.5	4.5	2017	8	US-11-514-704-23473	Sequence 23473, A	c 660	99.5	4.5	1854	1	US-10-547-956-507	Sequence 507, App
588	100.5	4.5	2068	8	US-11-514-704-1553	Sequence 1553, Ap	661	99.5	4.5	1878	1	US-10-438-246-785	Sequence 785, App
589	100.5	4.5	2162	8	US-11-649-663A-4103	Sequence 4103, Ap	662	99.5	4.5	1906	8	US-11-514-704-2679	Sequence 2679, Ap
c 590	100.5	4.5	2275	8	US-11-514-704-24366	Sequence 24366, A	c 663	99.5	4.5	1971	8	US-11-514-704-6335	Sequence 6335, Ap
591	100.5	4.5	2407	8	US-11-514-704-3569	Sequence 3569, Ap	664	99.5	4.5	1996	8	US-11-514-704-15047	Sequence 15047, A
592	100.5	4.5	2559	8	US-11-514-704-13889	Sequence 13889, A	665	99.5	4.5	2009	8	US-11-514-704-1281	Sequence 1281, Ap
593	100.5	4.5	2575	1	US-10-438-246-165	Sequence 165, App	c 666	99.5	4.5	2074	8	US-11-514-704-23188	Sequence 23188, A
594	100.5	4.5	2628	8	US-11-514-704-4184	Sequence 4184, Ap	667	99.5	4.5	2250	8	US-11-713-768-108346	Sequence 108346, A

C 668	99.5	4.5	2260	1	US-10-438-246-12799	Sequence 12799, A	741	98.5	4.5	1194	1	US-10-554-789-7	Sequence 7, Appli
C 669	99.5	4.5	2377	8	US-11-514-704-7309	Sequence 7309, Ap	742	98.5	4.5	1298	8	US-11-514-704-18243	Sequence 18243, A
C 670	99.5	4.5	2378	1	US-10-438-246-22227	Sequence 22227, A	743	98.5	4.5	1306	8	US-11-713-768-68388	Sequence 68388, A
C 671	99.5	4.5	2409	1	US-10-438-246-15529	Sequence 15529, A	744	98.5	4.5	1359	8	US-11-514-704-18592	Sequence 18592, A
C 672	99.5	4.5	2409	1	US-10-438-246-23427	Sequence 23427, A	745	98.5	4.5	1374	8	US-11-713-768-62916	Sequence 62916, A
C 673	99.5	4.5	2489	8	US-11-514-704-5448	Sequence 5448, Ap	746	98.5	4.5	1436	8	US-11-649-663A-4393	Sequence 4393, Ap
C 674	99.5	4.5	2994	8	US-11-407-888-54	Sequence 54, Appl	747	98.5	4.5	1468	8	US-11-514-704-16599	Sequence 16599, A
C 675	99.5	4.5	3109	8	US-11-514-704-7417	Sequence 7417, Ap	748	98.5	4.5	1504	8	US-11-514-704-3608	Sequence 3608, Ap
C 676	99.5	4.5	3260	8	US-11-514-704-8459	Sequence 8459, Ap	749	98.5	4.5	1517	1	US-10-438-246-20968	Sequence 20968, A
C 677	99.5	4.5	3482	8	US-11-514-704-16158	Sequence 16158, A	750	98.5	4.5	1516	1	US-10-438-246-21156	Sequence 21156, A
C 678	99.5	4.5	4162	8	US-11-514-704-10	Sequence 10, Appl	751	98.5	4.5	1620	1	US-10-438-246-1616	Sequence 1616, Ap
C 679	99.5	4.5	4290	8	US-11-514-704-5407	Sequence 5407, Ap	752	98.5	4.5	1672	1	US-10-438-246-21326	Sequence 21326, A
C 680	99.5	4.5	6603	1	US-10-594-266-55	Sequence 55, Appl	753	98.5	4.5	1676	8	US-11-713-768-10252	Sequence 10252, A
C 681	99.5	4.5	7119	8	US-11-514-704-20569	Sequence 20569, A	754	98.5	4.5	1692	8	US-11-614-098-13	Sequence 13, Appl
C 682	99	4.5	837	8	US-11-561-363-53	Sequence 53, Appl	755	98.5	4.5	1692	1	US-10-438-246-28383	Sequence 28383, A
C 683	99	4.5	915	8	US-11-713-768-111259	Sequence 111259, A	756	98.5	4.5	1757	1	US-10-438-246-21156	Sequence 21156, A
C 684	99	4.5	916	8	US-11-649-663A-947	Sequence 947, App	757	98.5	4.5	1767	8	US-11-713-768-59929	Sequence 59929, A
C 685	99	4.5	916	8	US-11-713-768-16344	Sequence 16344, A	758	98.5	4.5	1836	1	US-11-514-704-22177	Sequence 22177, A
C 686	99	4.5	976	1	US-10-438-246-28231	Sequence 28231, A	759	98.5	4.5	1854	1	US-10-547-956-17	Sequence 17, Appl
C 687	99	4.5	989	8	US-11-514-704-25032	Sequence 25032, A	760	98.5	4.5	1867	8	US-11-649-663A-3355	Sequence 3355, Ap
C 688	99	4.5	1036	1	US-10-438-246-11427	Sequence 11427, A	761	98.5	4.5	1909	8	US-11-649-663A-3777	Sequence 3777, Ap
C 689	99	4.5	1045	1	US-10-438-246-27141	Sequence 27141, A	762	98.5	4.5	1931	8	US-11-514-704-6529	Sequence 6529, Ap
C 690	99	4.5	1074	8	US-11-699-588-14	Sequence 14, Appl	763	98.5	4.5	1956	8	US-11-514-704-4783	Sequence 4783, Ap
C 691	99	4.5	1116	8	US-11-713-768-68953	Sequence 68953, A	764	98.5	4.5	2149	8	US-11-649-663A-271	Sequence 271, App
C 692	99	4.5	1157	8	US-11-713-768-6941	Sequence 6941, Ap	765	98.5	4.5	2159	8	US-11-514-704-943	Sequence 943, App
C 693	99	4.5	1173	1	US-10-438-246-11485	Sequence 11485, A	766	98.5	4.5	2313	8	US-11-514-704-390	Sequence 390, App
C 694	99	4.5	1178	8	US-11-649-663A-4045	Sequence 4045, Ap	767	98.5	4.5	2384	8	US-11-514-704-16088	Sequence 16088, A
C 695	99	4.5	1188	1	US-10-438-246-21120	Sequence 21120, A	768	98.5	4.5	2550	8	US-11-514-704-13928	Sequence 13928, A
C 696	99	4.5	1353	8	US-11-713-768-65219	Sequence 65219, A	769	98.5	4.5	2744	8	US-11-514-704-1358	Sequence 1358, Ap
C 697	99	4.5	1489	8	US-11-713-768-19277	Sequence 19277, A	770	98.5	4.5	3203	8	US-11-514-704-11302	Sequence 11302, A
C 698	99	4.5	1520	8	US-10-438-246-15285	Sequence 15285, A	771	98.5	4.5	3319	1	US-10-533-069-566	Sequence 566, App
C 699	99	4.5	1596	1	US-10-438-246-13222	Sequence 13222, A	772	98.5	4.5	4314	8	US-11-514-704-24321	Sequence 24321, A
C 700	99	4.5	1631	8	US-11-614-098-9	Sequence 9, Appl	773	98.5	4.5	4766	1	US-10-438-246-8137	Sequence 8137, Ap
C 701	99	4.5	1636	8	US-11-514-704-2451	Sequence 2451, Ap	774	98.5	4.5	4881	1	US-10-438-246-14505	Sequence 14505, A
C 702	99	4.5	1676	8	US-11-713-768-18691	Sequence 18691, A	775	98.5	4.5	5406	1	US-10-438-246-12260	Sequence 12260, A
C 703	99	4.5	1696	8	US-11-649-663A-629	Sequence 629, App	776	98.5	4.5	5622	1	US-10-438-246-12261	Sequence 12261, A
C 704	99	4.5	1696	8	US-11-713-768-7273	Sequence 7273, Ap	777	98.5	4.5	5941	1	US-10-438-246-21796	Sequence 21796, A
C 705	99	4.5	1741	8	US-11-649-663A-725	Sequence 725, App	778	98.5	4.5	6258	8	US-11-514-704-7695	Sequence 7695, Ap
C 706	99	4.5	1741	8	US-11-713-768-3093	Sequence 3093, Ap	779	98.5	4.5	6718	8	US-11-514-704-38	Sequence 38, Appl
C 707	99	4.5	1766	8	US-11-514-704-14695	Sequence 14695, A	780	98.5	4.5	9475	8	US-11-514-704-21252	Sequence 21252, A
C 708	99	4.5	1849	8	US-11-713-768-66298	Sequence 66298, A	781	98.5	4.5	13290	8	US-11-585-666-24	Sequence 24, Appl
C 709	99	4.5	1855	8	US-11-560-738A-27	Sequence 27, Appl	782	98.5	4.5	13302	8	US-11-585-666-23	Sequence 23, Appl
C 710	99	4.5	1855	8	US-11-713-768-17659	Sequence 17659, A	783	98.5	4.5	100534	8	US-11-257-477-160	Sequence 160, App
C 711	99	4.5	1861	8	US-11-713-768-4319	Sequence 4319, Ap	784	98	4.4	550	8	US-11-196-018A-63	Sequence 63, Appl
C 712	99	4.5	1955	1	US-10-438-246-22511	Sequence 22511, A	785	98	4.4	721	8	US-11-713-768-96116	Sequence 96116, A
C 713	99	4.5	1982	8	US-11-514-704-15233	Sequence 15233, A	786	98	4.4	734	8	US-11-649-663A-247	Sequence 247, App
C 714	99	4.5	1984	8	US-11-514-704-13232	Sequence 13232, A	787	98	4.4	734	8	US-11-713-768-76466	Sequence 76466, A
C 715	99	4.5	2058	8	US-11-514-704-22438	Sequence 22438, A	788	98	4.4	735	8	US-11-713-768-1363	Sequence 1363, Ap
C 716	99	4.5	2117	8	US-11-514-704-4842	Sequence 4842, Ap	789	98	4.4	810	1	US-10-438-246-27133	Sequence 27133, A
C 717	99	4.5	2135	8	US-11-713-768-65492	Sequence 65492, A	790	98	4.4	859	8	US-11-514-704-5542	Sequence 5542, Ap
C 718	99	4.5	2408	8	US-11-514-704-6643	Sequence 6643, Ap	791	98	4.4	978	8	US-11-649-663A-3619	Sequence 3619, Ap
C 719	99	4.5	2869	8	US-11-514-704-5917	Sequence 5917, Ap	792	98	4.4	1121	8	US-11-728-567-431	Sequence 431, App
C 720	99	4.5	3041	8	US-11-514-704-3853	Sequence 3853, Ap	793	98	4.4	1152	8	US-11-728-567-431	Sequence 431, App
C 721	99	4.5	3093	8	US-11-514-704-22100	Sequence 22100, A	794	98	4.4	1282	8	US-11-514-704-4249	Sequence 4249, Ap
C 722	99	4.5	3101	8	US-11-514-704-57160	Sequence 57160, A	795	98	4.4	1306	8	US-11-713-768-16765	Sequence 16765, A
C 723	99	4.5	3162	8	US-11-514-704-22100	Sequence 5762, Ap	796	98	4.4	1316	8	US-11-713-768-10382	Sequence 10382, A
C 724	99	4.5	4189	8	US-11-514-704-14870	Sequence 14870, A	797	98	4.4	1317	1	US-11-713-768-60707	Sequence 60707, A
C 725	99	4.5	4777	8	US-11-713-768-101107	Sequence 101107, A	798	98	4.4	1426	8	US-10-438-246-11476	Sequence 11476, A
C 726	99	4.5	5265	1	US-10-438-246-13848	Sequence 13848, A	799	98	4.4	1426	8	US-11-713-768-11115	Sequence 11115, A
C 727	99	4.5	5567	1	US-10-438-246-22996	Sequence 22996, A	800	98	4.4	1449	8	US-11-713-768-5574	Sequence 5574, Ap
C 728	99	4.5	5746	8	US-11-551-744-158	Sequence 158, App	801	98	4.4	1478	8	US-11-514-704-17827	Sequence 17827, Ap
C 729	99	4.5	6182	1	US-10-533-069-1283	Sequence 1283, Ap	802	98	4.4	1509	8	US-11-713-768-43466	Sequence 43466, A
C 730	99	4.5	6803	8	US-11-625-795-10	Sequence 10, Appl	803	98	4.4	1509	8	US-11-713-768-47031	Sequence 47031, A
C 731	99	4.5	7226	8	US-11-625-795-8	Sequence 8, Appl	804	98	4.4	1520	8	US-11-713-768-2243	Sequence 2243, Ap
C 732	98.5	4.5	803	1	US-10-438-246-380	Sequence 380, App	805	98	4.4	1640	8	US-11-514-704-5358	Sequence 5358, Ap
C 733	98.5	4.5	818	8	US-11-514-704-5500	Sequence 5500, Ap	806	98	4.4	1640	8	US-10-438-246-22340	Sequence 22340, A
C 734	98.5	4.5	1042	8	US-11-713-768-62185	Sequence 62185, A	807	98	4.4	1703	1	US-11-713-768-14192	Sequence 14192, A
C 735	98.5	4.5	1058	8	US-11-649-663A-5083	Sequence 5083, Ap	808	98	4.4	1854	1	US-10-547-956-731	Sequence 731, App
C 736	98.5	4.5	1080	8	US-11-514-704-20174	Sequence 20174, A	809	98	4.4	1854	1	US-10-547-956-731	Sequence 731, App
C 737	98.5	4.5	1108	8	US-11-713-768-6348	Sequence 6348, Ap	810	98	4.4	2108	8	US-11-347-780-15	Sequence 15, Appl
C 738	98.5	4.5	1164	1	US-10-438-246-11742	Sequence 11742, A	811	98	4.4	2259	8	US-11-514-704-17033	Sequence 17033, A
C 739	98.5	4.5	1174	8	US-11-649-663A-665	Sequence 665, App	812	98	4.4	2342	8	US-11-649-663A-4475	Sequence 4475, Ap
C 740	98.5	4.5	1174	8	US-11-713-768-9315	Sequence 9315, Ap	813	98	4.4	2518	8	US-11-514-704-19723	Sequence 19723, A

C 814	98	4.4	2522	8	US-11-514-704-15691	Sequence 15691, A	C 887	97.5	4.4	3237	8	US-11-514-704-13601	Sequence 13601, A
C 815	98	4.4	2691	8	US-11-513-768-73159	Sequence 73159, A	C 888	97.5	4.4	3261	8	US-11-514-704-17265	Sequence 17265, A
C 816	98	4.4	2749	8	US-11-514-704-13631	Sequence 13631, A	C 889	97.5	4.4	3303	8	US-11-514-704-11827	Sequence 11827, A
C 817	98	4.4	2831	8	US-11-514-704-11133	Sequence 11133, A	C 890	97.5	4.4	3481	8	US-11-514-704-1065	Sequence 1065, Ap
C 818	98	4.4	2935	1	US-10-438-246-29134	Sequence 29134, A	C 891	97.5	4.4	3485	8	US-11-514-704-6536	Sequence 6536, Ap
C 819	98	4.4	3172	8	US-11-514-704-15622	Sequence 15622, A	C 892	97.5	4.4	4589	8	US-11-514-704-10133	Sequence 10133, A
C 820	98	4.4	4144	8	US-11-514-704-10517	Sequence 10517, A	C 893	97.5	4.4	4764	8	US-11-514-704-4025	Sequence 4025, Ap
C 821	98	4.4	4179	8	US-11-514-704-19149	Sequence 19149, A	C 894	97.5	4.4	4886	8	US-11-514-704-3107	Sequence 3107, Ap
C 822	98	4.4	4314	8	US-11-514-704-22589	Sequence 22589, A	C 895	97.5	4.4	5004	8	US-11-514-704-19387	Sequence 19387, Ap
C 823	98	4.4	4603	8	US-11-514-704-21510	Sequence 21510, A	C 896	97.5	4.4	5349	8	US-11-514-704-2622	Sequence 2622, Ap
C 824	98	4.4	4637	8	US-11-514-704-6273	Sequence 6273, Ap	C 897	97.5	4.4	5632	1	US-11-514-704-7909	Sequence 7909, Ap
C 825	98	4.4	7741	8	US-11-514-704-20803	Sequence 20803, A	C 898	97.5	4.4	6282	1	US-10-438-246-5301	Sequence 5301, Ap
C 826	98	4.4	10057	1	US-10-533-069-212	Sequence 212, App	C 899	97.5	4.4	8212	1	US-11-407-888-24	Sequence 24, Appl
C 827	97.5	4.4	705	8	US-11-713-768-27777	Sequence 27777, A	C 900	97	4.4	673	1	US-10-438-246-13115	Sequence 13115, A
C 828	97.5	4.4	705	8	US-11-713-768-1367	Sequence 3367, A	C 901	97	4.4	715	8	US-11-713-768-38229	Sequence 38229, A
C 829	97.5	4.4	810	8	US-11-713-768-39374	Sequence 39374, A	C 902	97	4.4	866	1	US-10-438-246-28875	Sequence 28875, A
C 830	97.5	4.4	810	8	US-11-713-768-32964	Sequence 32964, A	C 903	97	4.4	936	1	US-10-438-246-11247	Sequence 11247, A
C 831	97.5	4.4	816	8	US-11-514-704-23143	Sequence 23143, A	C 904	97	4.4	996	8	US-11-713-768-62416	Sequence 62416, A
C 832	97.5	4.4	877	8	US-11-649-663A-3615	Sequence 3615, Ap	C 905	97	4.4	1026	8	US-11-514-704-6099	Sequence 6099, Ap
C 833	97.5	4.4	931	8	US-11-713-768-56066	Sequence 56066, A	C 906	97	4.4	1046	8	US-11-514-704-6062	Sequence 6062, Ap
C 834	97.5	4.4	939	8	US-11-713-768-68081	Sequence 68081, A	C 907	97	4.4	1147	8	US-11-713-768-7289	Sequence 7289, Ap
C 835	97.5	4.4	985	8	US-11-514-704-643	Sequence 643, App	C 908	97	4.4	1230	1	US-10-438-246-27294	Sequence 27294, A
C 836	97.5	4.4	994	1	US-10-438-246-11171	Sequence 11171, A	C 909	97	4.4	1230	8	US-11-514-704-11984	Sequence 11984, A
C 837	97.5	4.4	1002	1	US-10-438-246-12547	Sequence 12547, A	C 910	97	4.4	1378	8	US-11-713-768-54632	Sequence 54632, A
C 838	97.5	4.4	1002	1	US-10-438-246-21982	Sequence 21982, A	C 911	97	4.4	1399	8	US-11-649-663A-2893	Sequence 2893, Ap
C 839	97.5	4.4	1014	1	US-10-438-246-13165	Sequence 13165, A	C 912	97	4.4	1440	8	US-11-514-704-3918	Sequence 3918, Ap
C 840	97.5	4.4	1014	1	US-10-438-246-22454	Sequence 22454, A	C 913	97	4.4	1459	8	US-11-514-704-19150	Sequence 19150, A
C 841	97.5	4.4	1090	8	US-11-713-768-35686	Sequence 35686, A	C 914	97	4.4	1478	8	US-11-649-663A-3167	Sequence 3167, Ap
C 842	97.5	4.4	1090	8	US-11-713-768-50873	Sequence 50873, A	C 915	97	4.4	1488	1	US-10-554-789-6	Sequence 6, Appl
C 843	97.5	4.4	1128	8	US-11-514-704-13366	Sequence 13366, A	C 916	97	4.4	1490	8	US-11-713-768-65113	Sequence 65113, A
C 844	97.5	4.4	1157	8	US-11-713-768-65185	Sequence 65185, A	C 917	97	4.4	1501	8	US-11-713-768-9361	Sequence 9361, Ap
C 845	97.5	4.4	1189	8	US-11-514-704-9949	Sequence 9949, Ap	C 918	97	4.4	1599	8	US-11-649-663A-5079	Sequence 5079, Ap
C 846	97.5	4.4	1221	8	US-11-514-704-10375	Sequence 10375, A	C 919	97	4.4	1611	1	US-11-514-704-3506	Sequence 3506, Ap
C 847	97.5	4.4	1230	1	US-10-438-246-12456	Sequence 12456, A	C 920	97	4.4	1674	1	US-10-438-246-22399	Sequence 22399, Ap
C 848	97.5	4.4	1254	1	US-10-438-246-11187	Sequence 11187, A	C 921	97	4.4	1676	8	US-11-649-663A-627	Sequence 627, App
C 849	97.5	4.4	1277	8	US-11-713-768-3365	Sequence 3365, Ap	C 922	97	4.4	1768	8	US-11-713-768-7160	Sequence 7160, Ap
C 850	97.5	4.4	1336	8	US-11-713-768-2263	Sequence 2263, Ap	C 923	97	4.4	1810	8	US-11-649-663A-5201	Sequence 5201, Ap
C 851	97.5	4.4	1379	8	US-11-649-663A-645	Sequence 645, App	C 924	97	4.4	1810	8	US-11-514-704-11106	Sequence 11106, A
C 852	97.5	4.4	1379	8	US-11-713-768-2038	Sequence 2038, Ap	C 925	97	4.4	1922	8	US-11-514-704-15275	Sequence 15275, A
C 853	97.5	4.4	1411	1	US-10-438-246-21917	Sequence 21917, A	C 926	97	4.4	1928	1	US-10-438-246-3534	Sequence 3534, Ap
C 854	97.5	4.4	1415	1	US-10-438-246-29894	Sequence 29894, A	C 927	97	4.4	1953	8	US-11-514-704-18492	Sequence 18492, A
C 855	97.5	4.4	1461	8	US-11-713-768-11236	Sequence 11236, A	C 928	97	4.4	1957	8	US-11-649-663A-2319	Sequence 2319, Ap
C 856	97.5	4.4	1502	1	US-10-438-246-23476	Sequence 23476, A	C 929	97	4.4	1957	8	US-11-713-768-10679	Sequence 10679, A
C 857	97.5	4.4	1573	8	US-11-713-768-18605	Sequence 18605, A	C 930	97	4.4	1983	8	US-11-552-440-5	Sequence 5, Appl
C 858	97.5	4.4	1653	8	US-11-713-768-67411	Sequence 67411, A	C 931	97	4.4	2047	8	US-11-514-704-3910	Sequence 3910, Ap
C 859	97.5	4.4	1680	8	US-11-649-663A-711	Sequence 711, App	C 932	97	4.4	2050	8	US-11-514-704-13979	Sequence 13979, A
C 860	97.5	4.4	1680	8	US-11-713-768-16332	Sequence 16332, A	C 933	97	4.4	2111	8	US-11-713-768-66139	Sequence 66139, A
C 861	97.5	4.4	1709	8	US-11-713-768-16544	Sequence 16544, A	C 934	97	4.4	2223	8	US-11-514-704-1364	Sequence 1364, Ap
C 862	97.5	4.4	1716	8	US-11-514-704-21441	Sequence 21441, A	C 935	97	4.4	2268	8	US-11-514-704-12477	Sequence 12477, A
C 863	97.5	4.4	1745	8	US-11-649-663A-959	Sequence 959, App	C 936	97	4.4	2254	8	US-11-514-704-20954	Sequence 20954, A
C 864	97.5	4.4	1745	8	US-11-713-768-16127	Sequence 16127, A	C 937	97	4.4	2573	8	US-11-489-234-4	Sequence 4, Appl
C 865	97.5	4.4	1803	8	US-11-514-704-19484	Sequence 19484, A	C 938	97	4.4	3004	8	US-11-713-768-86311	Sequence 86311, A
C 866	97.5	4.4	1830	1	US-10-438-246-20923	Sequence 20923, A	C 939	97	4.4	3039	8	US-11-514-704-16346	Sequence 16346, A
C 867	97.5	4.4	1855	8	US-11-514-704-7910	Sequence 7910, Ap	C 940	97	4.4	3088	8	US-11-347-780-3	Sequence 3, Appl
C 868	97.5	4.4	1866	8	US-11-514-704-17035	Sequence 17035, A	C 941	97	4.4	3152	8	US-11-713-768-86282	Sequence 86282, A
C 869	97.5	4.4	1937	8	US-11-514-704-14872	Sequence 14872, A	C 942	97	4.4	3162	8	US-10-438-246-12905	Sequence 12905, A
C 870	97.5	4.4	1993	8	US-11-649-663A-3539	Sequence 3539, Ap	C 943	97	4.4	3459	1	US-10-438-246-22284	Sequence 22284, A
C 871	97.5	4.4	2008	8	US-11-713-768-35296	Sequence 35296, A	C 944	97	4.4	3578	1	US-11-514-704-22955	Sequence 22955, A
C 872	97.5	4.4	2024	8	US-11-514-704-2748	Sequence 2748, Ap	C 945	97	4.4	3594	1	US-10-438-246-22884	Sequence 22884, A
C 873	97.5	4.4	2119	8	US-11-514-704-11354	Sequence 11354, A	C 946	97	4.4	3796	8	US-11-514-704-22687	Sequence 22687, A
C 874	97.5	4.4	2161	8	US-11-514-704-17160	Sequence 17160, A	C 947	97	4.4	3836	8	US-11-514-704-20349	Sequence 20349, A
C 875	97.5	4.4	2230	8	US-11-514-704-23185	Sequence 23185, A	C 948	97	4.4	4098	8	US-11-514-704-18491	Sequence 18491, Ap
C 876	97.5	4.4	2254	8	US-11-514-704-1489	Sequence 1489, Ap	C 949	97	4.4	4503	8	US-11-514-704-1305	Sequence 1305, Ap
C 877	97.5	4.4	2355	1	US-10-438-246-13672	Sequence 13672, A	C 950	97	4.4	4517	8	US-11-514-704-8829	Sequence 8829, Ap
C 878	97.5	4.4	2594	8	US-11-514-704-17647	Sequence 17647, A	C 951	97	4.4	5336	8	US-11-514-704-24001	Sequence 24001, A
C 879	97.5	4.4	2627	8	US-11-514-704-20218	Sequence 20218, A	C 952	97	4.4	5718	8	US-11-514-704-20708	Sequence 20708, A
C 880	97.5	4.4	2724	8	US-11-713-768-90278	Sequence 90278, A	C 953	97	4.4	6519	8	US-11-796-730-2605	Sequence 2605, Ap
C 881	97.5	4.4	2724	8	US-11-713-768-94034	Sequence 94034, A	C 954	97	4.4	7419	8	US-11-514-704-21253	Sequence 21253, A
C 882	97.5	4.4	2912	8	US-11-514-704-5887	Sequence 5887, Ap	C 955	96.5	4.4	514	1	US-10-567-764-24	Sequence 24, Appl
C 883	97.5	4.4	2981	8	US-11-514-704-7251	Sequence 7251, Ap	C 956	96.5	4.4	770	1	US-11-713-768-3329	Sequence 3329, Ap
C 884	97.5	4.4	3073	8	US-11-514-704-21267	Sequence 21267, A	C 957	96.5	4.4	791	1	US-10-438-246-3273	Sequence 3273, Ap
C 885	97.5	4.4	3219	1	US-10-438-246-622	Sequence 622, App	C 958	96.5	4.4	861	8	US-11-514-704-17347	Sequence 17347, A
C 886	97.5	4.4	3234	8	US-11-514-704-6142	Sequence 6142, App	C 959	96.5	4.4	870	1	US-10-438-246-12057	Sequence 12057, A

c 960	96.5	4.4	924	8	US-11-514-704-21056	Sequence 21056, A	c1033	96	4.3	1508	8	US-11-713-768-56858	Sequence 56858, A
961	96.5	4.4	1062	8	US-11-713-768-61508	Sequence 61508, A	1034	96	4.3	1334	8	US-11-713-768-109087	Sequence 109087, A
962	96.5	4.4	1067	8	US-11-713-768-61508	Sequence 15998, A	c1035	96	4.3	1363	8	US-11-713-768-90350	Sequence 90350, A
c 963	96.5	4.4	1213	8	US-11-728-567-553	Sequence 553, App	c1036	96	4.3	1563	8	US-11-713-768-94106	Sequence 94106, A
c 964	96.5	4.4	1235	8	US-11-713-768-35705	Sequence 35705, A	1037	96	4.3	1568	8	US-10-533-069-1185	Sequence 1185, App
965	96.5	4.4	1241	8	US-11-514-704-15282	Sequence 15282, A	1038	96	4.3	1725	8	US-11-713-768-66173	Sequence 66173, A
c 966	96.5	4.4	1327	8	US-11-713-768-104901	Sequence 104901, A	c1039	96	4.3	1772	8	US-11-514-704-18079	Sequence 18079, A
c 967	96.5	4.4	1344	8	US-11-713-768-70617	Sequence 70617, A	1040	96	4.3	1839	8	US-11-713-768-86035	Sequence 86035, A
c 968	96.5	4.4	1346	8	US-11-514-704-23101	Sequence 23101, A	c1041	96	4.3	1854	1	US-10-547-956-131	Sequence 131, App
c 969	96.5	4.4	1347	8	US-11-649-663A-843	Sequence 843, App	c1042	96	4.3	1860	8	US-11-514-704-20274	Sequence 20274, A
c 970	96.5	4.4	1347	8	US-11-713-768-29732	Sequence 29732, A	1043	96	4.3	1863	8	US-11-713-768-15756	Sequence 15756, A
c 971	96.5	4.4	1347	8	US-11-713-768-33322	Sequence 33322, A	1044	96	4.3	1885	8	US-11-713-768-69234	Sequence 69234, A
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973	96.5	4.4	1409	8	US-11-713-768-64374	Sequence 64374, A	1046	96	4.3	1902	8	US-11-514-704-4311	Sequence 4311, App
974	96.5	4.4	1425	8	US-11-713-768-62920	Sequence 62920, A	c1047	96	4.3	1960	8	US-11-514-704-3160	Sequence 3160, App
975	96.5	4.4	1428	8	US-11-713-768-64624	Sequence 64624, A	c1048	96	4.3	1965	1	US-10-438-246-21361	Sequence 21361, A
976	96.5	4.4	1478	8	US-11-713-768-16191	Sequence 16191, A	1049	96	4.3	2115	8	US-11-713-768-13273	Sequence 13273, A
977	96.5	4.4	1479	8	US-11-514-704-13364	Sequence 13364, A	1050	96	4.3	2127	8	US-11-514-704-3348	Sequence 3348, App
978	96.5	4.4	1482	8	US-11-713-768-67114	Sequence 67114, A	1051	96	4.3	2180	8	US-11-514-704-23625	Sequence 23625, A
979	96.5	4.4	1494	8	US-11-514-704-15247	Sequence 15247, A	1052	96	4.3	2206	8	US-11-713-768-58992	Sequence 58992, A
980	96.5	4.4	1513	8	US-11-713-768-50788	Sequence 50788, A	1053	96	4.3	2240	8	US-11-514-704-4572	Sequence 4572, App
c 981	96.5	4.4	1663	8	US-11-514-704-6143	Sequence 6143, App	c1054	96	4.3	2376	1	US-10-438-246-4407	Sequence 4407, App
982	96.5	4.4	1755	8	US-11-514-704-13423	Sequence 13423, A	c1055	96	4.3	2449	8	US-11-514-704-11104	Sequence 11104, A
c 983	96.5	4.4	1756	8	US-11-713-768-1568	Sequence 1568, App	c1056	96	4.3	2563	8	US-11-514-704-6617	Sequence 6617, App
c 984	96.5	4.4	1762	8	US-11-713-768-17027	Sequence 17027, A	c1057	96	4.3	2629	8	US-11-514-704-19791	Sequence 19791, A
985	96.5	4.4	1856	8	US-11-713-768-65029	Sequence 65029, A	1058	96	4.3	2658	8	US-11-514-704-3329	Sequence 3329, App
986	96.5	4.4	1872	8	US-11-514-704-24976	Sequence 24976, A	c1059	96	4.3	2764	8	US-11-514-704-20411	Sequence 20411, A
c 987	96.5	4.4	1909	8	US-11-649-663A-3777	Sequence 3777, App	1060	96	4.3	2821	1	US-10-562-377-148	Sequence 148, App
c 988	96.5	4.4	1912	8	US-11-514-704-13395	Sequence 13395, A	c1061	96	4.3	2900	8	US-11-514-704-20426	Sequence 20426, A
c 989	96.5	4.4	2089	8	US-11-514-704-24996	Sequence 24996, A	c1062	96	4.3	3030	8	US-11-514-704-9448	Sequence 9448, App
c 990	96.5	4.4	2136	8	US-11-713-768-16390	Sequence 16390, A	c1063	96	4.3	3030	8	US-11-514-704-3591	Sequence 3591, App
991	96.5	4.4	2157	1	US-10-438-246-13677	Sequence 13677, A	c1064	96	4.3	3729	8	US-11-713-768-799047	Sequence 799047, A
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993	96.5	4.4	2157	1	US-10-438-246-14483	Sequence 14483, A	1066	96	4.3	3959	8	US-11-514-704-4962	Sequence 4962, App
994	96.5	4.4	2247	1	US-10-438-246-1483	Sequence 1483, A	1067	96	4.3	4102	1	US-10-562-377-139	Sequence 139, App
995	96.5	4.4	2289	1	US-10-438-246-11250	Sequence 11250, A	c1068	96	4.3	4102	1	US-10-562-377-139	Sequence 139, App
c 996	96.5	4.4	2316	8	US-11-514-704-13034	Sequence 13034, App	1069	96	4.3	4168	8	US-11-514-704-12307	Sequence 12307, A
c 997	96.5	4.4	3005	8	US-11-514-704-22954	Sequence 22954, A	1070	96	4.3	4612	8	US-11-514-704-5691	Sequence 5691, App
998	96.5	4.4	3093	8	US-11-514-704-23986	Sequence 23986, A	c1071	96	4.3	4650	8	US-11-514-704-21769	Sequence 21769, A
999	96.5	4.4	3198	8	US-11-713-768-30942	Sequence 30942, A	c1072	96	4.3	5095	8	US-11-514-704-10099	Sequence 10099, A
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c1002	96.5	4.4	3332	8	US-11-514-704-13369	Sequence 1369, App	1075	95.5	4.3	5431	8	US-11-713-768-4298	Sequence 4298, App
c1003	96.5	4.4	3788	8	US-11-514-704-23621	Sequence 23621, A	1076	95.5	4.3	5431	8	US-11-713-768-11444	Sequence 11444, A
c1004	96.5	4.4	4419	8	US-11-514-704-3106	Sequence 3106, App	1077	95.5	4.3	1005	1	US-10-438-246-26636	Sequence 26636, A
c1005	96.5	4.4	4506	1	US-10-438-246-14504	Sequence 14504, A	1078	95.5	4.3	1031	1	US-10-438-246-26636	Sequence 26636, A
1006	96.5	4.4	4698	1	US-10-438-246-13852	Sequence 13852, A	1079	95.5	4.3	1048	8	US-11-514-704-5633	Sequence 5633, App
1007	96.5	4.4	4995	8	US-10-438-246-23006	Sequence 23006, A	1080	95.5	4.3	1113	8	US-11-796-730-2120	Sequence 2120, App
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c1009	96.5	4.4	7907	1	US-10-438-246-23342	Sequence 23342, A	1082	95.5	4.3	1120	8	US-11-713-768-62844	Sequence 62844, A
c1010	96.5	4.4	102790	8	US-11-257-477-163	Sequence 163, App	c1083	95.5	4.3	1146	8	US-11-514-704-15737	Sequence 15737, A
1011	96	4.3	617	8	US-11-514-704-19532	Sequence 19532, A	1084	95.5	4.3	1179	8	US-11-514-704-24397	Sequence 24397, A
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c1013	96	4.3	958	8	US-11-713-768-4183	Sequence 4183, App	1086	95.5	4.3	1244	8	US-11-713-768-9407	Sequence 9407, App
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1016	96	4.3	976	8	US-11-514-704-20333	Sequence 20333, A	1089	95.5	4.3	1321	8	US-11-713-768-67877	Sequence 67877, A
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1018	96	4.3	1041	8	US-11-713-768-67076	Sequence 67076, A	1091	95.5	4.3	1329	8	US-11-713-768-95678	Sequence 95678, A
1019	96	4.3	1056	8	US-11-713-768-8147	Sequence 8147, App	c1092	95.5	4.3	1344	8	US-11-713-768-88600	Sequence 88600, A
1020	96	4.3	1098	1	US-10-438-246-21455	Sequence 21455, A	c1093	95.5	4.3	1344	8	US-11-713-768-92356	Sequence 92356, A
c1021	96	4.3	1106	8	US-11-514-704-20472	Sequence 20472, A	c1094	95.5	4.3	1354	1	US-10-438-246-22196	Sequence 22196, A
1022	96	4.3	1273	8	US-11-514-704-4042	Sequence 4042, App	1095	95.5	4.3	1365	8	US-11-713-768-16447	Sequence 16447, A
1023	96	4.3	1300	8	US-11-713-768-68979	Sequence 68979, A	1096	95.5	4.3	1368	8	US-11-713-768-14150	Sequence 14150, A
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1027	96	4.3	1327	1	US-10-438-246-369	Sequence 369, App	1100	95.5	4.3	1497	1	US-10-438-246-2936	Sequence 2936, A
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1032	96	4.3	1504	8	US-11-713-768-9376	Sequence 9376, App	1105	95.5	4.3	1562	8	US-11-713-768-60275	Sequence 60275, A

1106	95.5	4.3	1580	8	US-11-649-663A-1607	Sequence 3607, Ap	1179	95	4.3	1374	8	US-11-713-768-68134	Sequence 68134, A
1107	95.5	4.3	1582	8	US-11-713-768-17681	Sequence 17681, Ap	cl180	95	4.3	1391	8	US-11-713-768-7039	Sequence 7039, Ap
1108	95.5	4.3	1589	8	US-11-713-768-57022	Sequence 57022, A	1181	95	4.3	1422	8	US-11-582-540-54	Sequence 54, Appl
1109	95.5	4.3	1593	8	US-11-629-727-53	Sequence 53, Appl	1182	95	4.3	1463	8	US-11-514-704-5543	Sequence 5543, Ap
cl1110	95.5	4.3	1599	8	US-11-514-704-23279	Sequence 23279, A	1183	95	4.3	1495	8	US-11-514-704-20080	Sequence 20080, A
cl1111	95.5	4.3	1632	8	US-11-713-768-62601	Sequence 62601, A	1184	95	4.3	1523	8	US-11-713-768-68428	Sequence 68428, A
cl1112	95.5	4.3	1656	8	US-11-514-704-9725	Sequence 9725, Ap	1185	95	4.3	1549	8	US-11-514-704-23187	Sequence 23187, A
1113	95.5	4.3	1691	8	US-11-649-663A-5437	Sequence 5437, Ap	1186	95	4.3	1544	8	US-11-713-768-2719	Sequence 2719, Ap
1114	95.5	4.3	1758	8	US-11-514-704-6513	Sequence 6513, Ap	1187	95	4.3	1555	8	US-11-514-704-12359	Sequence 12359, A
1115	95.5	4.3	1788	1	US-10-547-956-351	Sequence 351, App	1188	95	4.3	1583	1	US-10-438-246-22615	Sequence 22615, A
1116	95.5	4.3	1828	8	US-11-713-768-63031	Sequence 63031, A	1189	95	4.3	1614	8	US-11-713-768-1798	Sequence 1798, Ap
1117	95.5	4.3	1894	8	US-11-514-704-24587	Sequence 24587, A	1190	95	4.3	1614	8	US-11-713-768-2664	Sequence 2664, Ap
cl1118	95.5	4.3	1910	8	US-11-514-704-19872	Sequence 19872, A	1191	95	4.3	1614	8	US-11-713-768-8349	Sequence 8349, Ap
cl1119	95.5	4.3	1913	8	US-11-713-768-17553	Sequence 17553, A	1192	95	4.3	1635	8	US-11-514-704-17860	Sequence 17860, A
1120	95.5	4.3	1971	8	US-11-713-768-89083	Sequence 89083, A	cl1193	95	4.3	1714	8	US-11-713-768-11200	Sequence 11200, A
1121	95.5	4.3	1971	8	US-11-713-768-92839	Sequence 92839, A	cl1194	95	4.3	1712	8	US-11-713-768-53798	Sequence 53798, A
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1123	95.5	4.3	1991	8	US-11-713-768-35009	Sequence 35009, A	1196	95	4.3	1732	8	US-11-713-768-66557	Sequence 66557, A
1124	95.5	4.3	2025	8	US-11-713-768-69474	Sequence 69474, A	1197	95	4.3	1741	8	US-11-713-768-66088	Sequence 66088, A
1125	95.5	4.3	2103	8	US-11-629-727-52	Sequence 52, Appl	1198	95	4.3	1794	8	US-11-514-704-16159	Sequence 16159, A
1126	95.5	4.3	2152	8	US-11-514-704-271	Sequence 271, App	cl1199	95	4.3	1797	1	US-10-438-246-2819	Sequence 2819, Ap
1127	95.5	4.3	2231	8	US-11-560-738A-19	Sequence 19, Appl	1200	95	4.3	1808	1	US-11-514-704-1539	Sequence 1539, Ap
1128	95.5	4.3	2286	8	US-11-713-768-17343	Sequence 17343, A	1201	95	4.3	1863	8	US-11-713-768-91379	Sequence 91379, A
1129	95.5	4.3	2314	8	US-11-514-704-23666	Sequence 23666, A	1202	95	4.3	1863	8	US-11-713-768-95135	Sequence 95135, A
1130	95.5	4.3	2324	8	US-11-514-704-8390	Sequence 8390, Ap	1203	95	4.3	1870	8	US-11-514-704-16348	Sequence 16348, A
1131	95.5	4.3	2333	8	US-11-514-704-14673	Sequence 14673, A	cl1204	95	4.3	1881	1	US-10-438-246-10978	Sequence 10978, A
1132	95.5	4.3	2362	8	US-11-514-704-20974	Sequence 20974, A	1205	95	4.3	1921	1	US-10-438-246-835	Sequence 835, App
1133	95.5	4.3	2416	8	US-11-713-768-46469	Sequence 46469, A	1206	95	4.3	1929	8	US-11-489-234-34	Sequence 34, Appl
1134	95.5	4.3	2704	8	US-11-713-768-46304	Sequence 46304, A	1207	95	4.3	1953	8	US-11-514-704-9098	Sequence 9098, Ap
1135	95.5	4.3	2729	8	US-11-514-704-18450	Sequence 18450, A	1208	95	4.3	1957	1	US-10-438-246-14255	Sequence 14255, A
1136	95.5	4.3	2957	8	US-11-514-704-12333	Sequence 12333, A	1209	95	4.3	1973	8	US-11-514-704-2472	Sequence 2472, Ap
cl1137	95.5	4.3	3011	8	US-11-514-704-19103	Sequence 19103, A	1210	95	4.3	2058	8	US-11-514-704-15872	Sequence 15872, A
cl1138	95.5	4.3	3214	8	US-11-514-704-6297	Sequence 6297, Ap	1211	95	4.3	2077	1	US-10-438-246-315	Sequence 315, App
1139	95.5	4.3	3248	8	US-11-514-704-9848	Sequence 9848, Ap	1212	95	4.3	2183	8	US-11-713-768-108593	Sequence 108593, A
cl1140	95.5	4.3	3283	8	US-11-514-704-15803	Sequence 15803, A	1213	95	4.3	2230	8	US-11-713-768-47147	Sequence 47147, A
1141	95.5	4.3	3763	8	US-11-544-679-1	Sequence 1, Appl	1214	95	4.3	2242	8	US-11-514-704-11809	Sequence 11809, A
1142	95.5	4.3	3764	8	US-11-514-704-22440	Sequence 22440, A	1215	95	4.3	2264	8	US-11-713-768-77314	Sequence 77314, A
cl1143	95.5	4.3	3901	8	US-11-514-704-14532	Sequence 14532, A	1216	95	4.3	2345	8	US-11-514-704-18720	Sequence 18720, A
cl1144	95.5	4.3	3936	8	US-11-514-704-19592	Sequence 19592, A	1217	95	4.3	2361	8	US-11-713-768-69822	Sequence 69822, A
1145	95.5	4.3	4662	1	US-10-438-246-14649	Sequence 14649, A	1218	95	4.3	2481	8	US-11-713-768-75176	Sequence 75176, A
1146	95.5	4.3	4783	1	US-10-533-069-1020	Sequence 1020, Ap	1219	95	4.3	2666	8	US-11-643-077-3	Sequence 3, Appl
1147	95.5	4.3	5027	8	US-11-514-704-168	Sequence 168, App	1220	95	4.3	2856	8	US-11-713-768-96889	Sequence 96889, A
1148	95.5	4.3	5195	8	US-11-514-704-6906	Sequence 6906, Ap	1221	95	4.3	2937	1	US-11-514-704-24343	Sequence 2434, Ap
1149	95.5	4.3	5373	1	US-10-438-246-12713	Sequence 12713, A	cl1222	95	4.3	2954	1	US-10-438-246-1423	Sequence 1423, Ap
1150	95.5	4.3	6579	1	US-10-438-246-11658	Sequence 11658, A	1223	95	4.3	3060	8	US-11-649-663A-1531	Sequence 1531, Ap
cl1151	95.5	4.3	7001	1	US-10-438-246-21266	Sequence 21266, A	cl1224	95	4.3	3152	8	US-11-514-704-5225	Sequence 5225, Ap
cl1152	95.5	4.3	7371	8	US-11-514-704-23944	Sequence 23944, A	1225	95	4.3	3191	8	US-11-514-704-12080	Sequence 12080, A
1153	95.5	4.3	7425	8	US-11-700-462-1	Sequence 1, Appl	cl1226	95	4.3	3199	8	US-11-514-704-1368	Sequence 1368, Ap
1154	95	4.3	421	1	US-10-567-764-20	Sequence 20, Appl	1227	95	4.3	3405	8	US-11-514-704-15027	Sequence 15027, A
1155	95	4.3	755	8	US-11-514-704-22876	Sequence 22876, A	1228	95	4.3	3405	1	US-10-533-069-130	Sequence 130, App
1156	95	4.3	855	8	US-11-713-768-38540	Sequence 38540, A	cl1229	95	4.3	4038	1	US-10-438-246-12715	Sequence 12715, A
1157	95	4.3	855	8	US-11-713-768-50066	Sequence 50066, A	1230	95	4.3	4090	8	US-11-514-704-21486	Sequence 21486, A
1158	95	4.3	899	8	US-11-514-704-13673	Sequence 13673, A	cl1231	95	4.3	4275	1	US-10-438-246-29026	Sequence 29026, A
1159	95	4.3	947	8	US-11-713-768-109717	Sequence 109717, A	cl1232	95	4.3	5004	1	US-10-438-246-14367	Sequence 14367, A
1160	95	4.3	957	1	US-10-438-246-11197	Sequence 11197, A	1233	95	4.3	5422	8	US-11-514-704-13098	Sequence 13098, A
1161	95	4.3	969	8	US-11-514-704-22762	Sequence 22762, A	1234	95	4.3	5727	1	US-10-533-069-1036	Sequence 1026, Ap
cl1162	95	4.3	990	8	US-11-514-704-6035	Sequence 6035, Ap	1235	95	4.3	6056	1	US-10-438-246-5045	Sequence 5045, Ap
1163	95	4.3	1026	8	US-11-514-704-5483	Sequence 5483, Ap	1236	95	4.3	8612	8	US-11-514-704-12624	Sequence 12624, A
1164	95	4.3	1033	1	US-10-438-246-21052	Sequence 21052, A	1237	95	4.3	15059	1	US-10-533-069-1601	Sequence 1601, Ap
1165	95	4.3	1064	8	US-11-713-768-11647	Sequence 11647, A	1238	95	4.3	51860	8	US-11-257-477-125	Sequence 125, App
1166	95	4.3	1080	8	US-11-514-704-11985	Sequence 11985, A	1239	94.5	4.3	484	8	US-11-713-768-14959	Sequence 14959, A
1167	95	4.3	1108	8	US-11-514-704-9363	Sequence 9363, Ap	1240	94.5	4.3	603	1	US-10-438-246-12633	Sequence 12633, A
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1169	95	4.3	1161	1	US-10-438-246-13488	Sequence 13488, A	1242	94.5	4.3	870	1	US-10-438-246-12058	Sequence 12058, A
cl1170	95	4.3	1187	8	US-11-514-704-24030	Sequence 24030, A	1243	94.5	4.3	870	1	US-10-438-246-21636	Sequence 21636, A
1171	95	4.3	1244	8	US-11-713-768-5890	Sequence 5890, Ap	1244	94.5	4.3	897	1	US-10-438-246-12461	Sequence 12461, A
1172	95	4.3	1257	8	US-11-713-768-68476	Sequence 68476, A	1245	94.5	4.3	944	8	US-11-713-768-55779	Sequence 55779, A
1173	95	4.3	1264	8	US-11-713-768-52196	Sequence 52196, A	cl1246	94.5	4.3	990	8	US-11-713-768-97390	Sequence 97390, A
1174	95	4.3	1330	8	US-11-514-704-12846	Sequence 12846, A	cl1247	94.5	4.3	1079	8	US-11-514-704-11668	Sequence 11668, Ap
1175	95	4.3	1337	8	US-11-514-704-12845	Sequence 12845, A	1248	94.5	4.3	1099	8	US-11-514-704-8507	Sequence 8507, Ap
1176	95	4.3	1356	1	US-10-554-789-9	Sequence 9, Appl	cl1249	94.5	4.3	1203	8	US-11-713-768-764	Sequence 764, App
1177	95	4.3	1356	8	US-11-713-768-4714	Sequence 4714, Ap	1250	94.5	4.3	1275	8	US-11-713-768-46007	Sequence 46007, A
cl1178	95	4.3	1368	8	US-11-514-704-4251	Sequence 4251, Ap	cl1251	94.5	4.3	1323	8	US-11-713-768-84014	Sequence 84014, A

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1253	94.5	4.3	1353	8	US-11-713-768-65360	Sequence 65360, A	1326	94	4.3	1422	8	US-11-713-768-6340	Sequence 6340, Ap
1254	94.5	4.3	1466	8	US-11-514-704-11228	Sequence 11228, A	1327	94	4.3	1430	8	US-11-713-768-62773	Sequence 62773, A
c1255	94.5	4.3	1480	1	US-10-438-246-21874	Sequence 21874, A	c1328	94	4.3	1458	8	US-11-713-768-59086	Sequence 59086, A
1256	94.5	4.3	1532	8	US-11-649-663A-3149	Sequence 3149, Ap	1329	94	4.3	1529	8	US-11-713-768-59086	Sequence 59086, A
c1257	94.5	4.3	1543	8	US-11-514-704-5627	Sequence 5627, Ap	c1330	94	4.3	1534	8	US-11-713-768-9871	Sequence 9871, Ap
1258	94.5	4.3	1607	8	US-11-649-663A-4529	Sequence 4529, Ap	1331	94	4.3	1571	8	US-11-713-768-2621	Sequence 2621, Ap
1259	94.5	4.3	1625	8	US-11-713-768-112014	Sequence 112014, A	1332	94	4.3	1630	8	US-11-514-704-22029	Sequence 22029, A
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1261	94.5	4.3	1746	8	US-11-713-768-8939	Sequence 8939, Ap	1334	94	4.3	1645	8	US-11-514-704-7929	Sequence 7929, Ap
1262	94.5	4.3	1761	8	US-11-552-061A-6	Sequence 6, Appli	1335	94	4.3	1722	8	US-11-514-704-16155	Sequence 16155, A
1263	94.5	4.3	1768	8	US-11-713-768-107895	Sequence 107895, A	1336	94	4.3	1728	8	US-11-514-704-4040	Sequence 4040, Ap
c1264	94.5	4.3	1774	8	US-11-514-704-19481	Sequence 19481, A	1337	94	4.3	1743	8	US-11-713-768-6967	Sequence 6967, Ap
1265	94.5	4.3	1776	8	US-11-514-704-15956	Sequence 15956, A	1338	94	4.3	1773	8	US-11-713-768-66589	Sequence 66589, A
c1266	94.5	4.3	1899	8	US-11-713-768-86765	Sequence 86765, A	c1339	94	4.3	1776	8	US-11-713-768-43830	Sequence 43830, A
1267	94.5	4.3	1916	8	US-11-713-768-66646	Sequence 66646, A	c1340	94	4.3	1776	8	US-11-713-768-46043	Sequence 46043, A
1268	94.5	4.3	1929	8	US-11-514-704-13450	Sequence 13450, A	c1341	94	4.3	1776	8	US-11-713-768-87563	Sequence 87563, A
1269	94.5	4.3	1929	8	US-11-514-704-19956	Sequence 19956, A	1342	94	4.3	1814	8	US-11-514-704-12318	Sequence 12318, A
c1270	94.5	4.3	2027	8	US-11-713-768-86761	Sequence 86761, A	c1343	94	4.3	1830	8	US-11-713-768-67547	Sequence 67547, A
1271	94.5	4.3	2044	8	US-11-713-768-83108	Sequence 83108, A	1344	94	4.3	1833	1	US-10-533-069-1167	Sequence 1167, Ap
c1272	94.5	4.3	2050	8	US-11-713-768-97910	Sequence 97910, A	1345	94	4.3	1857	8	US-11-728-567-223	Sequence 223, App
1273	94.5	4.3	2117	8	US-11-713-768-100681	Sequence 100681, A	c1346	94	4.3	2106	8	US-11-514-704-6144	Sequence 6144, Ap
c1274	94.5	4.3	2182	8	US-11-514-704-12360	Sequence 12360, A	c1347	94	4.3	2140	8	US-11-713-768-63279	Sequence 63279, A
1275	94.5	4.3	2195	8	US-11-514-704-10740	Sequence 10740, A	1348	94	4.3	2178	1	US-10-438-246-12412	Sequence 12412, A
c1276	94.5	4.3	2203	8	US-11-514-704-8544	Sequence 8544, Ap	c1349	94	4.3	2181	8	US-11-342-364-1	Sequence 1, Appli
1277	94.5	4.3	2256	8	US-11-713-768-46280	Sequence 46280, A	c1350	94	4.3	2346	1	US-10-562-377-189	Sequence 189, App
c1278	94.5	4.3	2292	8	US-11-544-679-10	Sequence 10, Appl	1351	94	4.3	2441	8	US-11-514-704-7870	Sequence 7870, Ap
1279	94.5	4.3	2382	8	US-11-514-704-6853	Sequence 6853, Ap	c1352	94	4.3	2451	8	US-11-342-364-8	Sequence 8, Appli
c1280	94.5	4.3	2421	8	US-11-514-704-16888	Sequence 16888, A	c1353	94	4.3	2487	8	US-11-342-364-7	Sequence 7, Appli
1281	94.5	4.3	2473	1	US-10-562-377-145	Sequence 145, App	1354	94	4.3	2527	1	US-11-514-704-2378	Sequence 2378, Ap
c1282	94.5	4.3	2484	1	US-10-438-246-15791	Sequence 15791, A	1355	94	4.3	2580	1	US-10-594-266-37	Sequence 37, Appl
1283	94.5	4.3	2534	8	US-11-552-437-25	Sequence 25, Appl	c1356	94	4.3	2637	8	US-11-342-364-6	Sequence 6, Appli
1284	94.5	4.3	2665	8	US-11-677-509-1	Sequence 1, Appli	1357	94	4.3	2781	8	US-11-342-364-5	Sequence 5, Appli
c1285	94.5	4.3	2830	8	US-11-514-704-8941	Sequence 8941, Ap	c1358	94	4.3	2808	1	US-11-342-364-4	Sequence 4, Appli
1286	94.5	4.3	2860	8	US-11-514-704-2211	Sequence 2211, Ap	1359	94	4.3	2830	1	US-10-438-246-12330	Sequence 12330, A
c1287	94.5	4.3	3025	8	US-11-514-704-2803	Sequence 2803, Ap	c1360	94	4.3	2850	8	US-11-514-704-18858	Sequence 18858, A
1288	94.5	4.3	3162	1	US-10-533-069-2073	Sequence 2073, Ap	c1361	94	4.3	2971	8	US-11-342-364-3	Sequence 3, Appli
c1289	94.5	4.3	3280	8	US-11-514-704-626	Sequence 626, App	c1362	94	4.3	3030	8	US-11-342-364-11	Sequence 11, Appl
1290	94.5	4.3	3472	8	US-11-514-704-18777	Sequence 18777, A	c1363	94	4.3	3060	8	US-11-342-364-4	Sequence 4, Appli
c1291	94.5	4.3	3558	8	US-11-514-704-737	Sequence 737, App	c1364	94	4.3	3091	8	US-11-514-704-6763	Sequence 6763, Ap
1292	94.5	4.3	3639	1	US-10-438-246-13781	Sequence 13781, A	1365	94	4.3	3237	8	US-11-514-704-7092	Sequence 7092, Ap
1293	94.5	4.3	4121	1	US-10-533-069-1010	Sequence 1010, Ap	1366	94	4.3	3349	1	US-10-533-069-1778	Sequence 1778, Ap
c1294	94.5	4.3	4692	1	US-10-438-246-12656	Sequence 12656, A	c1367	94	4.3	3467	8	US-11-514-704-17702	Sequence 17702, A
1295	94.5	4.3	4849	8	US-11-514-704-2116	Sequence 2116, Ap	c1368	94	4.3	3474	8	US-11-342-364-9	Sequence 9, Appli
c1296	94.5	4.3	4957	1	US-10-438-246-22084	Sequence 22084, A	1369	94	4.3	3821	8	US-11-514-704-11096	Sequence 11096, A
1297	94.5	4.3	5033	8	US-11-646-784-1	Sequence 1, Appli	1370	94	4.3	4129	8	US-11-514-704-3507	Sequence 3507, Ap
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1299	94.5	4.3	5055	8	US-11-514-704-21476	Sequence 21476, A	1372	94	4.3	4755	8	US-11-514-704-17666	Sequence 17666, A
c1300	94.5	4.3	5101	8	US-11-514-704-5287	Sequence 5287, Ap	1373	94	4.3	4974	1	US-10-438-246-15454	Sequence 15454, A
c1301	94.5	4.3	7398	8	US-11-514-704-24782	Sequence 24782, A	1374	94	4.3	4990	8	US-11-514-704-11110	Sequence 11110, A
1302	94.5	4.3	7893	1	US-10-438-246-11666	Sequence 11666, A	1375	94	4.3	5638	1	US-10-438-246-22902	Sequence 22902, A
c1303	94.5	4.3	8425	1	US-10-438-246-21268	Sequence 21268, A	1376	94	4.3	6484	8	US-11-514-704-13921	Sequence 13921, A
1304	94.5	4.3	9731	1	US-10-438-246-23019	Sequence 23019, A	c1377	94	4.3	7705	8	US-11-514-704-21078	Sequence 21078, A
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
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Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	1981	76	US-11-443-428A-108935
2	2211	100.0	2099	27	US-09-606-680-3263
3	2211	100.0	2284	21	US-09-254-311-90
4	2211	100.0	2284	34	US-09-929-404-71
55	2211	100.0	2284	37	US-09-937-428-514
69	2211	100.0	2284	47	US-10-429-667-82
70	2211	100.0	2284	50	US-10-677-471-82
71	2211	100.0	2284	50	US-10-677-669-82
72	2211	100.0	2284	56	US-10-735-014-82
73	2211	100.0	2284	58	US-10-854-947-82
74	2211	100.0	2284	58	US-10-858-961-82
75	2211	100.0	2284	58	US-10-858-993-82
76	2211	100.0	2284	58	US-10-899-671-82
77	2211	100.0	2284	59	US-10-901-400-82
78	2211	100.0	2284	60	US-10-943-353-82
79	2211	100.0	2284	60	US-10-950-374-514
80	2211	100.0	2284	70	US-11-296-092-82
81	2211	100.0	2284	70	US-11-296-155-82
82	2211	100.0	2284	82	US-11-814-136-9
83	2211	100.0	2297	27	US-09-629-469A-17949
84	2211	100.0	2297	29	US-10-917-503-17949
85	2211	100.0	2297	59	US-10-917-503B-17949
86	2211	100.0	2297	59	US-10-917-503C-17949
87	2211	100.0	2297	69	US-11-266-748A-30338
88	2211	100.0	2297	80	US-11-640-517-3678
89	2211	100.0	2297	93	US-60-751-455-3678
90	2211	100.0	2323	39	US-10-170-235-37529
91	2211	100.0	2342	1	PCT-US000-07285-105
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95	2210	99.9	1296	74	US-11-371-354-6204
96	2210	99.9	1296	74	US-11-371-354-62568
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129	1851	83.7	1423	41	US-10-296-115-675
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	219	510	23.1	542	24	US-09-522-251-1756	Sequence 1756, App	292	313.5	14.2	380	34	US-09-933-524-35994	Sequence 35994, A		
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	224	493.5	22.3	508	11	US-08-220-691B-7457	Sequence 7457, App	297	302	13.7	204	84	US-60-023-236-921	Sequence 921, App		
	225	493.5	22.3	508	32	US-09-813-155-7457	Sequence 7457, App	298	290	13.1	544	38	US-10-021-720-61	Sequence 61, Appl		
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	232	463	20.9	286	84	US-60-039-128-818	Sequence 818, App	305	280	12.7	316	18	US-08-923-903-2023	Sequence 2023, App		
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	237	443	20.0	285	84	US-60-015-377-1468	Sequence 1468, App	310	275	12.4	339	27	US-09-614-387-942	Sequence 942, App		
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	C	243	424	19.2	1000	69	US-11-266-748A-471590	Sequence 471590, A	C	316	264	11.9	519	85	US-60-172-360-7291	Sequence 7291, App
	244	414	18.7	541	22	US-09-366-691A-260	Sequence 260, App	317	261	11.8	141	1	PCT-US03-26780-195	Sequence 195, App		
	245	414	18.7	541	34	US-09-912-293-8036	Sequence 8036, App	318	260	11.8	693	76	US-11-443-428A-699758	Sequence 699758, A		
	246	411	18.6	390	22	US-09-332-782-11182	Sequence 11182, A	319	257	11.6	201	89	US-60-452-680-34096	Sequence 34096, A		
	247	411	18.6	390	24	US-09-515-694-11182	Sequence 11182, A	C	320	250.5	11.3	233	76	US-11-443-428A-488259	Sequence 488259, A	
	248	409	18.5	280	25	US-09-533-331D-33139	Sequence 33139, A	321	250.5	11.3	233	28	US-09-649-163-2508	Sequence 2508, App		
	249	402	18.2	334	25	US-09-540-212A-47536	Sequence 47536, A	322	237	10.7	383	28	US-09-652-916-3749	Sequence 3749, App		
	250	390	17.6	238	13	US-08-416-401-3033	Sequence 3033, App	323	227	10.3	242	3	PCT-US99-24206-1775	Sequence 1775, App		
	251	390	17.6	238	25	US-09-534-856-24638	Sequence 24638, A	324	227	10.3	242	35	US-09-807-521-1775	Sequence 1775, App		
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	254	384	17.4	487	22	US-09-399-932-3411	Sequence 3411, App	327	214	9.7	133	25	US-09-534-856-24646	Sequence 24646, A		
	255	384	17.4	487	28	US-09-649-163-3048	Sequence 3048, App	328	212	9.6	1870	24	US-09-532-857-45	Sequence 45, Appl		
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	257	374	16.9	207	11	US-08-296-757B-8104	Sequence 8104, App	C	330	211	9.5	893	76	US-11-443-428A-687368	Sequence 687368, A	
	258	374	16.9	207	25	US-09-534-856-24651	Sequence 24651, A	331	205.5	9.3	1890	39	US-10-144-771-972	Sequence 972, App		
	259	359	16.2	220	16	US-08-725-863-279	Sequence 279, App	332	205.5	9.3	1890	88	US-60-360-207-972	Sequence 972, App		
	260	359	16.2	220	25	US-09-534-856-24636	Sequence 24636, A	333	205	9.3	1766	1	PCT-US01-01565-27	Sequence 27, Appl		
	261	355	16.1	347	30	US-09-726-789-1183	Sequence 1183, App	334	205	9.3	1766	39	US-10-100-683-2086	Sequence 2086, App		
	262	346	15.6	201	89	US-60-452-680-34098	Sequence 34098, A	335	205	9.3	1766	62	US-11-001-793-2086	Sequence 2086, App		
	263	346	15.6	201	89	US-60-452-680-34106	Sequence 34106, A	336	205	9.3	1766	80	US-11-689-173-2086	Sequence 2086, App		
	264	346	15.6	214	17	US-08-879-863-4222	Sequence 4222, App	337	204.5	9.2	1979	76	US-11-443-428A-50588	Sequence 50588, A		
	265	346	15.6	214	17	US-08-879-863A-4222	Sequence 4222, App	338	204.5	9.2	2042	76	US-11-443-428A-50590	Sequence 50590, A		
	266	346	15.6	214	25	US-09-534-856-24643	Sequence 24643, A	339	204.5	9.2	2050	3	PCT-US05-22501-4598	Sequence 4598, App		
	267	345	15.6	201	89	US-60-452-680-34097	Sequence 34097, A	340	204.5	9.2	2050	48	US-10-531-147-163	Sequence 163, App		
	268	345	15.6	201	89	US-60-452-680-34105	Sequence 34105, A	341	204.5	9.2	2050	48	US-10-531-147-3308	Sequence 3308, App		
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354	204.5	9.2	2092	30	US-09-726-175-2925	Sequence 2925, Ap	869	188	8.5	1661	59	US-10-931-886-223	Sequence 223, App
355	204.5	9.2	2104	76	US-11-443-428A-50576	Sequence 50576, A	870	188	8.5	1661	60	US-10-955-952-223	Sequence 223, App
356	204.5	9.2	2132	76	US-11-443-428A-50581	Sequence 50581, A	871	188	8.5	1661	60	US-10-964-241-223	Sequence 223, App
357	204.5	9.2	2315	76	US-11-443-428A-50582	Sequence 50582, A	872	188	8.5	1661	60	US-10-964-241B-223	Sequence 223, App
358	204.5	9.2	2535	2	PCT-US03-38193-5035	Sequence 5035, Ap	873	188	8.5	1661	60	US-10-964-241C-223	Sequence 223, App
359	204.5	9.2	2535	56	US-10-723-860-5035	Sequence 5035, Ap	874	188	8.5	1661	60	US-10-973-115B-223	Sequence 223, App
360	204.5	9.2	2538	76	US-11-443-428A-50589	Sequence 50589, A	875	188	8.5	1661	70	US-11-290-153-223	Sequence 223, App
361	203.5	9.2	1719	85	US-60-172-373-10434	Sequence 10434, A	876	188	8.5	1661	78	US-11-553-810-223	Sequence 223, App
362	198.5	9.0	349	30	US-09-704-424-1165	Sequence 1165, Ap	877	188	8.5	1661	78	US-11-553-810-223	Sequence 223, App
363	197	8.9	1716	35	US-09-937-059-30	Sequence 30, Appl	878	188	8.5	17866	22	US-09-358-001-21	Sequence 21, Appl
364	197	8.9	1716	85	US-60-125-537-18	Sequence 18, Appl	879	188	8.5	17866	26	US-09-578-334-21	Sequence 21, Appl
365	197	8.9	1854	87	US-60-278-258-13359	Sequence 13359, A	880	188	8.5	17866	26	US-09-578-334B-21	Sequence 21, Appl
366	197	8.9	1854	84	US-60-324-185-25730	Sequence 25730, A	881	188	8.5	17866	26	US-09-578-517-21	Sequence 21, Appl
367	197	8.9	6000	94	US-60-873-737-414	Sequence 414, App	882	188	8.5	17866	26	US-09-578-518-21	Sequence 21, Appl
368	197	8.9	6000	94	US-60-873-739-1160	Sequence 1160, Ap	883	188	8.5	17866	26	US-09-578-518B-21	Sequence 21, Appl
369	197	8.9	6000	94	US-60-873-882-1306	Sequence 1306, Ap	884	188	8.5	17866	26	US-09-578-519-21	Sequence 21, Appl
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371	197	8.9	10346	62	US-11-001-793-12711	Sequence 12711, A	886	188	8.5	17866	26	US-09-578-520-21	Sequence 21, Appl
372	197	8.9	10346	80	US-11-689-173-12711	Sequence 12711, A	887	188	8.5	17866	26	US-09-578-520B-21	Sequence 21, Appl
373	197	8.9	10615	62	PCT-US02-01222-228	Sequence 38342, A	888	188	8.5	17866	26	US-09-578-831B-21	Sequence 21, Appl
374	196.5	8.9	1826	1	US-10-461-673-2112	Sequence 228, App	889	188	8.5	17866	26	US-09-579-237-21	Sequence 21, Appl
375	196.5	8.9	1826	47	US-10-461-673-2112	Sequence 2112, Ap	890	188	8.5	17866	26	US-09-579-243-21	Sequence 21, Appl
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377	195.5	8.8	1932	22	US-09-358-001-8	Sequence 8, Appl	892	188	8.5	17866	26	US-09-579-262-21	Sequence 21, Appl
378	195.5	8.8	1932	26	US-09-578-334B-8	Sequence 8, Appl	893	188	8.5	17866	26	US-09-579-280-21	Sequence 21, Appl
379	195.5	8.8	1932	26	US-09-578-517-8	Sequence 8, Appl	894	188	8.5	17866	26	US-09-579-280B-21	Sequence 21, Appl
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392	195.5	8.8	1932	26	US-09-579-262B-8	Sequence 8, Appl	907	186.5	8.4	2049	28	US-09-652-127-7508	Sequence 7508, Ap
393	195.5	8.8	1932	26	US-09-579-280-8	Sequence 8, Appl	908	186.5	8.4	2049	28	US-09-652-128-8163	Sequence 8163, Ap
394	195.5	8.8	1932	26	US-09-579-280B-8	Sequence 8, Appl	909	186.5	8.4	2049	28	US-09-652-913-9410	Sequence 9410, Ap
395	195.5	8.8	1969	74	US-11-371-354-10439	Sequence 10439, A	910	186.5	8.4	2049	28	US-09-652-914-8320	Sequence 8320, Ap
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397	195.5	8.8	2095	23	US-09-496-914A-992	Sequence 992, App	912	186.5	8.4	2081	69	US-11-266-748A-74381	Sequence 74381, A
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399	195.5	8.8	2095	40	US-10-276-774-51	Sequence 51, Appl	914	185	8.4	263	20	US-09-112-371-823	Sequence 823, App
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401	195.5	8.8	2095	47	US-10-461-673-2523	Sequence 2523, Ap	916	183	8.3	398	28	US-09-649-163-1829	Sequence 1829, Ap
402	194.5	8.8	1642	3	PCT-US99-17130-70	Sequence 802, Appl	917	182	8.2	445	24	US-09-528-409-42767	Sequence 42767, A
403	194.5	8.8	1642	39	US-10-100-683-3775	Sequence 3775, Ap	918	182	8.2	445	34	US-09-933-524A-42767	Sequence 42767, A
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405	194.5	8.8	1642	46	US-10-472-532-802	Sequence 802, App	920	178.5	8.1	1053	76	US-11-443-428A-50592	Sequence 50592, A
406	194.5	8.8	1642	62	US-11-001-793-3775	Sequence 3775, Ap	921	175	7.9	30542	3	PCT-US04-42189-74	Sequence 74, Appl
407	194.5	8.8	1642	62	US-11-229-769-70	Sequence 70, Appl	922	175	7.9	30542	56	US-10-737-082-74	Sequence 74, Appl
408	194.5	8.8	1642	69	US-11-346-470-802	Sequence 802, App	923	175	7.9	30542	57	US-10-765-790-74	Sequence 74, Appl
409	194.5	8.8	1642	72	US-11-689-173-3775	Sequence 3775, Ap	924	172.5	7.8	7587	76	US-11-443-428A-732416	Sequence 732416, A
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960	172.5	7.8	15720	58	US-10-843-641A-695	Sequence 695, App	1033	160.5	7.3	116100	24	US-09-528-237A-868	Sequence 868, App
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963	172.5	7.8	15720	66	US-11-105-233-118	Sequence 118, App	1036	160	7.2	5564	60	US-10-956-157-4662	Sequence 4662, App
964	172.5	7.8	15720	66	US-11-108-172-1058	Sequence 1058, App	1037	160	7.2	5564	91	US-60-507-511-4662	Sequence 4662, App
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981	172.5	7.8	17689	76	US-11-490-374-1838	Sequence 1838, App	1054	160	7.2	9424	76	US-11-443-428A-304815	Sequence 304815, A
982	171.5	7.8	10395	85	US-60-172-373-21532	Sequence 21532, A	1055	160	7.2	9693	75	US-11-437-729-4425	Sequence 4425, App
983	169.5	7.7	1000	69	US-11-266-748A-223231	Sequence 223231, A	1056	160	7.2	9693	93	US-11-475-062-8638	Sequence 2159, App
984	169.5	7.7	1000	69	US-11-266-748A-290508	Sequence 290508, A	1057	160	7.2	9693	93	US-60-717-196-2159	Sequence 2159, App
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988	168.5	7.6	1481	87	US-60-278-258-11018	Sequence 11018, A	1061	160	7.2	10174	3	PCT-US04-24424-471	Sequence 471, App
989	167.5	7.6	1964	69	US-11-266-748A-369782	Sequence 369782, A	1062	160	7.2	10174	48	US-10-567-867-471	Sequence 471, App
990	167.5	7.6	1964	69	US-11-266-748A-389221	Sequence 389221, A	1063	160	7.2	10174	78	US-11-510-530-82	Sequence 82, Appl
C-991	167.5	7.6	1964	69	US-11-266-748A-453161	Sequence 453161, A	1064	160	7.2	10174	90	US-60-490-890-471	Sequence 471, App
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993	165.5	7.5	8008	39	US-10-144-771-21709	Sequence 21709, A	1066	160	7.2	10347	1	PCT-US00-23291-1	Sequence 1, Appl
994	165.5	7.5	8008	39	US-60-360-207-21709	Sequence 21709, A	1067	160	7.2	10347	28	US-09-645-591-1	Sequence 1, Appl
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996	164	7.4	3437	76	US-11-443-428A-73516	Sequence 73516, A	1069	160	7.2	10361	39	US-10-170-235-30193	Sequence 30193, A
997	164	7.4	6154	76	US-11-443-428A-73520	Sequence 73520, A	1070	160	7.2	10361	46	US-10-330-773-629	Sequence 629, App
998	164	7.4	7187	76	US-11-443-428A-73513	Sequence 73513, A	1071	160	7.2	10361	46	US-10-330-773A-629	Sequence 629, App
999	164	7.4	14094	94	US-60-836-986-24860	Sequence 24860, A	1072	160	7.2	10361	48	US-10-540-898-629	Sequence 629, App
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1002	164	7.4	17847	48	US-10-585-725A-25	Sequence 25, Appl	1075	160	7.2	10371	75	US-11-437-729-4428	Sequence 4428, App
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1004	163	7.4	971	44	US-10-301-480B-68221	Sequence 68221, A	1077	160	7.2	10371	76	US-11-475-062-8641	Sequence 8641, App
1005	163	7.4	971	45	US-10-301-480C-68221	Sequence 68221, A	1078	160	7.2	10371	93	US-60-717-196-2160	Sequence 2160, App
C1006	161.5	7.3	614	85	US-60-196-190-615	Sequence 615, App	1079	160	7.2	10371	93	US-60-717-196-2162	Sequence 2162, App
1007	161.5	7.3	11334	85	US-60-164-769-21676	Sequence 21676, A	1080	160	7.2	10378	75	US-11-437-729-4429	Sequence 4429, App
C1008	161	7.3	1345	88	US-60-250-830-2144	Sequence 2144, App	1081	160	7.2	10378	76	US-11-475-062-8642	Sequence 8642, App
C1009	161	7.3	1345	88	US-60-323-966-2144	Sequence 2144, App	1082	160	7.2	10378	93	US-60-717-196-2163	Sequence 2163, App
1010	161	7.3	2300	3	PCT-US06-46920-6423	Sequence 6423, App	1083	160	7.2	10383	3	PCT-US06-13172-42	Sequence 42, Appl
1011	161	7.3	2300	80	US-11-636-385-6423	Sequence 6423, App	1084	160	7.2	10383	78	US-11-582-861-12175	Sequence 12175, A
1012	161	7.3	2300	80	US-11-636-385A-6423	Sequence 6423, App	1085	160	7.2	10383	94	US-60-836-986-21479	Sequence 21479, A
1013	161	7.3	2300	93	US-60-762-056-6423	Sequence 6423, App	1086	160	7.2	10415	75	US-11-437-729-4427	Sequence 4427, App

1087	160	7.2	10415	76	US-11-475-062-8640	Sequence 8640, Ap	1160	155	7.0	2380	3	PCT-US05-23708-742	Sequence 742, App
1088	160	7.2	10415	93	US-60-717-196-2161	Sequence 2161, Ap	1161	155	7.0	2380	3	US-11-293-697-1446	Sequence 1446, Ap
1089	160	7.2	10586	76	US-11-443-428A-304813	Sequence 304813, Ap	1162	154.5	7.0	2380	21	US-09-288-001A-1328	Sequence 1328, Ap
1090	160	7.2	11275	76	US-11-443-428A-304810	Sequence 304810, Ap	1163	154.5	7.0	2380	22	US-09-540-225-176422	Sequence 176422, Ap
1091	160	7.2	11315	76	US-11-443-428A-304812	Sequence 304812, Ap	1164	154.5	7.0	2380	272	US-60-081-215-1328	Sequence 1328, Ap
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1099	159	7.2	7140	3	PCT-US04-10531-19	Sequence 19, App	1172	154.5	7.0	2380	1	PCT-US01-27760A-365	Sequence 365, App
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1102	158.5	7.2	1604	46	US-10-312-352-66	Sequence 66, Appl	1175	154.5	7.0	2380	46	US-10-399-103A-365	Sequence 365, App
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1104	158.5	7.2	2346	76	US-11-443-428A-72983	Sequence 72983, A	1177	154	7.0	2380	38	US-10-029-386-22985	Sequence 22985, A
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1106	158.5	7.2	2388	30	US-09-714-936-295	Sequence 295, App	1179	154	7.0	2380	76	US-11-443-428A-637773	Sequence 637773, Ap
1107	158.5	7.2	2388	39	US-10-115-635-295	Sequence 295, App	1180	154	7.0	2380	46	US-10-399-103A-365	Sequence 365, App
1108	158.5	7.2	2388	47	US-10-416-931-276	Sequence 276, App	1181	154	7.0	2380	46	US-10-399-103A-365	Sequence 365, App
1109	158.5	7.2	2388	47	US-10-461-673-1411	Sequence 1411, Ap	1182	154	7.0	2380	46	US-10-461-673-1054	Sequence 1054, Ap
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1114	158	7.1	12534	39	US-10-144-771-2670	Sequence 2670, Ap	1187	153.5	6.9	4293	38	US-10-029-386-22985	Sequence 22985, A
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1146	156	7.1	3161	65	US-11-097-143-39133	Sequence 39133, A	1219	152	6.9	882	30	US-10-144-771-28576	Sequence 28576, A
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1151	156	7.1	48626	85	US-60-161-932-426	Sequence 426, App	1224	152	6.9	882	30	US-10-144-771-28576	Sequence 28576, A
1152	156	7.1	7418	24	US-09-528-237A-142	Sequence 142, App	1225	152	6.9	882	30	US-10-144-771-28576	Sequence 28576, A
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1154	156	7.1	745443	19	US-09-012-031B-311	Sequence 311, App	1227	152	6.9	882	30	US-10-144-771-28576	Sequence 28576, A
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1156	156	7.1	745443	22	US-09-335-032A-12213	Sequence 12213, A	1229	152	6.9	882	30	US-10-144-771-28576	Sequence 28576, A
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1235	151.5	6.9	1396	73	US-11-360-355-76736	Sequence 76736, A	1308	149	6.7	3480	92	US-60-655-875-13116	Sequence 13116, A
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1237	151.5	6.9	2751	39	US-10-179-131-997	Sequence 997, App	1310	149	6.7	4830	88	US-60-360-039-25222	Sequence 25222, A
1238	151.5	6.9	3922	27	US-60-167-117-17339	Sequence 17339, A	1311	149	6.7	4830	94	US-60-851-434-25	Sequence 25, Appl
1239	151.5	6.9	4829	27	US-09-614-150-17339	Sequence 17339, A	1312	149	6.7	4911	59	US-10-932-182A-75783	Sequence 75783, A
1240	151.5	6.9	4829	27	US-09-614-150A-17339	Sequence 17339, A	1313	149	6.7	4911	69	US-11-217-529-75783	Sequence 75783, A
1241	151.5	6.9	4829	65	US-11-097-143-17339	Sequence 17339, A	1314	149	6.7	315341	19	US-09-012-031B-304	Sequence 304, App
1242	151.5	6.9	4829	65	US-60-171-625-362	Sequence 362, App	1315	149	6.7	315341	19	US-09-012-031B-304	Sequence 304, App
1243	151.5	6.9	4829	85	US-60-173-464-14245	Sequence 14245, A	1316	149	6.7	315341	22	US-09-012-031C-304	Sequence 304, App
1244	151.5	6.9	4829	85	US-60-191-637-17389	Sequence 17389, A	1317	149	6.7	315341	22	US-09-335-032-12206	Sequence 12206, A
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1247	151.5	6.9	4912	92	US-60-655-875-12974	Sequence 12974, A	1320	148.5	6.7	1515	76	US-11-443-428A-587458	Sequence 587458, A
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1249	151.5	6.9	8479	88	US-60-360-207-16337	Sequence 16337, A	1322	148	6.7	996	76	US-11-443-428A-71851	Sequence 71851, A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	122.5	5.5	1904	7	US-11-833-133-55	Sequence 55, Appl
4	121.5	5.5	2000	7	US-11-623-607A-13	Sequence 13, Appl
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6	121.5	5.5	2000	7	US-11-852-274-44	Sequence 44, Appl
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8	120.5	5.5	2444	7	US-11-781-665-2385	Sequence 2385, Ap
9	120.5	5.5	2445	7	US-11-235-701A-354	Sequence 354, App
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C 254	100	4.5	2740	7	US-11-833-133-43	Sequence 43, Appl	C 327	97	4.4	6519	7	US-11-801-963A-2605	Sequence 2605, Ap
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C 274	99	4.5	1431	8	US-60-914-361-86	Sequence 86, Appl	347	96	4.3	1422	8	US-60-970-876-204	Sequence 204, App
C 275	99	4.5	1480	7	US-11-781-151-19	Sequence 19, Appl	348	96	4.3	1446	7	US-11-833-133-12	Sequence 12, Appl
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C 277	99	4.5	1867	7	US-11-831-404-33	Sequence 33, Appl	350	96	4.3	1708	8	US-60-970-876-133	Sequence 133, App
C 278	99	4.5	2055	7	US-11-781-665-425	Sequence 425, App	351	96	4.3	2046	8	US-60-970-876-181	Sequence 181, App
C 279	99	4.5	2438	7	US-11-884-496-238	Sequence 238, App	352	96	4.3	2151	6	US-10-554-521-44	Sequence 44, Appl
C 280	99	4.5	3302	7	US-11-816-601-74	Sequence 74, Appl	353	96	4.3	2494	7	US-11-825-627-301	Sequence 301, App
C 281	99	4.5	7497	7	US-11-782-310-67	Sequence 67, Appl	354	96	4.3	2666	7	US-11-847-733-4	Sequence 4, Appli
C 282	98.5	4.5	954	1	PCT-US07-1776B-4368	Sequence 4368, Ap	355	96	4.3	2961	1	PCT-US07-16605-3	Sequence 3, Appli
C 283	98.5	4.5	1228	7	US-11-597-986A-9	Sequence 9, Appli	356	96	4.3	2961	7	US-11-490-374A-2010	Sequence 2010, Ap
C 284	98.5	4.5	1776	7	US-11-374-300-353	Sequence 353, App	357	96	4.3	3173	7	US-11-354-210-108	Sequence 108, App
C 285	98.5	4.5	2906	7	US-11-834-069-3	Sequence 3, Appli	358	96	4.3	3753	7	US-11-354-210-118	Sequence 118, App
C 286	98.5	4.5	3186	7	US-11-834-069-4	Sequence 4, Appli	359	96	4.3	4026	7	US-11-354-210-126	Sequence 126, App
C 287	98.5	4.5	3770	7	US-11-597-986A-8	Sequence 8, Appli	360	96	4.3	4536	7	US-11-354-210-112	Sequence 112, App
C 288	98.5	4.5	11893	7	US-11-781-865-8	Sequence 8, Appli	361	96	4.3	4710	7	US-11-354-210-114	Sequence 114, App
C 289	98	4.4	710	7	US-11-582-527A-3	Sequence 3, Appli	362	96	4.3	4884	7	US-11-354-210-104	Sequence 104, App
C 290	98	4.4	817	1	PCT-US07-1776B-7412	Sequence 7412, Ap	363	96	4.3	5198	7	US-11-816-601-725	Sequence 725, App
C 291	98	4.4	1185	7	US-11-833-133-9	Sequence 9, Appli	364	96	4.3	5198	7	US-11-816-601-798	Sequence 798, App
C 292	98	4.4	2226	7	US-11-781-665-2442	Sequence 2442, Ap	365	96	4.3	5776	7	US-11-354-210-128	Sequence 128, App
C 293	98	4.4	6953	7	US-11-847-733-73	Sequence 73, Appl	366	96	4.3	10550	7	US-11-235-701A-368	Sequence 368, App
C 294	97.5	4.4	1278	7	US-11-844-953-9	Sequence 9, Appli	367	96	4.3	13018	7	US-11-235-701A-369	Sequence 369, App
C 295	97.5	4.4	1278	7	US-11-844-956-9	Sequence 9, Appli	368	96	4.3	30729	7	US-11-884-086-2	Sequence 2, Appli
C 296	97.5	4.4	1278	7	US-11-844-963-9	Sequence 9, Appli	369	95.5	4.3	1044	7	US-11-880-377-2451	Sequence 2451, Ap
C 297	97.5	4.4	1278	7	US-11-844-967-9	Sequence 9, Appli	370	95.5	4.3	1113	7	US-11-801-963A-2120	Sequence 2120, Ap
C 298	97.5	4.4	1278	7	US-11-844-970-9	Sequence 9, Appli	371	95.5	4.3	1194	7	US-11-833-133-40	Sequence 40, Appl
C 299	97.5	4.4	1278	7	US-11-844-973-9	Sequence 9, Appli	372	95.5	4.3	1269	8	US-60-970-876-55	Sequence 55, Appl
C 300	97.5	4.4	2887	7	US-11-884-496-249	Sequence 249, App	373	95.5	4.3	1893	1	PCT-US07-75398-81	Sequence 81, Appl
C 301	97.5	4.4	3646	1	PCT-US07-13803-274	Sequence 274, App	374	95.5	4.3	1893	7	US-11-835-328-81	Sequence 81, Appl
C 302	97.5	4.4	3646	1	PCT-US07-13803-498	Sequence 498, App	375	95.5	4.3	2800	7	US-11-781-151-29	Sequence 29, Appl
C 303	97.5	4.4	5817	7	US-11-884-496-352	Sequence 352, App	C 376	95.5	4.3	2833	7	US-11-884-496-326	Sequence 326, App

377	95.5	4.3	3585	6	US-10-050-000C-2	Sequence 2, Appli	450	94	4.3	3574	7	US-11-815-559-5	Sequence 5, Appli
378	95.5	4.3	3633	7	US-11-649-155-13	Sequence 13, Appli	451	94	4.3	3585	1	PCT-US07-17013-29	Sequence 28, Appli
C 379	95.5	4.3	4790	7	US-11-838-500-70	Sequence 70, Appli	452	94	4.3	3965	7	US-11-795-824-28	Sequence 29, Appli
C 380	95.5	4.3	8679	8	US-60-914-361-115	Sequence 115, Appli	453	94	4.3	4000	7	US-11-235-701A-508	Sequence 508, Appli
C 381	95.5	4.3	14760	7	US-11-490-374A-1331	Sequence 1331, Appli	454	94	4.3	5184	7	US-11-235-701A-509	Sequence 509, Appli
C 382	95.5	4.3	14760	7	US-11-490-374A-1332	Sequence 1332, Appli	455	94	4.3	8548	7	US-11-884-496-256	Sequence 256, Appli
C 383	95.5	4.3	14760	7	US-11-490-374A-1333	Sequence 1333, Appli	456	94	4.3	9944	7	US-11-490-374A-2183	Sequence 2183, Appli
C 384	95	4.3	834	8	US-60-970-876-156	Sequence 156, Appli	457	94	4.3	9959	7	US-11-490-374A-2181	Sequence 2181, Appli
385	95	4.3	891	1	PCT-US07-17776B-2703	Sequence 2703, Appli	458	94	4.3	9962	7	US-11-490-374A-2180	Sequence 2180, Appli
386	95	4.3	1932	7	US-11-649-155-15	Sequence 15, Appli	459	94	4.3	10061	7	US-11-490-374A-2182	Sequence 2182, Appli
387	95	4.3	1968	7	US-11-649-155-17	Sequence 17, Appli	460	94	4.3	10562	7	US-11-490-374A-2182	Sequence 2182, Appli
388	95	4.3	2791	7	US-11-781-665-1300	Sequence 1300, Appli	461	93.5	4.2	633	1	PCT-US07-17776B-211	Sequence 211, Appli
389	95	4.3	2791	7	US-11-781-665-1301	Sequence 1301, Appli	462	93.5	4.2	774	1	PCT-US07-17776B-1020	Sequence 1020, Appli
390	95	4.3	2961	1	PCT-US07-16605-5	Sequence 5, Appli	463	93.5	4.2	1012	1	PCT-US07-17776B-3410	Sequence 3410, Appli
391	95	4.3	3494	7	US-11-795-824-31	Sequence 31, Appli	464	93.5	4.2	1282	7	US-11-781-665-91	Sequence 91, Appli
392	95	4.3	3750	1	PCT-US07-18368A-136	Sequence 136, Appli	465	93.5	4.2	1884	7	US-11-833-133-51	Sequence 51, Appli
393	95	4.3	3812	8	US-60-956-093-74	Sequence 74, Appli	466	93.5	4.2	2004	7	US-11-817-499-7	Sequence 7, Appli
394	95	4.3	3812	8	US-60-956-094-74	Sequence 74, Appli	467	93.5	4.2	2029	7	US-11-833-133-4	Sequence 4, Appli
395	95	4.3	3938	7	US-11-847-733-1	Sequence 1, Appli	468	93.5	4.2	2076	7	US-11-817-499-1	Sequence 1, Appli
396	95	4.3	3958	8	US-60-956-093-73	Sequence 73, Appli	469	93.5	4.2	3034	7	US-11-708-858-44	Sequence 44, Appli
397	95	4.3	3958	8	US-60-956-094-73	Sequence 73, Appli	470	93.5	4.2	3270	7	US-11-835-336-38	Sequence 38, Appli
C 398	95	4.3	4270	7	US-11-884-496-228	Sequence 228, Appli	471	93.5	4.2	3971	7	US-11-816-601-155	Sequence 155, Appli
399	95	4.3	7407	1	PCT-US02-29565-3	Sequence 3, Appli	472	93.5	4.2	3971	7	US-11-816-601-295	Sequence 295, Appli
400	95	4.3	7848	7	US-11-490-374A-1485	Sequence 1485, Appli	473	93.5	4.2	4125	7	US-11-490-374A-2159	Sequence 2159, Appli
401	95	4.3	7959	7	US-11-490-374A-1475	Sequence 1475, Appli	474	93.5	4.2	4240	7	US-11-490-374A-2158	Sequence 2158, Appli
402	95	4.3	8013	7	US-11-490-374A-1483	Sequence 1483, Appli	475	93.5	4.2	4286	7	US-11-137-671A-14	Sequence 14, Appli
403	95	4.3	8226	7	US-11-490-374A-1492	Sequence 1492, Appli	476	93.5	4.2	4749	7	US-11-884-496-194	Sequence 194, Appli
404	95	4.3	8278	7	US-11-490-374A-1482	Sequence 1482, Appli	477	93.5	4.2	4749	7	US-11-884-496-362	Sequence 362, Appli
405	95	4.3	8278	7	US-11-490-374A-1484	Sequence 1484, Appli	478	93.5	4.2	4903	1	PCT-US07-15888-0	Sequence 0, Appli
406	95	4.3	8278	7	US-11-490-374A-1493	Sequence 1493, Appli	479	93	4.2	921	8	US-60-914-361-93	Sequence 93, Appli
407	95	4.3	8371	7	US-11-490-374A-1476	Sequence 1476, Appli	480	93	4.2	1310	7	US-11-833-133-76	Sequence 76, Appli
408	95	4.3	8374	7	US-11-490-374A-1478	Sequence 1478, Appli	481	93	4.2	1341	7	US-11-832-579-8	Sequence 8, Appli
409	95	4.3	8449	7	US-11-490-374A-1490	Sequence 1490, Appli	482	93	4.2	1341	7	US-11-832-579-15	Sequence 15, Appli
410	95	4.3	706	1	PCT-US07-17776B-363	Sequence 363, Appli	483	93	4.2	1341	7	US-11-832-579-31	Sequence 31, Appli
411	94.5	4.3	909	8	US-60-970-876-30	Sequence 30, Appli	484	93	4.2	1341	7	US-11-832-579-90	Sequence 90, Appli
412	94.5	4.3	1127	1	PCT-US07-17776B-3015	Sequence 3015, Appli	485	93	4.2	1341	7	US-11-832-579-90	Sequence 90, Appli
413	94.5	4.3	1368	7	US-11-833-133-15	Sequence 15, Appli	486	93	4.2	1350	8	US-60-914-361-95	Sequence 95, Appli
414	94.5	4.3	1410	6	US-10-343-663B-40	Sequence 40, Appli	487	93	4.2	1987	7	US-10-374-300-706	Sequence 706, Appli
415	94.5	4.3	1512	7	US-11-844-953-31	Sequence 31, Appli	488	93	4.2	2028	6	US-10-375-932A-202	Sequence 202, Appli
416	94.5	4.3	1512	7	US-11-844-953-31	Sequence 31, Appli	489	93	4.2	2157	7	US-11-832-579-91	Sequence 91, Appli
417	94.5	4.3	1512	7	US-11-844-953-31	Sequence 31, Appli	490	93	4.2	2441	7	US-11-832-579-1	Sequence 1, Appli
418	94.5	4.3	1512	7	US-11-844-967-31	Sequence 31, Appli	491	93	4.2	2641	7	US-11-374-300-63	Sequence 63, Appli
419	94.5	4.3	1512	7	US-11-844-970-31	Sequence 31, Appli	492	93	4.2	3072	8	US-60-914-361-121	Sequence 121, Appli
420	94.5	4.3	1512	7	US-11-844-973-31	Sequence 31, Appli	493	93	4.2	3318	8	US-60-970-876-117	Sequence 117, Appli
421	94.5	4.3	1746	7	US-11-665-276-4	Sequence 4, Appli	494	93	4.2	4189	8	US-60-970-876-115	Sequence 115, Appli
422	94.5	4.3	3158	1	PCT-US07-13803-430	Sequence 430, Appli	495	93	4.2	5880	7	US-11-802-321A-68	Sequence 68, Appli
423	94.5	4.3	3683	8	US-60-970-876-124	Sequence 124, Appli	496	93	4.2	5880	7	US-11-802-321A-69	Sequence 69, Appli
424	94.5	4.3	4045	7	US-11-794-690-11	Sequence 11, Appli	497	93	4.2	5880	7	US-11-802-321A-71	Sequence 71, Appli
425	94.5	4.3	4653	7	US-11-569-756-10	Sequence 10, Appli	498	93	4.2	5880	7	US-11-490-374A-1937	Sequence 1937, Appli
426	94.5	4.3	5304	7	US-11-569-756-2	Sequence 2, Appli	499	93	4.2	5903	7	US-11-802-321A-81	Sequence 81, Appli
427	94.5	4.3	5487	7	US-11-884-546-90	Sequence 90, Appli	500	93	4.2	5903	7	US-11-490-374A-1941	Sequence 1941, Appli
428	94.5	4.3	9200	7	US-11-235-701A-367	Sequence 367, Appli	501	93	4.2	9189	6	US-10-741-191B-1	Sequence 1, Appli
429	94.5	4.3	12050	7	US-11-884-496-41	Sequence 41, Appli	502	93	4.2	9765	7	US-11-825-627-494	Sequence 494, Appli
430	94.5	4.3	14123	7	US-11-569-756-6	Sequence 6, Appli	503	92.5	4.2	495	8	US-60-969-195-7500	Sequence 7500, Appli
431	94.5	4.3	14177	7	US-11-569-756-4	Sequence 4, Appli	504	92.5	4.2	821	1	PCT-US07-17776B-7307	Sequence 7307, Appli
432	94.5	4.3	33592	7	US-11-249-873A-1	Sequence 1, Appli	505	92.5	4.2	2115	7	US-11-833-133-10	Sequence 10, Appli
433	94.5	4.3	33699	7	US-11-249-873A-3	Sequence 3, Appli	506	92.5	4.2	2189	7	US-11-816-601-716	Sequence 716, Appli
434	94.5	4.3	33988	7	US-11-249-873A-14	Sequence 14, Appli	507	92.5	4.2	2377	7	US-11-829-058-3	Sequence 3, Appli
435	94.5	4.3	34341	7	US-11-249-873A-2	Sequence 2, Appli	508	92.5	4.2	2558	7	US-11-733-861-12	Sequence 12, Appli
436	94.5	4.3	34448	7	US-11-249-873A-4	Sequence 4, Appli	509	92.5	4.2	2757	8	US-60-970-876-120	Sequence 120, Appli
437	94.5	4.3	34555	6	US-10-559-596-5	Sequence 5, Appli	510	92.5	4.2	2830	7	US-11-884-496-575	Sequence 575, Appli
438	94.5	4.3	34737	7	US-11-249-873A-15	Sequence 15, Appli	511	92.5	4.2	3939	7	US-11-884-496-35	Sequence 35, Appli
439	94.5	4.3	35149	7	US-11-884-086-1	Sequence 1, Appli	512	92.5	4.2	5370	7	US-11-908-114-1	Sequence 1, Appli
440	94.5	4.3	35724	7	US-11-249-873A-13	Sequence 13, Appli	513	92.5	4.2	6000	1	PCT-US07-13803-154	Sequence 154, Appli
441	94.5	4.3	36114	7	US-11-249-873A-16	Sequence 16, Appli	514	92.5	4.2	7823	7	US-11-490-374A-1480	Sequence 1480, Appli
442	94.5	4.3	39301	7	US-11-712-794-17	Sequence 17, Appli	515	92.5	4.2	7823	7	US-11-490-374A-1487	Sequence 1487, Appli
443	94.5	4.3	50475	7	US-11-712-794-16	Sequence 16, Appli	516	92.5	4.2	8647	7	US-11-490-374A-1474	Sequence 1474, Appli
444	94	4.3	774	8	US-60-911-925A-40	Sequence 40, Appli	517	92.5	4.2	8815	7	US-11-490-374A-1481	Sequence 1481, Appli
445	94	4.3	1290	1	PCT-US07-17776B-3321	Sequence 3321, Appli	518	92.5	4.2	12021	7	US-11-884-496-428	Sequence 428, Appli
446	94	4.3	1499	7	US-11-781-665-1891	Sequence 1891, Appli	519	92	4.2	669	8	US-60-970-876-150	Sequence 150, Appli
447	94	4.3	2119	7	US-11-830-023-1	Sequence 1, Appli	520	92	4.2	757	1	PCT-US07-17776B-5272	Sequence 5272, Appli
448	94	4.3	2583	7	US-11-235-701A-510	Sequence 510, Appli	521	92	4.2	830	7	US-11-582-527A-1	Sequence 1, Appli
449	94	4.3	3497	8	US-60-911-925A-41	Sequence 41, Appli	522	92	4.2	850	7	US-11-582-527A-5	Sequence 5, Appli

523	92	4.2	1125	7	US-11-833-133-54	Sequence 54, Appl	596	91.5	4.1	1974	7	US-11-649-155-3	Sequence 3, Appli
524	92	4.2	1341	7	US-11-832-579-15	Sequence 15, Appl	c 597	91.5	4.1	1995	7	US-11-817-499-9	Sequence 9, Appli
525	92	4.2	1341	7	US-11-832-579-21	Sequence 21, Appl	c 598	91.5	4.1	2067	7	US-11-817-499-3	Sequence 3, Appli
526	92	4.2	1341	7	US-11-832-579-29	Sequence 29, Appl	c 599	91.5	4.1	2118	7	US-11-649-155-5	Sequence 5, Appli
527	92	4.2	1434	7	US-11-830-023-117	Sequence 117, Appl	c 600	91.5	4.1	2274	7	US-11-817-499-13	Sequence 13, Appl
528	92	4.2	1616	7	US-11-833-579-11	Sequence 11, Appl	c 601	91.5	4.1	2274	7	US-11-884-496-531	Sequence 531, App
529	92	4.2	1637	7	US-11-833-133-52	Sequence 52, Appl	c 602	91.5	4.1	2709	7	US-11-884-496-165	Sequence 165, App
530	92	4.2	1725	1	PCT-US07-06371-3	Sequence 3, Appli	c 603	91.5	4.1	2766	6	US-10-276-032-42	Sequence 42, Appl
c 531	92	4.2	1797	7	US-11-781-665-2915	Sequence 2915, Ap	c 604	91.5	4.1	3057	7	US-11-781-665-751	Sequence 751, App
532	92	4.2	2443	6	US-10-815-495A-17	Sequence 17, Appl	c 605	91.5	4.1	3434	1	PCT-US07-13803-515	Sequence 515, App
533	92	4.2	2443	7	US-11-837-279-17	Sequence 17, Appl	c 606	91.5	4.1	3474	8	US-60-970-876-118	Sequence 118, App
534	92	4.2	2520	6	US-10-815-495A-21	Sequence 21, Appl	c 607	91.5	4.1	5674	8	US-60-970-876-52	Sequence 52, Appl
535	92	4.2	2520	7	US-11-837-279-21	Sequence 21, Appl	c 608	91.5	4.1	6000	1	PCT-US07-13803-102	Sequence 102, App
c 536	92	4.2	2607	1	PCT-US07-18368A-177	Sequence 177, App	c 609	91	4.1	923	7	US-11-781-151-1	Sequence 1, Appli
c 537	92	4.2	2620	1	PCT-US07-18368A-178	Sequence 178, App	c 610	91	4.1	1122	8	US-60-914-361-11	Sequence 11, Appl
538	92	4.2	2784	1	PCT-US07-13803-391	Sequence 391, Appl	c 611	91	4.1	1415	7	US-11-884-496-67	Sequence 67, Appl
c 539	92	4.2	3107	7	US-11-835-336-81	Sequence 81, Appl	c 612	91	4.1	2022	6	US-10-554-521-53	Sequence 53, Appl
540	92	4.2	3542	7	US-11-884-496-307	Sequence 307, App	c 613	91	4.1	2469	7	US-11-817-478-3	Sequence 3, Appli
541	92	4.2	3693	1	PCT-US07-06371-5	Sequence 5, Appli	c 614	91	4.1	2728	6	US-10-587-995-1	Sequence 1, Appli
542	92	4.2	4457	1	PCT-US07-06371-6	Sequence 6, Appli	c 615	91	4.1	2771	7	US-11-733-861-59	Sequence 59, Appl
543	92	4.2	6177	7	US-11-781-861-15	Sequence 15, Appl	c 616	91	4.1	3263	7	US-11-847-733-69	Sequence 69, Appl
544	92	4.2	6177	7	US-11-781-867-15	Sequence 15, Appl	c 617	91	4.1	3387	7	US-11-884-496-496	Sequence 496, App
545	92	4.2	6177	7	US-11-781-870-15	Sequence 15, Appl	c 618	91	4.1	3387	7	US-11-884-496-535	Sequence 535, App
546	92	4.2	6177	7	US-11-781-871-15	Sequence 15, Appl	c 619	91	4.1	8085	7	US-11-835-336-72	Sequence 72, Appl
547	92	4.2	6177	7	US-11-884-956-36	Sequence 36, Appl	c 620	91	4.1	11185	1	PCT-US07-13803-307	Sequence 307, App
548	92	4.2	6177	7	US-11-781-875-15	Sequence 15, Appl	c 621	91	4.1	11466	6	US-10-466-960B-4	Sequence 4, Appli
549	92	4.2	6177	7	US-11-781-877-15	Sequence 15, Appl	c 622	91	4.1	155470	6	US-10-910-811B-373	Sequence 373, App
550	92	4.2	6177	7	US-11-781-880-15	Sequence 15, Appl	c 623	91	4.1	155470	6	US-10-945-565B-373	Sequence 373, App
551	92	4.2	6177	7	US-11-781-882-15	Sequence 15, Appl	c 624	90.5	4.1	594	1	PCT-US07-17776B-8962	Sequence 8962, Ap
c 552	92	4.2	6180	7	US-11-844-953-3	Sequence 3, Appli	c 625	90.5	4.1	711	8	US-60-970-876-42	Sequence 42, Appl
c 553	92	4.2	6180	7	US-11-844-953-36	Sequence 36, Appl	c 626	90.5	4.1	827	1	PCT-US07-17776B-5707	Sequence 5707, Ap
554	92	4.2	6180	7	US-11-844-953-37	Sequence 37, Appl	c 627	90.5	4.1	1002	7	US-11-781-665-306	Sequence 306, App
555	92	4.2	6180	7	US-11-844-953-69	Sequence 69, Appl	c 628	90.5	4.1	1038	8	US-60-970-876-57	Sequence 57, Appl
556	92	4.2	6180	7	US-11-844-953-63	Sequence 63, Appli	c 629	90.5	4.1	1434	1	PCT-US07-18368A-218	Sequence 218, App
c 557	92	4.2	6180	7	US-11-844-956-3	Sequence 3, Appli	c 630	90.5	4.1	2212	7	US-11-708-858-41	Sequence 41, Appl
558	92	4.2	6180	7	US-11-844-956-36	Sequence 36, Appl	c 631	90.5	4.1	2545	7	US-11-880-377-2455	Sequence 2455, Ap
559	92	4.2	6180	7	US-11-844-956-69	Sequence 69, Appl	c 632	90.5	4.1	2749	7	US-11-880-377-2461	Sequence 2461, Ap
560	92	4.2	6180	7	US-11-844-963-37	Sequence 37, Appl	c 633	90.5	4.1	3207	7	US-11-884-496-125	Sequence 125, App
c 561	92	4.2	6180	7	US-11-844-963-36	Sequence 36, Appl	c 634	90.5	4.1	3211	7	US-11-884-496-132	Sequence 132, App
562	92	4.2	6180	7	US-11-844-963-37	Sequence 37, Appl	c 635	90.5	4.1	5452	7	US-11-235-701A-495	Sequence 495, App
563	92	4.2	6180	7	US-11-844-963-69	Sequence 69, Appl	c 636	90	4.1	964	1	PCT-US07-17776B-5428	Sequence 5428, Ap
564	92	4.2	6180	7	US-11-844-967-3	Sequence 3, Appli	c 637	90	4.1	1026	8	US-60-970-876-168	Sequence 168, App
565	92	4.2	6180	7	US-11-844-967-37	Sequence 37, Appl	c 638	90	4.1	1149	8	US-60-914-361-132	Sequence 132, App
c 566	92	4.2	6180	7	US-11-844-967-36	Sequence 36, Appl	c 639	90	4.1	1350	7	US-11-844-953-27	Sequence 27, Appl
567	92	4.2	6180	7	US-11-844-967-69	Sequence 69, Appl	c 640	90	4.1	1350	7	US-11-844-956-27	Sequence 27, Appl
c 568	92	4.2	6180	7	US-11-844-970-3	Sequence 3, Appli	c 641	90	4.1	1350	7	US-11-844-963-27	Sequence 27, Appl
c 569	92	4.2	6180	7	US-11-844-970-36	Sequence 36, Appl	c 642	90	4.1	1350	7	US-11-844-967-27	Sequence 27, Appl
570	92	4.2	6180	7	US-11-844-970-37	Sequence 37, Appl	c 643	90	4.1	1350	7	US-11-844-970-27	Sequence 27, Appl
571	92	4.2	6180	7	US-11-844-970-69	Sequence 69, Appl	c 644	90	4.1	1350	7	US-11-844-973-27	Sequence 27, Appl
572	92	4.2	6180	7	US-11-844-973-3	Sequence 3, Appli	c 645	90	4.1	1392	7	US-11-781-151-21	Sequence 21, Appl
c 573	92	4.2	6180	7	US-11-844-973-37	Sequence 37, Appl	c 646	90	4.1	1392	7	US-11-769-327A-13	Sequence 13, Appl
574	92	4.2	6180	7	US-11-844-973-37	Sequence 37, Appl	c 647	90	4.1	1407	7	US-11-557-761-4	Sequence 4, Appli
575	92	4.2	6180	7	US-11-844-973-69	Sequence 69, Appl	c 648	90	4.1	1407	7	US-11-557-783-4	Sequence 4, Appli
576	92	4.2	17534	1	PCT-US07-06371-7	Sequence 7, Appli	c 649	90	4.1	1407	7	US-11-769-327A-10	Sequence 10, Appl
c 577	92	4.2	21001	1	PCT-US07-75297-3	Sequence 3, Appli	c 650	90	4.1	2344	7	US-11-833-133-49	Sequence 49, Appl
578	92	4.2	30756	1	PCT-US07-06371-16	Sequence 16, Appl	c 651	90	4.1	2766	8	US-60-970-876-126	Sequence 126, App
579	91.5	4.1	752	1	PCT-US07-17776B-6870	Sequence 6870, Ap	c 652	90	4.1	2855	7	US-11-884-496-563	Sequence 563, App
c 580	91.5	4.1	784	1	PCT-US07-17776B-1624	Sequence 1624, Ap	c 653	90	4.1	3217	7	US-11-207-739B-7	Sequence 7, Appli
c 581	91.5	4.1	794	1	PCT-US07-17776B-5692	Sequence 5692, Ap	c 654	90	4.1	3325	1	PCT-US07-13803-518	Sequence 518, App
c 582	91.5	4.1	1061	1	PCT-US07-17776B-8342	Sequence 8342, Ap	c 655	90	4.1	3332	7	US-11-733-861-21	Sequence 21, Appl
583	91.5	4.1	1189	7	US-11-374-300-54	Sequence 54, Appl	c 656	90	4.1	3807	7	US-11-557-761-2	Sequence 2, Appli
584	91.5	4.1	1218	7	US-11-649-155-9	Sequence 9, Appli	c 657	90	4.1	3807	7	US-11-557-783-2	Sequence 2, Appli
585	91.5	4.1	1530	7	US-11-844-953-25	Sequence 25, Appl	c 658	90	4.1	4131	1	PCT-US07-13803-343	Sequence 343, App
586	91.5	4.1	1530	7	US-11-844-956-25	Sequence 25, Appl	c 659	90	4.1	4673	7	US-11-816-601-779	Sequence 779, App
587	91.5	4.1	1530	7	US-11-844-963-25	Sequence 25, Appl	c 660	90	4.1	5898	7	US-11-557-761-1	Sequence 1, Appli
588	91.5	4.1	1530	7	US-11-844-967-25	Sequence 25, Appl	c 661	90	4.1	5898	7	US-11-557-783-1	Sequence 1, Appli
589	91.5	4.1	1530	7	US-11-844-970-25	Sequence 25, Appl	c 662	90	4.1	6000	1	PCT-US07-13803-76	Sequence 76, Appl
590	91.5	4.1	1530	7	US-11-844-973-25	Sequence 25, Appl	c 663	90	4.1	34555	6	US-10-559-596-5	Sequence 5, Appli
591	91.5	4.1	1595	7	US-11-816-601-713	Sequence 713, App	c 664	89.5	4.0	811	1	PCT-US07-17776B-6415	Sequence 6415, Ap
592	91.5	4.1	1786	7	US-11-374-300-709	Sequence 709, App	c 665	89.5	4.0	811	1	PCT-US07-17776B-7081	Sequence 7081, Ap
593	91.5	4.1	1854	1	PCT-US07-75398-64	Sequence 64, Appl	c 666	89.5	4.0	839	1	PCT-US07-17776B-7896	Sequence 7896, Ap
594	91.5	4.1	1854	7	US-11-835-328-64	Sequence 64, Appl	c 667	89.5	4.0	840	8	US-60-970-876-141	Sequence 141, App
595	91.5	4.1	1887	7	US-11-649-155-7	Sequence 7, Appli	c 668	89.5	4.0	842	1	PCT-US07-17776B-9643	Sequence 9643, Ap

669	89.5	4.0	934	7	US-11-374-300-581	Sequence 581, App	742	88.5	4.0	3774	8	US-60-951-363-182	Sequence 182, App
c 670	89.5	4.0	1260	8	US-60-970-876-171	Sequence 171, App	743	88.5	4.0	3774	8	US-60-951-363-184	Sequence 184, App
c 671	89.5	4.0	1449	8	US-60-914-361-58	Sequence 58, App	744	88.5	4.0	4147	1	PCT-US07-13803-404	Sequence 404, App
c 672	89.5	4.0	1500	7	US-11-844-953-63	Sequence 63, App	c 745	88.5	4.0	5477	7	US-11-835-336-108	Sequence 108, App
c 673	89.5	4.0	1500	7	US-11-844-956-63	Sequence 63, App	746	88.5	4.0	6470	7	US-11-884-496-258	Sequence 258, App
c 674	89.5	4.0	1500	7	US-11-844-963-63	Sequence 63, App	747	88.5	4.0	8115	7	US-11-825-627-322	Sequence 322, App
c 675	89.5	4.0	1500	7	US-11-844-967-63	Sequence 63, App	c 748	88.5	4.0	9155	7	US-11-884-496-412	Sequence 412, App
c 676	89.5	4.0	1500	7	US-11-844-970-63	Sequence 63, App	c 749	88	4.0	768	1	PCT-US07-177768-1951	Sequence 1951, App
c 677	89.5	4.0	1500	7	US-11-844-973-63	Sequence 63, App	750	88	4.0	885	1	PCT-US07-177768-5636	Sequence 5636, App
c 678	89.5	4.0	1569	8	US-60-970-876-169	Sequence 169, App	c 751	88	4.0	921	1	PCT-US07-177768-9587	Sequence 9587, App
c 679	89.5	4.0	1782	1	PCT-US07-17013-77	Sequence 77, App	c 752	88	4.0	966	7	US-11-883-506-4	Sequence 4, Appli
c 680	89.5	4.0	1965	7	US-11-835-328-87	Sequence 87, App	c 753	88	4.0	1006	7	US-11-883-499-4	Sequence 9498, App
c 681	89.5	4.0	2004	1	PCT-US07-75398-80	Sequence 80, App	754	88	4.0	1032	6	PCT-US07-177768-9498	Sequence 27, Appl
c 682	89.5	4.0	2004	7	US-11-835-328-80	Sequence 80, App	755	88	4.0	1032	1	PCT-US07-177768-4418	Sequence 4418, App
c 683	89.5	4.0	2043	6	US-10-375-932A-216	Sequence 216, App	c 757	88	4.0	1040	1	PCT-US07-177768-3442	Sequence 3442, App
c 684	89.5	4.0	2243	7	US-11-847-733-54	Sequence 54, App	c 758	88	4.0	1106	1	PCT-US07-177768-8283	Sequence 8283, App
c 685	89.5	4.0	2858	7	US-11-781-665-741	Sequence 741, App	759	88	4.0	1592	7	US-11-833-133-7	Sequence 7, Appli
c 686	89.5	4.0	4410	7	US-11-781-861-23	Sequence 23, App	c 760	88	4.0	1844	7	US-11-781-665-1615	Sequence 1615, App
c 687	89.5	4.0	4410	7	US-11-781-867-23	Sequence 23, App	761	88	4.0	2136	7	US-11-832-009-20	Sequence 20, Appl
c 688	89.5	4.0	4410	7	US-11-781-867-23	Sequence 23, App	762	88	4.0	4374	7	US-11-884-496-217	Sequence 217, App
c 689	89.5	4.0	4410	7	US-11-781-870-23	Sequence 23, App	763	88	4.0	4702	7	US-11-490-374A-1567	Sequence 1567, App
c 690	89.5	4.0	4410	7	US-11-781-871-23	Sequence 23, App	764	88	4.0	5862	7	US-11-816-601-20	Sequence 20, Appl
c 691	89.5	4.0	4410	7	US-11-781-874-23	Sequence 23, App	c 765	88	4.0	6000	1	PCT-US07-13803-248	Sequence 248, App
c 692	89.5	4.0	4410	7	US-11-781-875-23	Sequence 23, App	c 766	88	4.0	6127	1	PCT-US07-13803-424	Sequence 424, App
c 693	89.5	4.0	4410	7	US-11-781-877-23	Sequence 23, App	767	88	4.0	6233	7	US-11-793-909-82	Sequence 82, Appl
c 694	89.5	4.0	4410	7	US-11-781-880-23	Sequence 23, App	768	88	4.0	9778	7	US-11-884-496-164	Sequence 164, App
c 695	89.5	4.0	4410	7	US-11-781-882-23	Sequence 23, App	c 769	87.5	4.0	546	1	PCT-US07-177768-4719	Sequence 4719, App
c 696	89.5	4.0	4410	7	US-11-844-953-61	Sequence 61, App	c 770	87.5	4.0	711	1	PCT-US07-17321A-61	Sequence 61, Appl
c 697	89.5	4.0	4410	7	US-11-844-956-61	Sequence 61, App	771	87.5	4.0	750	7	PCT-US07-17321A-156	Sequence 156, App
c 698	89.5	4.0	4410	7	US-11-844-963-61	Sequence 61, App	772	87.5	4.0	930	7	US-11-374-300-332	Sequence 332, App
c 699	89.5	4.0	4410	7	US-11-844-967-61	Sequence 61, App	773	87.5	4.0	1088	7	US-11-852-274-61	Sequence 61, Appl
c 700	89.5	4.0	4410	7	US-11-844-970-61	Sequence 61, App	c 774	87.5	4.0	1188	7	US-11-781-151-3	Sequence 3, Appli
c 701	89.5	4.0	4410	7	US-11-844-973-61	Sequence 61, App	775	87.5	4.0	1309	1	PCT-US07-177768-3528	Sequence 3528, App
c 702	89.5	4.0	5119	7	US-11-884-496-255	Sequence 255, App	c 776	87.5	4.0	1401	7	US-11-833-133-85	Sequence 85, Appl
c 703	89.5	4.0	6187	7	US-11-793-909-75	Sequence 75, App	777	87.5	4.0	1431	7	US-11-374-300-80	Sequence 80, Appl
c 704	89.5	4.0	8312	7	US-11-884-496-221	Sequence 221, App	778	87.5	4.0	1573	7	US-11-781-665-1819	Sequence 1819, App
c 705	89.5	4.0	11883	7	US-11-796-131-4	Sequence 4, Appli	779	87.5	4.0	1804	1	PCT-US07-75398-11	Sequence 11, Appl
c 706	89.5	4.0	11916	7	US-11-796-131-1	Sequence 1, Appli	780	87.5	4.0	1804	7	US-11-835-328-11	Sequence 11, Appl
c 707	89	4.0	681	8	US-60-970-876-63	Sequence 63, App	781	87.5	4.0	1821	7	US-11-538-319-29	Sequence 29, Appl
c 708	89	4.0	684	7	US-11-833-133-42	Sequence 42, App	782	87.5	4.0	2022	7	US-11-573-744-9	Sequence 9, Appli
c 709	89	4.0	1388	7	US-11-825-627-182	Sequence 182, App	783	87.5	4.0	2103	6	US-10-815-495A-5	Sequence 5, Appli
c 710	89	4.0	1718	8	US-60-970-876-76	Sequence 76, App	784	87.5	4.0	2361	7	US-11-650-345-8	Sequence 8, Appli
c 711	89	4.0	1741	7	US-11-374-300-664	Sequence 664, App	785	87.5	4.0	2692	1	PCT-US07-15762-2	Sequence 2, Appli
c 712	89	4.0	2047	7	US-11-781-665-863	Sequence 863, App	c 786	87.5	4.0	3728	7	US-11-711-146-12	Sequence 12, Appl
c 713	89	4.0	2378	7	US-11-884-496-283	Sequence 283, App	787	87.5	4.0	3728	7	US-11-711-146-13	Sequence 13, Appl
c 714	89	4.0	2509	7	US-11-781-665-2430	Sequence 2430, App	788	87.5	4.0	5144	7	US-11-490-374A-1684	Sequence 34, Appl
c 715	89	4.0	4403	7	US-11-825-627-330	Sequence 330, App	c 789	87.5	4.0	5288	7	US-11-708-858-34	Sequence 34, Appl
c 716	89	4.0	4683	7	US-11-490-374A-1647	Sequence 1647, App	790	87.5	4.0	5288	7	US-11-708-858-34	Sequence 34, Appl
c 717	89	4.0	4683	7	US-11-490-374A-1648	Sequence 1648, App	c 791	87	3.9	698	1	PCT-US07-177768-3319	Sequence 3319, App
c 718	89	4.0	4838	7	US-11-490-374A-1650	Sequence 1650, App	c 792	87	3.9	698	1	PCT-US07-177768-4098	Sequence 4098, App
c 719	89	4.0	6000	1	PCT-US07-13803-247	Sequence 247, App	c 793	87	3.9	832	1	PCT-US07-177768-8015	Sequence 8015, App
c 720	89	4.0	7108	7	US-11-847-733-21	Sequence 21, App	c 794	87	3.9	919	1	PCT-US07-177768-3280	Sequence 3280, App
c 721	89	4.0	8515	7	US-11-884-496-15	Sequence 15, App	795	87	3.9	963	7	US-11-833-133-78	Sequence 78, Appl
c 722	89	4.0	9263	7	US-11-884-496-191	Sequence 191, App	796	87	3.9	1034	8	US-60-970-876-144	Sequence 144, App
c 723	88.5	4.0	689	1	PCT-US07-177768-3803	Sequence 3803, App	c 797	87	3.9	1034	1	PCT-US07-177768-4552	Sequence 4552, App
c 724	88.5	4.0	972	1	PCT-US07-177768-4620	Sequence 4620, App	c 798	87	3.9	1052	1	PCT-US07-177768-9473	Sequence 9473, App
c 725	88.5	4.0	1056	7	US-11-800-955-17	Sequence 17, App	c 799	87	3.9	1077	7	US-11-830-023-125	Sequence 125, App
c 726	88.5	4.0	1215	1	PCT-US07-18368A-148	Sequence 148, App	800	87	3.9	1170	1	PCT-US07-18368A-54	Sequence 54, Appl
c 727	88.5	4.0	1215	1	PCT-US07-18368A-149	Sequence 149, App	801	87	3.9	1214	6	PCT-US07-177768-8200	Sequence 8200, App
c 728	88.5	4.0	1215	1	PCT-US07-18368A-150	Sequence 150, App	802	87	3.9	1314	6	US-10-552-571-1	Sequence 1, Appli
c 729	88.5	4.0	1460	8	US-60-970-876-85	Sequence 85, App	803	87	3.9	1366	1	PCT-US07-13803-273	Sequence 273, App
c 730	88.5	4.0	1501	7	US-11-847-733-32	Sequence 32, App	804	87	3.9	1388	7	US-11-781-665-970	Sequence 970, App
c 731	88.5	4.0	1839	7	US-11-781-151-13	Sequence 13, App	c 805	87	3.9	1398	7	US-11-804-222-55	Sequence 55, Appl
c 732	88.5	4.0	1897	7	US-11-836-667-34	Sequence 34, App	806	87	3.9	1695	7	PCT-US07-18368A-167	Sequence 167, App
c 733	88.5	4.0	2136	7	US-11-374-300-163	Sequence 163, App	807	87	3.9	1885	7	US-11-781-665-181	Sequence 181, App
c 734	88.5	4.0	2637	7	US-11-781-199-3	Sequence 3, Appli	c 808	87	3.9	1959	7	US-11-801-963A-1756	Sequence 1756, App
c 735	88.5	4.0	2637	1	PCT-US07-13803-399	Sequence 399, App	809	87	3.9	2049	8	US-60-914-361-52	Sequence 52, Appl
c 736	88.5	4.0	2912	7	US-11-781-665-2818	Sequence 2818, App	810	87	3.9	2403	7	US-11-816-294-7	Sequence 7, Appli
c 737	88.5	4.0	3299	7	US-11-781-665-186	Sequence 186, App	811	87	3.9	2476	7	US-11-374-300-320	Sequence 320, App
c 738	88.5	4.0	3747	8	US-60-951-363-186	Sequence 186, App	c 812	87	3.9	2814	7	US-11-783-064-4	Sequence 4, Appli
c 739	88.5	4.0	3762	8	US-60-951-363-178	Sequence 178, App	813	87	3.9	2855	7	US-11-374-300-7	Sequence 7, Appli
c 740	88.5	4.0	3762	8	US-60-951-363-180	Sequence 180, App	c 814	87	3.9	2931	7	US-11-783-064-10	Sequence 10, Appli
c 741	88.5	4.0	3774	8	US-60-951-363-179	Sequence 179, App							

C 815	87	3.9	3144	7	US-11-783-064-9	Sequence 9, Appli	888	86	3.9	4562	7	US-11-847-733-59	Sequence 59, Appli
C 816	87	3.9	3174	7	US-11-783-064-7	Sequence 7, Appli	889	86	3.9	5469	7	US-11-490-374A-1608	Sequence 1608, Ap
C 817	87	3.9	3809	7	US-11-783-064-6	Sequence 6, Appli	890	86	3.9	5648	7	US-11-490-374A-1605	Sequence 1605, Ap
C 818	87	3.9	3865	7	US-11-783-064-3	Sequence 3, Appli	891	86	3.9	5648	7	US-11-490-374A-1609	Sequence 1609, Ap
819	87	3.9	5096	7	US-11-881-406-40	Sequence 40, Appl	892	86	3.9	5695	7	US-11-490-374A-1597	Sequence 1597, Ap
820	87	3.9	5432	7	US-11-838-500-29	Sequence 29, Appl	893	86	3.9	5715	7	US-11-490-374A-1598	Sequence 1598, Ap
821	87	3.9	5432	7	US-11-838-500-57	Sequence 57, Appl	894	86	3.9	5778	7	US-11-490-374A-1604	Sequence 1604, Ap
822	87	3.9	6000	1	PCT-US07-13803-249	Sequence 249, App	895	86	3.9	5829	7	US-11-490-374A-1603	Sequence 1603, Ap
823	87	3.9	6096	1	PCT-US07-78059-10	Sequence 10, Appl	896	86	3.9	5829	7	US-11-490-374A-1607	Sequence 1607, Ap
824	87	3.9	6519	7	US-11-801-963A-2605	Sequence 2605, Ap	897	86	3.9	5866	7	US-11-490-374A-1600	Sequence 1600, Ap
825	87	3.9	6753	7	US-11-816-601-75	Sequence 75, Appl	898	86	3.9	5920	7	US-11-490-374A-1599	Sequence 1599, Ap
826	87	3.9	7028	7	US-11-881-406-39	Sequence 39, Appl	899	86	3.9	5925	7	US-11-815-198-28	Sequence 28, Appl
827	87	3.9	7822	7	US-11-830-023-144	Sequence 144, App	900	86	3.9	5925	7	US-11-490-374A-1601	Sequence 1601, Ap
828	87	3.9	8165	7	US-11-749-889-22	Sequence 22, Appl	901	86	3.9	5988	7	US-11-490-374A-1602	Sequence 1602, Ap
829	87	3.9	8165	7	US-11-830-023-164	Sequence 164, App	902	86	3.9	5988	7	US-11-490-374A-1606	Sequence 1606, Ap
830	87	3.9	8841	7	US-11-884-496-131	Sequence 131, App	903	86	3.9	6000	1	PCT-US07-13803-69	Sequence 69, Appl
831	87	3.9	12690	7	US-11-830-023-124	Sequence 124, App	C 904	86	3.9	6000	1	PCT-US07-13803-148	Sequence 148, App
C 832	87	3.9	12690	7	US-11-830-023-124	Sequence 124, App	905	86	3.9	8230	7	US-11-490-374A-1253	Sequence 1253, Ap
833	87	3.9	13313	6	US-10-552-571-16	Sequence 16, Appl	906	86	3.9	8481	7	US-11-490-374A-1254	Sequence 1254, Ap
834	87	3.9	13711	7	US-11-490-374A-1308	Sequence 1308, Ap	907	86	3.9	8481	7	US-11-847-733-36	Sequence 36, Appl
835	87	3.9	13711	7	US-11-490-374A-1310	Sequence 1310, Ap	908	86	3.9	8679	8	PCT-US07-17776B-5023	Sequence 115, App
836	87	3.9	13711	7	US-11-490-374A-1311	Sequence 1311, Ap	909	85.5	3.9	582	1	PCT-US07-17776B-5023	Sequence 5023, Ap
837	87	3.9	14194	7	US-11-490-374A-1309	Sequence 1309, Ap	910	85.5	3.9	819	7	US-11-749-889-25	Sequence 25, Appl
C 838	87	3.9	35937	7	US-11-249-873A-28	Sequence 28, Appl	911	85.5	3.9	819	7	US-11-830-023-119	Sequence 119, App
839	86.5	3.9	741	7	US-11-833-133-18	Sequence 18, Appl	C 912	85.5	3.9	933	7	US-11-834-069-2	Sequence 2, Appli
840	86.5	3.9	765	8	US-60-970-876-39	Sequence 39, Appl	913	85.5	3.9	1040	1	PCT-US07-17776B-4386	Sequence 4386, Ap
841	86.5	3.9	787	1	PCT-US07-17776B-5805	Sequence 5805, Ap	914	85.5	3.9	1307	8	US-60-970-876-40	Sequence 40, Appl
842	86.5	3.9	867	1	PCT-US07-17776B-7887	Sequence 7887, Ap	915	85.5	3.9	1368	7	US-11-631-698-23	Sequence 23, Appl
843	86.5	3.9	908	7	US-11-374-300-293	Sequence 293, App	916	85.5	3.9	1477	6	US-10-860-724B-63	Sequence 63, Appl
844	86.5	3.9	939	7	US-11-833-133-63	Sequence 63, Appl	917	85.5	3.9	1962	7	US-11-817-499-11	Sequence 11, Appl
845	86.5	3.9	958	1	PCT-US07-17776B-6868	Sequence 6868, Ap	918	85.5	3.9	2710	7	US-11-884-496-166	Sequence 166, App
846	86.5	3.9	1055	7	US-11-825-627-158	Sequence 158, App	919	85.5	3.9	3720	7	US-11-835-336-37	Sequence 37, Appl
C 847	86.5	3.9	1057	1	PCT-US07-17776B-3304	Sequence 3304, Ap	920	85.5	3.9	3980	6	US-10-488-672A-17	Sequence 17, Appl
848	86.5	3.9	1083	7	US-11-883-996-59	Sequence 59, Appl	921	85.5	3.9	5535	7	US-11-908-114-2	Sequence 2, Appli
849	86.5	3.9	1265	7	US-11-795-824-11	Sequence 11, Appl	922	85.5	3.9	5868	1	PCT-US07-13803-288	Sequence 288, App
850	86.5	3.9	1265	7	US-11-795-824-12	Sequence 12, Appl	923	85.5	3.9	5868	1	PCT-US07-13803-526	Sequence 526, App
851	86.5	3.9	1265	7	US-11-795-824-13	Sequence 13, Appl	924	85.5	3.9	6453	7	US-11-816-601-136	Sequence 136, App
852	86.5	3.9	1265	7	US-11-795-824-14	Sequence 14, Appl	C 925	85.5	3.9	6621	7	US-11-835-336-15	Sequence 15, Appl
853	86.5	3.9	1265	7	US-11-795-824-35	Sequence 35, Appl	926	85	3.8	513	1	PCT-US07-17776B-5040	Sequence 5040, Ap
C 854	86.5	3.9	1492	7	US-11-374-300-197	Sequence 197, App	927	85	3.8	521	1	PCT-US07-17776B-10024	Sequence 10024, A
C 855	86.5	3.9	1493	7	US-11-884-496-433	Sequence 433, App	928	85	3.8	654	1	PCT-US07-17776B-7776	Sequence 7776, Ap
C 856	86.5	3.9	1845	7	US-11-374-300-341	Sequence 341, App	929	85	3.8	705	6	US-10-532-681-17	Sequence 17, Appl
857	86.5	3.9	1936	7	US-11-830-023-130	Sequence 130, App	C 930	85	3.8	782	1	PCT-US07-17776B-7901	Sequence 7901, Ap
858	86.5	3.9	2087	7	US-11-490-374A-1449	Sequence 1449, Ap	931	85	3.8	933	8	US-60-970-876-84	Sequence 84, Appl
859	86.5	3.9	2180	7	US-11-708-858-51	Sequence 51, Appl	C 932	85	3.8	1030	1	PCT-US07-17776B-3173	Sequence 3173, Ap
860	86.5	3.9	2287	7	US-11-781-665-2270	Sequence 2270, Ap	933	85	3.8	1042	7	US-11-374-300-467	Sequence 467, App
861	86.5	3.9	2615	7	US-11-884-496-444	Sequence 444, App	934	85	3.8	1047	7	US-11-654-358-18	Sequence 18, Appl
C 862	86.5	3.9	2988	7	US-11-354-210-90	Sequence 90, Appl	935	85	3.8	1134	8	US-60-970-876-7	Sequence 7, Appli
C 863	86.5	3.9	3034	7	US-11-708-858-44	Sequence 44, Appl	936	85	3.8	1335	8	US-60-970-876-102	Sequence 102, App
C 864	86.5	3.9	3077	7	US-11-708-858-45	Sequence 45, Appl	937	85	3.8	1371	7	US-11-623-607A-3	Sequence 3, Appli
865	86.5	3.9	3145	7	US-11-884-496-409	Sequence 409, App	938	85	3.8	1371	7	US-11-623-689-36	Sequence 36, Appl
866	86.5	3.9	3393	7	US-11-354-210-92	Sequence 92, Appl	939	85	3.8	1371	7	US-11-852-274-36	Sequence 36, Appl
867	86.5	3.9	3726	8	US-60-914-361-128	Sequence 128, App	940	85	3.8	1380	7	US-11-631-698-2	Sequence 2, Appli
868	86.5	3.9	5045	7	US-11-884-496-530	Sequence 530, App	941	85	3.8	1491	7	US-11-374-300-87	Sequence 87, Appl
C 869	86.5	3.9	5372	7	US-11-908-114-13	Sequence 13, Appl	942	85	3.8	1515	1	PCT-US07-77281-15	Sequence 15, Appl
C 870	86.5	3.9	5468	7	US-11-235-701A-489	Sequence 489, App	943	85	3.8	1515	7	US-11-490-374A-1839	Sequence 1839, Ap
871	86.5	3.9	6000	1	PCT-US07-13803-81	Sequence 81, Appl	944	85	3.8	1515	7	US-11-490-374A-1968	Sequence 1968, Ap
C 872	86.5	3.9	6705	1	PCT-US07-13803-188	Sequence 188, App	945	85	3.8	1515	7	US-11-490-374A-2136	Sequence 2136, Ap
C 873	86.5	3.9	6705	1	US-11-781-665-3045	Sequence 3045, Ap	C 946	85	3.8	1520	7	US-11-374-300-185	Sequence 185, App
874	86	3.9	813	1	PCT-US07-17776B-8024	Sequence 8024, Ap	947	85	3.8	1630	7	US-11-374-300-559	Sequence 559, App
875	86	3.9	1080	8	US-60-914-361-131	Sequence 131, App	948	85	3.8	1751	7	US-11-884-496-226	Sequence 226, App
876	86	3.9	1269	8	US-60-970-876-165	Sequence 165, App	949	85	3.8	2025	6	US-10-375-932A-204	Sequence 204, App
877	86	3.9	1326	7	US-11-883-197-12	Sequence 12, Appl	950	85	3.8	2193	7	US-11-781-665-3063	Sequence 3063, App
878	86	3.9	1497	7	US-11-795-824-29	Sequence 29, Appl	951	85	3.8	2238	8	US-60-970-876-100	Sequence 100, App
879	86	3.9	1603	6	US-10-583-089-9	Sequence 9, Appli	952	85	3.8	2583	7	US-11-785-365B-1	Sequence 1, Appli
880	86	3.9	1651	7	US-11-781-665-845	Sequence 845, App	C 953	85	3.8	2714	7	US-11-816-601-805	Sequence 805, App
881	86	3.9	1671	8	US-60-970-876-28	Sequence 28, Appl	C 954	85	3.8	2811	7	US-11-781-818-51	Sequence 51, Appl
882	86	3.9	1746	8	US-60-970-876-139	Sequence 139, App	C 955	85	3.8	2811	7	US-11-781-818-52	Sequence 13, Appl
C 883	86	3.9	1751	7	US-11-884-496-226	Sequence 226, App	956	85	3.8	3212	7	US-11-785-365B-13	Sequence 13, Appl
884	86	3.9	2329	7	US-11-884-496-271	Sequence 271, App	957	85	3.8	3288	7	US-11-785-365B-18	Sequence 18, Appl
885	86	3.9	2636	7	US-11-781-665-862	Sequence 862, App	958	85	3.8	3329	7	US-11-785-365B-15	Sequence 15, Appl
886	86	3.9	3192	7	US-11-884-496-29	Sequence 29, Appl	959	85	3.8	3740	7	US-11-733-861-18	Sequence 18, Appl
887	86	3.9	3494	7	US-11-795-824-33	Sequence 33, Appl	960	85	3.8	3872	7	US-11-884-496-524	Sequence 524, App

c 961	85	3.8	4501	7	US-11-835-336-63	Sequence 63, Appl	1034	84	3.8	2220	6	US-10-554-521-58	Sequence 58, Appl
962	85	3.8	4853	7	US-11-884-496-600	Sequence 600, App	1035	84	3.8	2694	7	US-11-490-374A-1446	Sequence 1446, Ap
963	85	3.8	5053	7	US-11-235-701A-500	Sequence 500, App	1036	84	3.8	2694	7	US-11-490-374A-1447	Sequence 1447, Ap
964	85	3.8	30612	7	US-11-665-940-64	Sequence 64, Appl	1037	84	3.8	2694	7	US-11-490-374A-1448	Sequence 1448, Ap
965	84.5	3.8	633	8	US-60-914-361-101	Sequence 101, Appl	c1038	84	3.8	2940	7	US-11-802-321A-18	Sequence 18, Appl
966	84.5	3.8	690	8	US-60-970-876-159	Sequence 159, App	c1039	84	3.8	2940	7	US-11-802-321A-20	Sequence 20, Appl
967	84.5	3.8	699	1	PCT-US07-17776B-9251	Sequence 9251, Ap	c1040	84	3.8	2940	7	US-11-802-321A-21	Sequence 21, Appl
968	84.5	3.8	814	7	US-11-374-300-56	Sequence 56, Appl	c1041	84	3.8	2940	7	US-11-802-321A-22	Sequence 22, Appl
969	84.5	3.8	844	1	PCT-US07-17776B-2765	Sequence 2765, Ap	c1042	84	3.8	3000	7	US-11-623-607A-9	Sequence 9, Appl
970	84.5	3.8	893	1	PCT-US07-18368A-190	Sequence 190, App	c1043	84	3.8	3000	7	US-11-623-689-42	Sequence 42, Appl
971	84.5	3.8	1052	1	PCT-US07-18368A-52	Sequence 52, Appl	c1044	84	3.8	3000	7	US-11-852-274-42	Sequence 42, Appl
972	84.5	3.8	1059	1	PCT-US07-17776B-4547	Sequence 4547, Ap	1045	84	3.8	3018	1	PCT-US07-13803-349	Sequence 349, App
973	84.5	3.8	1099	8	US-60-970-876-157	Sequence 157, App	1046	84	3.8	3120	7	US-11-802-321A-53	Sequence 53, Appl
c 974	84.5	3.8	1176	6	US-10-552-571-15	Sequence 15, Appl	1047	84	3.8	3349	7	US-11-825-627-252	Sequence 252, App
975	84.5	3.8	1257	1	PCT-US07-17776B-3260	Sequence 3260, Ap	1048	84	3.8	3349	7	US-11-825-627-252	Sequence 54, Appl
976	84.5	3.8	1308	8	US-60-970-876-145	Sequence 145, App	1049	84	3.8	3305	7	US-11-802-321A-55	Sequence 55, Appl
977	84.5	3.8	1432	7	US-11-374-300-390	Sequence 390, App	1050	84	3.8	3319	7	US-11-802-321A-80	Sequence 80, Appl
978	84.5	3.8	1462	7	US-11-374-300-207	Sequence 207, App	1051	84	3.8	3387	7	US-11-490-374A-1243	Sequence 1243, Ap
979	84.5	3.8	1489	7	US-11-591-361B-1	Sequence 1, Appl	c1052	84	3.8	4060	7	US-11-733-861-60	Sequence 60, Appl
980	84.5	3.8	1492	7	US-11-374-300-197	Sequence 197, App	1053	84	3.8	4143	7	US-11-490-374A-1450	Sequence 1450, Ap
c 981	84.5	3.8	1900	7	US-11-374-300-356	Sequence 356, App	c1054	84	3.8	4502	7	US-11-490-374A-2152	Sequence 2152, Ap
982	84.5	3.8	2050	7	US-11-884-546-68	Sequence 68, Appl	c1055	84	3.8	4502	7	US-11-490-374A-2154	Sequence 2154, Ap
983	84.5	3.8	2619	7	US-11-490-374A-1989	Sequence 1989, Ap	1056	84	3.8	4504	7	US-11-884-496-435	Sequence 435, App
984	84.5	3.8	2659	1	PCT-US07-13803-293	Sequence 293, App	c1057	84	3.8	5119	7	US-11-884-496-255	Sequence 255, App
985	84.5	3.8	3128	7	US-11-490-374A-1990	Sequence 1990, Ap	1058	84	3.8	5143	7	US-11-781-665-31	Sequence 31, Appl
986	84.5	3.8	3128	7	US-11-490-374A-1991	Sequence 1991, Ap	c1059	84	3.8	5898	7	US-11-557-761-1	Sequence 1, Appl
987	84.5	3.8	3216	6	US-10-419-296A-32	Sequence 32, Appl	c1060	84	3.8	5898	7	US-11-557-783-1	Sequence 1, Appl
988	84.5	3.8	3263	7	US-11-137-671A-15	Sequence 15, Appl	1061	84	3.8	6444	8	US-11-831-404-85	Sequence 85, Appl
989	84.5	3.8	3444	1	PCT-US07-17013-27	Sequence 27, Appl	1062	84	3.8	6444	8	US-60-956-153-7	Sequence 7, Appl
990	84.5	3.8	3729	7	US-11-795-913-155	Sequence 155, App	1063	84	3.8	36909	8	US-60-968-754-7	Sequence 7, Appl
991	84.5	3.8	3922	7	US-11-881-406-161	Sequence 161, App	1064	84	3.8	36909	8	US-60-970-269-7	Sequence 7, Appl
992	84.5	3.8	5619	7	US-11-235-701A-493	Sequence 493, App	1065	84	3.8	36909	8	US-60-970-281-7	Sequence 7, Appl
993	84.5	3.8	5674	7	US-11-235-701A-488	Sequence 488, App	1066	84	3.8	49107	8	US-60-970-281-42	Sequence 42, Appl
994	84.5	3.8	5674	7	US-11-235-701A-490	Sequence 490, App	1067	84	3.8	49765	8	US-60-956-153-13	Sequence 13, Appl
995	84.5	3.8	5674	7	US-11-235-701A-501	Sequence 501, App	1068	84	3.8	49765	8	US-60-968-754-13	Sequence 13, Appl
c 996	84.5	3.8	5748	7	US-11-235-701A-491	Sequence 491, App	1069	84	3.8	49911	8	US-60-956-153-6	Sequence 6, Appl
997	84.5	3.8	6000	1	PCT-US07-13803-136	Sequence 136, App	1070	84	3.8	49911	8	US-60-968-754-6	Sequence 6, Appl
998	84.5	3.8	8206	7	US-11-490-374A-1902	Sequence 1902, Ap	1071	84	3.8	49911	8	US-60-970-269-6	Sequence 6, Appl
999	84.5	3.8	8206	7	US-11-490-374A-2123	Sequence 2123, Ap	1072	84	3.8	49911	8	US-60-970-281-6	Sequence 6, Appl
1000	84.5	3.8	8411	7	US-11-490-374A-1900	Sequence 1900, Ap	1073	84	3.8	52701	8	US-60-970-281-41	Sequence 41, Appl
1001	84.5	3.8	8435	7	US-11-490-374A-1903	Sequence 1903, Ap	1074	83.5	3.8	795	1	PCT-US07-17776B-1679	Sequence 1679, Ap
1002	84.5	3.8	8850	7	US-11-490-374A-1901	Sequence 1901, Ap	1075	83.5	3.8	831	1	PCT-US07-17776B-7083	Sequence 7083, Ap
1003	84.5	3.8	8850	7	US-11-490-374A-2120	Sequence 2120, Ap	c1076	83.5	3.8	852	1	PCT-US07-17776B-9542	Sequence 9542, Ap
c1004	84.5	3.8	8976	7	US-11-490-374A-2121	Sequence 2121, Ap	1077	83.5	3.8	867	1	PCT-US07-17776B-7919	Sequence 7919, Ap
c1005	84.5	3.8	8976	7	US-11-490-374A-2122	Sequence 2122, Ap	1078	83.5	3.8	1078	7	US-11-781-665-1288	Sequence 1288, Ap
c1006	84.5	3.8	8976	7	US-11-490-374A-2124	Sequence 2124, Ap	1079	83.5	3.8	1178	8	US-60-970-876-64	Sequence 64, Appl
1007	84.5	3.8	9448	7	US-11-490-374A-2125	Sequence 2125, Ap	1080	83.5	3.8	1227	1	PCT-US07-17776B-3300	Sequence 3300, Ap
1008	84.5	3.8	10448	7	US-11-830-023-129	Sequence 129, App	1081	83.5	3.8	1630	7	US-11-374-300-559	Sequence 559, App
c1009	84.5	3.8	12563	7	US-11-816-601-789	Sequence 789, App	1082	83.5	3.8	1736	7	US-11-374-300-717	Sequence 717, App
c1010	84.5	3.8	18099	7	US-11-884-496-169	Sequence 169, App	c1083	83.5	3.8	1795	7	US-11-490-374A-1307	Sequence 1307, Ap
1011	84	3.8	690	1	PCT-US07-17776B-4072	Sequence 4072, Ap	1084	83.5	3.8	2213	1	PCT-US07-18368A-117	Sequence 117, App
1012	84	3.8	705	8	US-60-970-876-66	Sequence 66, Appl	1085	83.5	3.8	2393	7	US-11-825-627-97	Sequence 97, Appl
c1013	84	3.8	746	1	PCT-US07-17776B-1175	Sequence 1175, Ap	1086	83.5	3.8	2793	7	US-11-816-601-98	Sequence 98, Appl
1014	84	3.8	762	1	PCT-US07-17776B-1438	Sequence 1438, Ap	1087	83.5	3.8	2831	7	US-11-829-545-24	Sequence 24, Appl
1015	84	3.8	768	7	US-11-374-300-180	Sequence 180, App	1088	83.5	3.8	2831	7	US-11-782-545-24	Sequence 24, Appl
1016	84	3.8	795	7	US-11-677-866A-4	Sequence 4, Appl	1089	83.5	3.8	2831	7	US-11-829-011-24	Sequence 24, Appl
c1017	84	3.8	841	1	PCT-US07-17776B-9383	Sequence 9383, Ap	1090	83.5	3.8	3033	6	US-11-781-665-2408	Sequence 2408, Ap
1018	84	3.8	885	1	PCT-US07-18368A-5	Sequence 5, Appl	1091	83.5	3.8	3221	6	US-10-910-811B-379	Sequence 379, App
1019	84	3.8	1103	7	US-11-374-300-525	Sequence 525, App	1092	83.5	3.8	3221	6	US-10-945-565B-379	Sequence 379, App
c1020	84	3.8	1108	1	PCT-US07-17776B-3067	Sequence 3067, Ap	1093	83.5	3.8	3822	1	PCT-US07-77281-24	Sequence 24, Appl
c1021	84	3.8	1284	7	US-11-801-963A-968	Sequence 968, App	1094	83.5	3.8	4279	7	US-11-060-659A-41	Sequence 41, Appl
c1022	84	3.8	1300	7	US-11-374-300-505	Sequence 505, App	1095	83.5	3.8	4279	7	US-11-060-659A-43	Sequence 43, Appl
1023	84	3.8	1305	7	US-11-833-133-16	Sequence 16, Appl	1096	83.5	3.8	4311	6	US-10-494-333A-5	Sequence 5, Appl
1024	84	3.8	1310	7	US-11-137-671A-13	Sequence 13, Appl	c1097	83.5	3.8	4451	7	US-11-847-733-47	Sequence 47, Appl
1025	84	3.8	1368	7	US-11-631-698-25	Sequence 25, Appl	1098	83.5	3.8	5451	7	US-11-815-198-1	Sequence 1, Appl
1026	84	3.8	1462	7	US-11-374-300-630	Sequence 630, App	1099	83.5	3.8	5774	8	US-60-956-437-3	Sequence 3, Appl
1027	84	3.8	1628	7	US-11-374-300-130	Sequence 130, App	1100	83.5	3.8	6000	1	PCT-US07-13803-202	Sequence 202, App
c1028	84	3.8	1759	7	US-11-781-665-792	Sequence 792, App	c1101	83.5	3.8	6112	7	US-11-835-336-65	Sequence 65, Appl
1029	84	3.8	1834	7	US-11-374-300-644	Sequence 644, App	1102	83.5	3.8	6156	7	US-11-816-601-739	Sequence 739, App
1030	84	3.8	1855	7	US-11-831-468-97	Sequence 97, Appl	1103	83.5	3.8	6349	7	US-11-793-909-16	Sequence 16, Appl
c1031	84	3.8	2001	7	US-11-881-406-3178	Sequence 3178, Ap	1104	83.5	3.8	6372	7	US-11-793-909-31	Sequence 31, Appl
1032	84	3.8	2025	6	US-10-375-932A-256	Sequence 256, App	1105	83.5	3.8	6386	7	US-11-793-909-21	Sequence 21, Appl
1033	84	3.8	2048	1	PCT-US07-13803-460	Sequence 460, App	c1106	83.5	3.8	6389	7	US-11-793-909-36	Sequence 36, Appl

1107	83.5	3.8	6394	7	US-11-793-909-26	Sequence 26, Appl	cl180	83	3.8	9944	7	US-11-490-374A-2183	Sequence 2183, Ap
1108	83.5	3.8	6450	7	US-11-793-909-58	Sequence 58, Appl	cl181	83	3.8	9959	7	US-11-490-374A-2181	Sequence 2181, Ap
1109	83.5	3.8	6464	7	US-11-793-909-42	Sequence 42, Appl	cl182	83	3.8	9962	7	US-11-490-374A-2180	Sequence 2180, Ap
1110	83.5	3.8	6573	7	US-11-490-374A-1572	Sequence 1572, Ap	cl183	83	3.8	10362	7	US-11-490-374A-2182	Sequence 2182, Ap
1111	83.5	3.8	6583	7	US-11-793-909-55	Sequence 55, Appl	cl184	83	3.8	33592	7	US-11-249-873A-1	Sequence 1, Appl
1112	83.5	3.8	6604	7	US-11-793-909-45	Sequence 45, Appl	cl185	83	3.8	33592	7	US-11-249-873A-3	Sequence 3, Appl
1113	83.5	3.8	6609	7	US-11-793-909-52	Sequence 52, Appl	cl186	83	3.8	33988	7	US-11-249-873A-14	Sequence 14, Appl
1114	83.5	3.8	6759	7	US-11-793-909-59	Sequence 59, Appl	cl187	83	3.8	34341	7	US-11-249-873A-2	Sequence 2, Appl
1115	83.5	3.8	6780	7	US-11-793-909-60	Sequence 60, Appl	cl188	83	3.8	34448	7	US-11-249-873A-4	Sequence 4, Appl
1116	83.5	3.8	8666	7	US-11-835-336-95	Sequence 95, Appl	cl189	83	3.8	34737	7	US-11-249-873A-15	Sequence 15, Appl
1117	83.5	3.8	11025	7	US-11-712-794-1	Sequence 1, Appl	cl190	83	3.8	35724	7	US-11-249-873A-13	Sequence 13, Appl
1118	83.5	3.8	11933	7	US-11-712-794-2	Sequence 2, Appl	cl191	83	3.8	36114	7	US-11-249-873A-16	Sequence 16, Appl
1119	83	3.8	654	7	US-11-538-319-5	Sequence 5, Appl	cl192	83	3.8	39301	7	US-11-712-794-17	Sequence 17, Appl
1120	83	3.8	657	7	US-11-538-319-31	Sequence 31, Appl	cl193	83	3.8	50475	7	US-11-712-794-16	Sequence 16, Appl
1121	83	3.8	705	6	US-10-532-681-9	Sequence 9, Appl	cl194	82.5	3.7	750	8	US-60-970-876-87	Sequence 87, Appl
1122	83	3.8	705	1	US-11-374-300-458	Sequence 458, Appl	cl195	82.5	3.7	751	1	PCT-US07-1776B-9238	Sequence 9238, Ap
1123	83	3.8	775	1	PCT-US07-1776B-655	Sequence 655, Appl	cl196	82.5	3.7	758	7	US-11-816-601-785	Sequence 785, Appl
1124	83	3.8	831	1	PCT-US07-1776B-4104	Sequence 4104, Appl	cl197	82.5	3.7	826	1	PCT-US07-1776B-3965	Sequence 3965, Appl
1125	83	3.8	884	1	PCT-US07-1776B-9354	Sequence 9354, Appl	cl198	82.5	3.7	1196	7	US-11-374-300-241	Sequence 241, Appl
1126	83	3.8	1098	1	PCT-US07-1776B-3453	Sequence 3453, Appl	cl199	82.5	3.7	1232	1	PCT-US07-1776B-3554	Sequence 3554, Appl
1127	83	3.8	1143	7	US-11-833-133-24	Sequence 24, Appl	cl200	82.5	3.7	1275	7	US-11-833-133-61	Sequence 61, Appl
1128	83	3.8	1198	1	PCT-US07-1776B-3330	Sequence 3330, Appl	cl201	82.5	3.7	1284	7	US-11-801-963A-1279	Sequence 1279, Appl
1129	83	3.8	1269	1	PCT-US07-18368A-356	Sequence 356, Appl	cl202	82.5	3.7	1455	8	US-60-970-876-82	Sequence 82, Appl
1130	83	3.8	1416	1	PCT-US02-29565-15	Sequence 15, Appl	cl203	82.5	3.7	1658	7	US-11-833-133-22	Sequence 22, Appl
1131	83	3.8	1500	7	US-11-844-953-23	Sequence 23, Appl	cl204	82.5	3.7	1731	1	PCT-US07-77297-13	Sequence 13, Appl
1132	83	3.8	1500	7	US-11-844-956-23	Sequence 23, Appl	cl205	82.5	3.7	1887	1	PCT-US07-77297-7	Sequence 7, Appl
1133	83	3.8	1500	7	US-11-844-963-23	Sequence 23, Appl	cl206	82.5	3.7	2059	7	US-11-884-496-430	Sequence 430, Appl
1134	83	3.8	1500	7	US-11-844-967-23	Sequence 23, Appl	cl207	82.5	3.7	2432	7	US-11-832-579-17	Sequence 17, Appl
1135	83	3.8	1500	7	US-11-844-970-23	Sequence 23, Appl	cl208	82.5	3.7	2461	7	US-11-832-579-7	Sequence 7, Appl
1136	83	3.8	1500	7	US-11-844-973-23	Sequence 23, Appl	cl209	82.5	3.7	3003	6	US-10-836-063B-69	Sequence 69, Appl
1137	83	3.8	1603	6	US-10-583-089-1	Sequence 1, Appl	cl210	82.5	3.7	3060	6	US-10-836-063B-95	Sequence 95, Appl
1138	83	3.8	1613	7	US-11-374-300-734	Sequence 734, Appl	cl211	82.5	3.7	3060	7	US-11-781-151-27	Sequence 27, Appl
1139	83	3.8	1614	7	US-11-538-319-1	Sequence 1, Appl	cl212	82.5	3.7	3515	7	US-11-490-374A-2111	Sequence 2111, Appl
1140	83	3.8	1652	7	US-11-781-665-490	Sequence 490, Appl	cl213	82.5	3.7	3529	7	US-11-490-374A-2112	Sequence 2112, Appl
1141	83	3.8	1701	7	US-11-538-319-15	Sequence 15, Appl	cl214	82.5	3.7	3530	7	US-11-490-374A-2114	Sequence 2114, Appl
1142	83	3.8	1728	8	US-60-970-876-109	Sequence 109, Appl	cl215	82.5	3.7	3585	1	PCT-US07-17013-3	Sequence 3, Appl
1143	83	3.8	2034	7	US-11-817-499-5	Sequence 5, Appl	cl216	82.5	3.7	5083	7	US-11-781-665-2337	Sequence 2337, Appl
1144	83	3.8	2053	7	US-11-781-665-1399	Sequence 1399, Appl	cl217	82.5	3.7	6000	1	PCT-US07-13803-48	Sequence 48, Appl
1145	83	3.8	2056	7	US-11-884-496-554	Sequence 554, Appl	cl218	82.5	3.7	6050	7	US-11-835-336-20	Sequence 20, Appl
1146	83	3.8	2121	7	US-11-816-601-87	Sequence 87, Appl	cl219	82.5	3.7	6644	7	US-11-847-733-88	Sequence 88, Appl
1147	83	3.8	2195	6	US-10-276-032-40	Sequence 40, Appl	cl220	82.5	3.7	7085	8	US-60-911-925A-29	Sequence 29, Appl
1148	83	3.8	2395	7	US-11-831-404-17	Sequence 17, Appl	cl221	82.5	3.7	7085	8	US-60-911-925A-30	Sequence 30, Appl
1149	83	3.8	2589	6	US-10-836-063B-71	Sequence 71, Appl	cl222	82.5	3.7	7872	8	US-60-911-925A-30	Sequence 30, Appl
1150	83	3.8	2632	7	US-11-847-733-14	Sequence 14, Appl	cl223	82.5	3.7	8671	7	US-11-749-889-93	Sequence 93, Appl
1151	83	3.8	3145	7	US-11-781-665-1360	Sequence 1360, Appl	cl224	82.5	3.7	11706	8	US-60-911-925A-39	Sequence 39, Appl
1152	83	3.8	3145	7	US-11-781-665-1361	Sequence 1361, Appl	cl225	82.5	3.7	74424	7	US-11-829-279-153	Sequence 153, Appl
1153	83	3.8	3195	7	US-11-781-665-1362	Sequence 1362, Appl	cl226	82	3.7	495	7	US-11-801-963A-1467	Sequence 1467, Appl
1154	83	3.8	3195	7	US-11-781-665-1363	Sequence 1363, Appl	cl227	82	3.7	564	7	US-11-838-500-43	Sequence 43, Appl
1155	83	3.8	3294	7	US-11-781-151-73	Sequence 73, Appl	cl228	82	3.7	725	1	PCT-US07-1776B-971	Sequence 971, Appl
1156	83	3.8	3294	7	US-11-781-151-75	Sequence 75, Appl	cl229	82	3.7	731	1	PCT-US07-1776B-9221	Sequence 9221, Appl
1157	83	3.8	3387	8	US-60-951-363-185	Sequence 185, Appl	cl230	82	3.7	732	1	PCT-US07-14648-3	Sequence 3, Appl
1158	83	3.8	3480	8	US-60-951-363-172	Sequence 172, Appl	cl231	82	3.7	752	1	PCT-US07-14648-60	Sequence 60, Appl
1159	83	3.8	3522	8	US-60-951-363-183	Sequence 183, Appl	cl232	82	3.7	756	1	PCT-US07-1776B-1614	Sequence 1614, Appl
1160	83	3.8	3621	8	US-60-951-363-177	Sequence 177, Appl	cl233	82	3.7	799	7	US-11-374-300-506	Sequence 506, Appl
1161	83	3.8	3663	8	US-60-951-363-171	Sequence 170, Appl	cl234	82	3.7	851	1	PCT-US07-1776B-4519	Sequence 4519, Appl
1162	83	3.8	3663	8	US-60-951-363-181	Sequence 181, Appl	cl235	82	3.7	870	8	US-60-914-361-137	Sequence 137, Appl
1163	83	3.8	3663	8	US-60-951-363-181	Sequence 181, Appl	cl236	82	3.7	994	1	PCT-US07-1776B-3465	Sequence 3465, Appl
1164	83	3.8	4744	7	US-11-884-496-632	Sequence 632, Appl	cl237	82	3.7	1017	1	PCT-US07-1776B-4539	Sequence 4539, Appl
1165	83	3.8	4840	7	US-11-838-500-58	Sequence 58, Appl	cl238	82	3.7	1124	7	US-11-374-300-249	Sequence 249, Appl
1166	83	3.8	5432	7	US-11-838-500-29	Sequence 29, Appl	cl239	82	3.7	1266	1	PCT-US07-1776B-4015	Sequence 4015, Appl
1167	83	3.8	5432	7	US-11-838-500-57	Sequence 57, Appl	cl240	82	3.7	1278	1	PCT-US02-29565-5	Sequence 5, Appl
1168	83	3.8	6000	1	PCT-US07-13803-164	Sequence 164, Appl	cl241	82	3.7	1319	1	PCT-US07-1776B-5934	Sequence 5934, Appl
1169	83	3.8	6249	7	US-11-787-237-4	Sequence 4, Appl	cl242	82	3.7	1368	7	US-11-631-698-6	Sequence 6, Appl
1170	83	3.8	6592	7	US-11-847-733-80	Sequence 80, Appl	cl243	82	3.7	1368	8	US-60-970-876-138	Sequence 138, Appl
1171	83	3.8	7303	1	PCT-US07-67567-17	Sequence 17, Appl	cl244	82	3.7	1380	7	US-11-830-023-3	Sequence 3, Appl
1172	83	3.8	7382	7	US-11-884-496-451	Sequence 451, Appl	cl245	82	3.7	1591	7	US-11-781-665-441	Sequence 441, Appl
1173	83	3.8	8733	7	US-11-844-953-35	Sequence 35, Appl	cl246	82	3.7	1599	7	US-11-781-665-3108	Sequence 3108, Appl
1174	83	3.8	8733	7	US-11-844-956-35	Sequence 35, Appl	cl247	82	3.7	1599	6	US-10-583-089-5	Sequence 5, Appl
1175	83	3.8	8733	7	US-11-844-963-35	Sequence 35, Appl	cl248	82	3.7	1716	1	PCT-US07-1776B-5003	Sequence 5003, Appl
1176	83	3.8	8733	7	US-11-844-967-35	Sequence 35, Appl	cl249	82	3.7	1721	1	PCT-US07-1776B-5003	Sequence 5003, Appl
1177	83	3.8	8733	7	US-11-844-970-35	Sequence 35, Appl	cl250	82	3.7	1905	7	US-11-573-744-4	Sequence 4, Appl
1178	83	3.8	8964	7	US-11-706-376-132	Sequence 132, Appl	cl251	82	3.7	2070	7	US-11-490-374A-1451	Sequence 1451, Appl
1179	83	3.8	9189	6	US-10-741-191B-1	Sequence 1, Appl	cl252	82	3.7	2130	7	US-11-354-210-94	Sequence 94, Appl

1253	82	3.7	2377	7	US-11-829-659-15	Sequence 15, Appl	1326	81	3.7	825	7	US-11-781-818-60	Sequence 60, Appl
1254	82	3.7	2377	7	US-11-829-667-15	Sequence 15, Appl	1327	81	3.7	825	7	US-11-781-818-61	Sequence 61, Appl
1255	82	3.7	2535	7	US-11-354-210-96	Sequence 96, Appl	1328	81	3.7	990	1	PCT-US07-1776B-3524	Sequence 3524, Ap
1256	82	3.7	2851	7	US-11-884-496-442	Sequence 442, Appl	1329	81	3.7	1000	1	PCT-US07-1776B-4513	Sequence 4513, Ap
1257	82	3.7	3300	7	US-11-490-374A-1570	Sequence 1570, Ap	1330	81	3.7	1003	1	PCT-US07-1776B-2991	Sequence 2991, Ap
1258	82	3.7	3300	7	US-11-490-374A-1571	Sequence 1571, Ap	1331	81	3.7	1037	1	PCT-US07-1776B-2945	Sequence 2945, Ap
1259	82	3.7	3300	7	US-11-490-374A-1573	Sequence 1573, Ap	1332	81	3.7	1072	1	US-11-374-300-495	Sequence 495, App
1260	82	3.7	3715	7	US-11-835-336-100	Sequence 100, App	1333	81	3.7	1098	1	PCT-US07-1776B-8263	Sequence 8263, Ap
1261	82	3.7	4698	1	PCT-US07-13803-440	Sequence 440, Appl	1334	81	3.7	1197	8	US-60-915-455-132	Sequence 416, App
1262	82	3.7	4889	7	US-11-816-601-86	Sequence 86, Appl	1335	81	3.7	1454	7	US-11-235-701A-416	Sequence 33, Appl
1263	82	3.7	4889	7	US-11-816-601-289	Sequence 289, App	1336	81	3.7	1497	7	US-11-815-095-33	Sequence 1175, Ap
1264	82	3.7	4889	7	US-11-816-601-810	Sequence 810, App	1337	81	3.7	1704	7	US-11-801-963A-1175	Sequence 342, App
1265	82	3.7	4915	7	US-11-884-496-682	Sequence 682, App	1338	81	3.7	1925	7	US-11-374-300-342	Sequence 342, App
1266	82	3.7	5175	7	US-11-733-744-15	Sequence 15, Appl	1339	81	3.7	1943	1	PCT-US07-1776B-10013	Sequence 10013, A
1267	82	3.7	5668	7	US-11-733-861-17	Sequence 17, Appl	1340	81	3.7	2000	1	PCT-US07-63132-1	Sequence 1, Appl
1268	82	3.7	5687	6	US-10-590-043-1	Sequence 1, Appl	1341	81	3.7	2000	7	US-11-681-285-1	Sequence 420, App
1269	82	3.7	6000	1	PCT-US07-13803-209	Sequence 209, App	1342	81	3.7	2002	7	US-11-374-300-420	Sequence 1038, Ap
1270	82	3.7	6072	6	US-10-741-191B-21	Sequence 21, Appl	1343	81	3.7	2092	7	US-11-781-665-1038	Sequence 136, App
1271	82	3.7	7407	1	PCT-US02-29565-3	Sequence 3, Appl	1344	81	3.7	2170	8	US-60-970-876-136	Sequence 1893, Ap
1272	82	3.7	7523	7	US-11-884-496-215	Sequence 215, App	1345	81	3.7	2397	7	US-11-781-665-1893	Sequence 616, App
1273	82	3.7	218241	7	US-11-765-730A-1	Sequence 1, Appl	1346	81	3.7	2526	7	US-11-884-496-616	Sequence 1600, Ap
1274	81.5	3.7	642	1	PCT-US07-1776B-4311	Sequence 4311, Ap	1347	81	3.7	2707	7	US-11-781-665-1600	Sequence 2113, Ap
1275	81.5	3.7	726	8	US-60-970-876-36	Sequence 36, Appl	1348	81	3.7	3419	7	US-11-490-374A-2113	Sequence 8, Appl
1276	81.5	3.7	782	1	PCT-US07-1776B-8791	Sequence 8791, Ap	1349	81	3.7	4015	7	US-11-851-267-8	Sequence 15, Appl
1277	81.5	3.7	992	6	US-10-669-757A-3	Sequence 3, Appl	1350	81	3.7	4015	7	US-11-851-267-15	Sequence 23, Appl
1278	81.5	3.7	1112	1	PCT-US07-1776B-8179	Sequence 8179, Ap	1351	81	3.7	4281	7	US-11-649-155-23	Sequence 24, Appl
1279	81.5	3.7	1122	1	PCT-US07-1776B-3482	Sequence 3482, Ap	1352	81	3.7	4281	7	US-11-649-155-24	Sequence 406, App
1280	81.5	3.7	1195	7	US-11-781-665-311	Sequence 311, App	1353	81	3.7	5776	1	PCT-US07-13803-406	Sequence 30, Appl
1281	81.5	3.7	1197	7	US-11-801-963A-747	Sequence 747, App	1354	81	3.7	8145	7	US-11-884-496-30	Sequence 2184, Ap
1282	81.5	3.7	1260	7	US-11-801-963A-747	Sequence 449, App	1355	81	3.7	10061	7	US-11-490-374A-2184	Sequence 63, Appl
1283	81.5	3.7	1311	1	PCT-US07-75236-14	Sequence 14, Appl	1356	81	3.7	10874	7	US-11-660-659A-63	Sequence 711, App
1284	81.5	3.7	1311	8	US-60-914-361-55	Sequence 55, Appl	1357	81	3.7	15346	7	US-11-884-496-711	Sequence 731, App
1285	81.5	3.7	1494	1	PCT-US07-18368A-41	Sequence 41, Appl	1358	80.5	3.6	753	1	PCT-US07-1776B-812	Sequence 812, App
1286	81.5	3.7	1494	1	PCT-US07-18368A-42	Sequence 42, Appl	1359	80.5	3.6	754	1	PCT-US07-1776B-5880	Sequence 5880, Ap
1287	81.5	3.7	1615	7	US-11-832-579-24	Sequence 24, Appl	1360	80.5	3.6	757	1	PCT-US07-1776B-5992	Sequence 5992, Ap
1288	81.5	3.7	1635	1	PCT-US07-18368A-40	Sequence 40, Appl	1361	80.5	3.6	774	1	PCT-US07-1776B-2506	Sequence 2506, Ap
1289	81.5	3.7	1680	7	US-11-881-406-2035	Sequence 2025, Ap	1362	80.5	3.6	778	7	US-11-815-559-4	Sequence 4, Appl
1290	81.5	3.7	1872	7	US-11-781-665-2525	Sequence 2525, Ap	1363	80.5	3.6	804	7	US-11-582-527A-7	Sequence 170, App
1291	81.5	3.7	1872	7	US-11-842-069-17	Sequence 17, Appl	1364	80.5	3.6	810	7	US-11-582-527A-7	Sequence 7, Appl
1292	81.5	3.7	1892	1	PCT-US07-63132-3	Sequence 3, Appl	1365	80.5	3.6	829	1	PCT-US07-1776B-7517	Sequence 7517, Ap
1293	81.5	3.7	1920	7	US-11-681-285-3	Sequence 3, Appl	1366	80.5	3.6	880	1	PCT-US07-1776B-6264	Sequence 6264, Ap
1294	81.5	3.7	1920	7	US-11-834-332-5	Sequence 5, Appl	1367	80.5	3.6	893	7	US-11-801-963A-1513	Sequence 1513, Ap
1295	81.5	3.7	2025	6	US-10-375-932A-208	Sequence 208, App	1368	80.5	3.6	1039	7	US-11-733-861-1	Sequence 1, Appl
1296	81.5	3.7	2182	7	US-11-781-665-30	Sequence 30, Appl	1369	80.5	3.6	1329	8	US-60-970-876-201	Sequence 201, App
1297	81.5	3.7	2257	7	US-11-490-374A-1248	Sequence 1248, Ap	1370	80.5	3.6	1431	8	US-60-914-361-105	Sequence 105, App
1298	81.5	3.7	2280	7	US-11-490-374A-1249	Sequence 1249, Ap	1371	80.5	3.6	1489	7	US-11-374-300-571	Sequence 571, App
1299	81.5	3.7	2338	7	US-11-490-374A-1246	Sequence 1246, Ap	1372	80.5	3.6	1571	7	US-11-374-300-107	Sequence 107, App
1300	81.5	3.7	2338	7	US-11-490-374A-1247	Sequence 1247, Ap	1373	80.5	3.6	1596	1	PCT-US07-1776B-9539	Sequence 9539, Ap
1301	81.5	3.7	2608	7	US-11-781-665-1579	Sequence 1579, Ap	1374	80.5	3.6	1629	8	US-60-970-876-199	Sequence 3, Appl
1302	81.5	3.7	2623	7	US-11-816-601-159	Sequence 159, App	1375	80.5	3.6	1718	8	PCT-US07-75398-7	Sequence 7, Appl
1303	81.5	3.7	2665	7	US-11-781-665-2346	Sequence 2346, Ap	1376	80.5	3.6	2239	7	US-11-835-328-7	Sequence 7, Appl
1304	81.5	3.7	2885	7	US-11-817-475-3	Sequence 3, Appl	1377	80.5	3.6	2239	7	US-11-835-328-7	Sequence 7, Appl
1305	81.5	3.7	2805	7	US-11-733-861-75	Sequence 75, Appl	1378	80.5	3.6	2395	1	PCT-US07-13803-292	Sequence 292, App
1306	81.5	3.7	3231	7	US-11-816-601-105	Sequence 105, App	1379	80.5	3.6	2395	1	PCT-US07-13803-531	Sequence 531, App
1307	81.5	3.7	3345	6	US-10-552-571-6	Sequence 6, Appl	1380	80.5	3.6	2447	7	US-11-832-579-20	Sequence 20, Appl
1308	81.5	3.7	3541	7	US-11-884-496-259	Sequence 259, App	1381	80.5	3.6	2459	7	US-11-832-579-14	Sequence 14, Appl
1309	81.5	3.7	3885	7	US-11-785-365B-3	Sequence 3, Appl	1382	80.5	3.6	2460	7	US-11-794-690-7	Sequence 7, Appl
1310	81.5	3.7	4334	7	US-11-649-155-21	Sequence 21, Appl	1383	80.5	3.6	2539	7	US-11-884-496-329	Sequence 329, App
1311	81.5	3.7	4156	1	PCT-US07-13803-342	Sequence 342, App	1384	80.5	3.6	2728	1	PCT-US07-13803-475	Sequence 475, App
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1313	81.5	3.7	5105	7	US-11-830-023-82	Sequence 82, Appl	1386	80.5	3.6	2731	7	US-11-781-665-3065	Sequence 3065, Ap
1314	81.5	3.7	5450	7	US-11-838-500-69	Sequence 69, Appl	1387	80.5	3.6	2772	7	US-11-800-272-1	Sequence 1, Appl
1315	81.5	3.7	5831	7	US-11-884-496-162	Sequence 162, App	1388	80.5	3.6	2904	8	US-60-970-876-123	Sequence 123, App
1316	81.5	3.7	7849	7	US-11-884-496-163	Sequence 163, App	1389	80.5	3.6	3160	7	US-11-884-496-134	Sequence 134, App
1317	81.5	3.7	18070	6	US-10-552-571-17	Sequence 17, Appl	1390	80.5	3.6	3160	7	US-11-884-496-277	Sequence 277, App
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1319	81	3.7	549	1	PCT-US07-18368A-275	Sequence 275, App	1392	80.5	3.6	3203	7	US-11-816-601-137	Sequence 137, App
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1322	81	3.7	658	1	PCT-US07-1776B-6018	Sequence 6018, Ap	1395	80.5	3.6	4220	7	US-11-816-601-149	Sequence 149, App
1323	81	3.7	684	1	PCT-US07-18368A-355	Sequence 355, App	1396	80.5	3.6	5463	1	PCT-US07-13803-505	Sequence 505, App
1324	81	3.7	708	7	US-11-665-940-61	Sequence 61, Appl	1397	80.5	3.6	6000	1	PCT-US07-13803-169	Sequence 169, App
1325	81	3.7	729	1	PCT-US07-1776B-6848	Sequence 6848, Ap	1398	80.5	3.6	6000	1	PCT-US07-13803-238	Sequence 238, App

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c1400	80.5	3.6	12065	7	US-11-884-496-426	Sequence 426, App	1473	80	3.6	11361	7	US-11-774-254A-24	Sequence 24, Appli
1401	80.5	3.6	14760	7	US-11-490-374A-1331	Sequence 1331, Ap	1474	80	3.6	12563	7	US-11-816-601-789	Sequence 789, App
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1403	80.5	3.6	14760	7	US-11-490-374A-1333	Sequence 1333, Ap	c1476	80	3.6	15534	7	US-11-490-374A-1805	Sequence 1805, Ap
1404	80.5	3.6	16382	7	US-11-490-374A-1332	Sequence 1332, Ap	c1477	80	3.6	36909	8	US-60-956-153-7	Sequence 7, Appli
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1407	80	3.6	776	7	US-11-374-300-714	Sequence 714, App	c1480	80	3.6	36909	8	US-60-970-281-7	Sequence 7, Appli
c1408	80	3.6	797	1	PCT-US07-17776B-8039	Sequence 8039, Ap	1481	80	3.6	38794	7	US-11-781-861-7	Sequence 7, Appli
1409	80	3.6	846	7	US-11-795-915-128	Sequence 128, App	1482	80	3.6	38794	7	US-11-781-867-7	Sequence 7, Appli
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c1411	80	3.6	1028	1	PCT-US07-17776B-3395	Sequence 3395, Ap	1484	80	3.6	38794	7	US-11-781-871-7	Sequence 7, Appli
1412	80	3.6	1107	8	US-60-951-363-158	Sequence 158, App	1485	80	3.6	38794	7	US-11-781-874-7	Sequence 7, Appli
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1419	80	3.6	1380	6	US-10-375-932A-190	Sequence 190, App	c1492	80	3.6	49765	8	US-60-968-754-13	Sequence 6, Appl
1420	80	3.6	1382	7	US-11-374-300-546	Sequence 546, App	c1493	80	3.6	49911	8	US-60-956-153-6	Sequence 6, Appli
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1437	80	3.6	2504	7	US-11-837-468-3	Sequence 3, Appli							
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1446	80	3.6	3350	7	US-11-884-496-167	Sequence 167, App							
1447	80	3.6	3350	7	US-60-970-876-148	Sequence 148, App							
1448	80	3.6	3382	8	US-60-970-876-148	Sequence 148, App							
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1450	80	3.6	3330	7	US-11-774-236A-26	Sequence 26, Appl							
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1459	80	3.6	4352	1	PCT-US07-13803-427	Sequence 427, App							
1460	80	3.6	4431	7	US-11-354-210-110	Sequence 110, App							
1461	80	3.6	4555	7	US-11-884-496-390	Sequence 390, App							
1462	80	3.6	4779	7	US-11-354-210-106	Sequence 106, App							
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1464	80	3.6	5337	1	PCT-US07-13803-312	Sequence 312, App							
1465	80	3.6	6000	1	PCT-US07-13803-198	Sequence 198, App							
1466	80	3.6	6328	1	PCT-US07-13803-485	Sequence 485, App							
c1467	80	3.6	7309	7	US-11-835-336-98	Sequence 98, Appl							
c1468	80	3.6	8111	7	US-11-835-336-85	Sequence 85, Appl							
c1469	80	3.6	9535	7	US-11-490-374A-1806	Sequence 1806, Ap							
c1470	80	3.6	11185	1	PCT-US07-13803-307	Sequence 307, App							
1471	80	3.6	11361	7	US-11-774-204A-24	Sequence 24, Appl							

Search completed: September 20, 2007, 01:46:40

Job time : 88 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 20, 2007, 00:32:37 ; Search time 6788 Seconds
(without alignments)
3939.258 Million cell updates/sec

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Perfect score: 2211
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107169730

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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90	588	26.6	584	14	DB201117	DB201117	163	547	24.7	574	14	DA299483	DA299483
91	588	26.6	584	14	DB261530	DB261530	164	547	24.7	575	14	DA278922	DA278922
92	588	26.6	590	14	DB206324	DB206324	165	547	24.7	575	14	DB204597	DB204597
93	588	26.6	591	14	DA529624	DA529624	166	543	24.6	573	14	DA016588	DA016588
94	588	26.6	764	13	DT848580	DT848580	167	542	24.5	561	14	DA017673	DA017673
95	586	26.5	1018	3	BI416048	BI416048	168	542	24.5	566	14	DA205264	DA205264
96	585	26.5	561	5	BY720875	BY720875	169	542	24.5	566	14	DA486096	DA486096
97	584.5	26.4	631	8	CF746243	UI-M-GVO-	170	542	24.5	568	14	DA629218	DA629218
98	584	26.4	527	3	BM790877	BM790877	171	542	24.5	573	14	DB035688	DB035688
99	581	26.3	583	14	DA769469	DA769469	172	542	24.5	575	14	DA588356	DA588356
100	581	26.3	585	14	DA293619	DA293619	173	541	24.5	560	14	DA440743	DA440743
101	581	26.3	588	14	DB055500	DB055500	174	541	24.5	571	14	DA873110	DA873110
102	581	26.3	590	14	DA583843	DA583843	175	541	24.5	573	14	DA942667	DA942667
103	581	26.3	591	3	BM828071	BM828071	176	536	24.2	557	14	DA922775	DA922775
104	581	26.3	592	14	DA527373	DA527373	177	536	24.2	558	14	DA885677	DA885677
105	576	26.1	578	14	DB107700	DB107700	178	536	24.2	561	14	DA558218	DA558218
106	576	26.1	580	14	DA925055	DA925055	179	536	24.2	562	14	DB173161	DB173161
107	576	26.1	581	14	DB204893	DB204893	180	536	24.2	562	14	DB245007	DB245007
108	576	26.1	583	14	DA303353	DA303353	181	536	24.2	564	14	DA261403	DA261403
109	576	26.1	583	14	DA354352	DA354352	182	536	24.2	565	14	DA889049	DA889049
110	576	26.1	592	14	DB264705	DB264705	183	536	24.2	566	14	DA175505	DA175505
111	575	26.0	595	14	DA672973	DA672973	184	536	24.2	566	14	DA886222	DA886222
112	572	25.9	583	14	DA207426	DA207426	185	536	24.2	566	14	DB258399	DB258399
113	572	25.9	601	14	DA263168	DA263168	186	536	24.2	569	14	DA075629	DA075629
114	572	25.9	826	5	BX926783	BX926783	187	536	24.2	569	14	DB241748	DB241748
115	571	25.8	342	11	F12992	F12992	188	536	24.2	571	14	DB202994	DB202994
116	570	25.8	589	14	DB112866	DB112866	189	536	24.2	571	14	DB262440	DB262440
117	567.5	25.7	886	4	BQ922735	AGENCOURT	190	535	24.2	559	14	DA950526	DA950526
118	565	25.6	570	14	DA750655	DA750655	191	535	24.2	570	14	DA293697	DA293697
119	565	25.6	576	14	DA706884	DA706884	192	534	24.2	566	14	DA513506	DA513506
120	565	25.6	576	14	DB201861	DB201861	193	534	24.2	567	3	BI682666	BI682666
121	565	25.6	577	14	DA711645	DA711645	194	531	24.0	563	14	DA451334	DA451334
122	565	25.6	578	14	DA866073	DA866073	195	530	24.0	562	12	DY048683	000510BPP
123	565	25.6	578	14	DB202346	DB202346	196	529	23.9	554	14	DA208636	DA208636
124	565	25.6	579	14	DA090848	DA090848	197	529	23.9	559	14	DA041769	DA041769
125	565	25.6	583	14	DA346289	DA346289	198	529	23.9	559	14	DB197453	DB197453
126	565	25.6	584	14	DA001661	DA001661	199	529	23.9	560	14	DA064734	DA064734
127	565	25.6	585	14	DB265991	DB265991	200	529	23.9	560	14	DB205717	DB205717
128	563.5	25.5	947	5	BY720818	BY720818	201	529	23.9	564	14	DA014288	DA014288
129	563.5	25.5	584	3	BM828163	K-EST0100	202	529	23.9	566	14	DA772851	DA772851
130	566	25.1	583	14	DA879394	DA879394	203	529	23.9	567	7	AU279841	AU279841
131	566	25.1	573	14	DA172736	DA172736	204	529	23.9	567	14	DA154103	DA154103
132	566	25.1	574	14	DA873470	DA873470	205	529	23.9	568	14	DA886847	DA886847
133	566	25.1	574	14	DB201824	DB201824	206	528	23.9	560	14	DA915048	DA915048
134	566	25.1	576	14	DB009591	DB009591	207	528	23.9	567	14	DB008431	DB008431
135	566	25.1	582	4	BP256186	BP256186	208	528	23.9	568	14	DA956476	DA956476
136	566	25.1	583	14	DA499290	DA499290	209	526	23.8	771	10	CO809298	AGENCOURT
137	566	25.1	583	14	DA590234	DA590234	210	522	23.6	584	4	BP248743	BP248743
138	566	25.1	584	14	DB256983	DB256983	211	520	23.5	555	14	DA884221	DA884221
139	565	25.1	570	14	DA766877	DA766877	212	520	23.5	556	14	DA747951	DA747951
140	565	25.1	581	14	DB265041	DB265041	213	520	23.5	557	14	DA669963	DA669963
141	564	25.1	574	4	BP375859	BP375859	214	520	23.5	557	14	DA715919	DA715919
142	563	25.0	579	14	DB198688	DB198688	215	520	23.5	558	14	DA566772	DA566772
143	562	25.0	566	14	DB244462	DB244462	216	520	23.5	558	14	DA916870	DA916870
144	562	25.0	567	14	DA583585	DA583585	217	520	23.5	560	14	DB258618	DB258618
145	562	25.0	568	14	DA999605	DA999605	218	520	23.5	562	14	DA009313	DA009313

219	520	23.5	562	14	DA885298	DA885298	292	475	21.5	549	14	DA347002	DA347002
220	520	23.5	563	4	BP375432	BP375432	293	475	21.5	735	9	CK963207	CK963207
221	520	23.5	565	14	DA874577	DA874577	294	470	21.3	528	14	DA761447	DA761447
222	520	23.5	571	14	DA494871	DA494871	295	470	21.3	538	14	DB255096	DB255096
223	519	23.5	585	14	DA527896	DA527896	296	470	21.3	539	14	DB255096	DB255096
224	519	23.5	710	2	BG964611	BG964611	297	470	21.3	540	14	DB001639	DB001639
225	515.5	23.3	673	7	BG661915	BG661915	298	470	21.3	540	14	DB244134	DB244134
226	514	23.2	549	14	DA885250	DA885250	299	470	21.3	571	14	DA890033	DA890033
227	514	23.2	553	14	DA885250	DA885250	300	465.5	21.1	341	7	AW478661	AW478661
228	514	23.2	557	14	DA171315	DA171315	301	465	21.0	537	14	DA489229	DA489229
229	514	23.2	561	14	DA749318	DA749318	302	465	21.0	566	14	DA693173	DA693173
230	514	23.2	561	14	DB257489	DB257489	303	465	21.0	566	14	DB265802	DB265802
231	513	23.2	553	14	DA446772	DA446772	304	465	21.0	568	14	DA706892	DA706892
232	513	23.2	559	14	DA922755	DA922755	305	464	21.0	534	14	DA625746	DA625746
233	513	23.2	559	14	DA932819	DA932819	306	462	20.9	552	14	DA158656	DA158656
234	510	23.1	561	14	DA534072	DA534072	307	460.5	20.8	560	2	BF046016	BF046016
235	508	23.0	544	14	DA850355	DA850355	308	456	20.6	530	3	BM753270	BM753270
236	508	23.0	546	14	DA753698	DA753698	309	456	20.6	543	14	DA688482	DA688482
237	508	23.0	546	14	DA793552	DA793552	310	456	20.6	560	14	DA022777	DA022777
238	508	23.0	547	14	DA060573	DA060573	311	455	20.6	534	14	DB263443	DB263443
239	508	23.0	550	14	DA887692	DA887692	312	455	20.6	566	14	DA453539	DA453539
240	508	23.0	551	14	DA882853	DA882853	313	451	20.4	534	14	DA149350	DA149350
241	508	23.0	558	14	DA663368	DA663368	314	451	20.4	557	14	DA275399	DA275399
242	508	23.0	560	14	DA821008	DA821008	315	451	20.4	559	14	DB249814	DB249814
243	508	23.0	562	14	DA505204	DA505204	316	448	20.3	561	14	DA884160	DA884160
244	508	23.0	569	14	DA711490	DA711490	317	445.5	20.1	530	14	DA133295	DA133295
245	507	22.9	550	14	DA479383	DA479383	318	444	20.1	569	14	DA149179	DA149179
246	507	22.9	562	14	DA765169	DA765169	319	444	20.1	701	4	BP147701	BP147701
247	507	22.9	564	14	DA276943	DA276943	320	444	20.1	880	8	CB959572	CB959572
248	506	22.9	555	14	DA710837	DA710837	321	443	20.0	518	14	DB208478	DB208478
249	506	22.9	559	14	DA632196	DA632196	322	443	20.0	517	3	BM838896	BM838896
250	506	22.9	581	4	BP247346	BP247346	323	435	19.7	520	14	DA624843	DA624843
251	504	22.8	543	14	DA886741	DA886741	324	435	19.7	521	14	DB248037	DB248037
252	504	22.8	546	14	DA670045	DA670045	325	434	19.6	526	14	DB207283	DB207283
253	504	22.8	551	14	DA103576	DA103576	326	432	19.5	287	2	BF361648	BF361648
254	504	22.8	555	14	DA881505	DA881505	327	429.5	19.4	555	13	DN339203	DN339203
255	503	22.7	546	5	CA397415	CA397415	328	429	19.4	516	14	DA008487	DA008487
256	503	22.7	551	14	DB105348	DB105348	329	428	19.4	598	7	AW913757	AW913757
257	501	22.7	564	14	DA564742	DA564742	330	420	19.0	496	14	DB195696	DB195696
258	499	22.6	542	14	DA653625	DA653625	331	417.5	18.9	762	13	DN870440	DN870440
259	498.5	22.5	447	17	CG620426	CG620426	332	410	18.5	503	14	DA604196	DA604196
260	497.5	22.5	663	7	BG645954	BG645954	333	410	18.5	533	14	DA624540	DA624540
261	497	22.5	540	14	DB212308	DB212308	334	408	18.5	514	14	DA701250	DA701250
262	497	22.5	544	14	DA297157	DA297157	335	405.5	18.3	691	14	DN117286	DN117286
263	497	22.5	550	14	DA869606	DA869606	336	405.5	18.3	691	14	DN117635	DN117635
264	497	22.5	551	14	DB002322	DB002322	337	398.5	18.0	457	8	CF788452	CF788452
265	497	22.5	552	14	DB023291	DB023291	338	398	18.0	506	14	DB208508	DB208508
266	497	22.5	583	14	DA250034	DA250034	339	396	17.9	583	4	BP248346	BP248346
267	496	22.4	542	14	DA882344	DA882344	340	394	17.8	530	5	BX512983	BX512983
268	495	22.4	539	14	DA689777	DA689777	341	393.5	17.8	671	8	CF789259	CF789259
269	495	22.4	548	14	DB129282	DB129282	342	393.5	17.8	862	9	CF788452	CF788452
270	491	22.2	560	14	DA349567	DA349567	343	399	17.6	463	12	DY136771	DY136771
271	490	22.2	554	14	DB207607	DB207607	344	388.5	17.6	862	14	DN132822	DN132822
272	488	22.1	538	14	DA649316	DA649316	345	385	17.4	515	14	DA701985	DA701985
273	488	22.1	545	14	DA866856	DA866856	346	380.5	17.2	848	9	CK449279	CK449279
274	488	22.1	547	14	DA885751	DA885751	347	380	17.2	479	14	DA739541	DA739541
275	488	22.1	549	14	DA888887	DA888887	348	380	17.2	488	14	DA699749	DA699749
276	488	22.1	552	14	DA259995	DA259995	349	379	17.1	475	14	DA129582	DA129582
277	488	22.1	552	14	DA680705	DA680705	350	374	16.9	528	14	DA698278	DA698278
278	488	22.1	553	14	DA885090	DA885090	351	373.5	16.9	540	2	BE750665	BE750665
279	488	22.1	585	14	DA442354	DA442354	352	372	16.8	571	14	DA707669	DA707669
280	487.5	22.0	574	2	BE533293	BE533293	353	370	16.7	446	13	DN384707	DN384707
281	487	22.0	578	14	DB203581	DB203581	354	368.5	16.7	502	2	BE481505	BE481505
282	484	21.9	550	14	DA841065	DA841065	355	368	16.6	223	2	BF793997	BF793997
283	484	21.9	641	7	BG624968	BG624968	356	366	16.6	472	14	DA017137	DA017137
284	482	21.8	537	14	DA516958	DA516958	357	366	16.6	572	14	DA130511	DA130511
285	482	21.8	541	14	DA625554	DA625554	358	361	16.3	564	14	DA269140	DA269140
286	482	21.8	545	14	DA647894	DA647894	359	358	16.2	668	11	EE216707	EE216707
287	482	21.8	547	14	DA999982	DA999982	360	353	16.0	500	14	DA835136	DA835136
288	482	21.8	576	14	DA878608	DA878608	361	352	15.9	557	14	DA278002	DA278002
289	480	21.7	695	3	BI146784	BI146784	362	352	15.9	557	14	DA707706	DA707706
290	478	21.6	579	14	DA955491	DA955491	363	347.5	15.7	620	5	BX926593	BX926593
291	477	21.6	542	14	DB059714	DB059714	364	346.5	15.7	686	7	BB625038	BB625038

365	344	15.6	510	3	BM481814	BM481814 534346 MA	438	200.5	9.1	888	8	CD757319	CD757319 AGENCOURT
366	343	15.5	559	14	DA130901	DA130901 DA130901	439	199.5	9.0	845	13	DT234157	DT234157 JGI CAAT8
C 367	343	15.5	630	9	CK963012	CK963012 4077498 B	440	198.5	9.0	804	13	DT226240	DT226240 JGI CAAT2
C 368	341	15.4	630	9	CK971129	CK971129 4086672 B	441	197.5	8.9	818	9	AK140617	AK140617 AGENCOURT
369	341	15.4	946	2	BQ242060	BQ242060 602354602	442	195.5	8.8	1987	6	AF370372	AF370372 Homo sapi
370	335	15.2	604	12	EC327580	EC327580 GUTP09168	443	195	8.8	1365	13	DR419675	DR419675 gpgc EST0
371	334	15.1	874	1	AJ456451	AJ456451 AJ456451	444	194.5	8.8	986	4	BUI11386	BUI11386 603127015
372	330	14.9	456	14	DB204351	DB204351 DB204351	445	193.5	8.8	841	8	CD752203	CD752203 AGENCOURT
C 373	328.5	14.9	1057	1	AL525390	AL525390 AL525390	446	192.5	8.7	451	9	CJ125832	CJ125832 CJ125832
C 374	318	14.4	462	12	DY135468	DY135468 000902BEM	447	192.5	8.7	455	9	CJ127942	CJ127942 CJ127942
C 375	314	14.2	587	13	DN279685	DN279685 1160739 M	448	192.5	8.7	782	13	DT235740	DT235740 JGI CAAT8
C 376	310	14.0	694	13	DT892500	DT892500 1474931 M	449	185.5	8.4	659	14	DB418741	DB418741
377	309	14.0	874	2	BQ967218	BQ967218 602833706	450	185.5	8.4	732	14	CK603031	CK603031 CT02034A2
378	307	13.9	667	1	AJ445959	AJ445959 AJ445959	451	183.5	8.3	722	4	BU480164	BU480164 603845869
379	305.5	13.8	506	3	BM439543	BM439543 pgr1c.pk0	C 452	183.5	8.3	916	5	BX363088	BX363088 BX363088
380	305	13.8	657	13	DN74275	DN74275 LIB38529	C 453	181	8.2	630	1	AJ735763	AJ735763 AJ735763
381	303	13.7	549	18	DU218553	DU218553 109855369	C 454	178	8.1	836	9	CK139504	CK139504 AGENCOURT
C 382	302	13.7	600	7	AW937332	AW937332 PM2-DT004	455	178	8.1	1350	19	DO054172	DO054172 Homo sapi
383	302	13.7	784	9	CJ462354	CJ462354 CJ462354	C 456	176.5	8.0	301	2	BE927563	BE927563 MR0-CT045
384	299	13.5	641	9	CK979245	CK979245 4111113 B	C 457	175	7.9	1033	5	BX343326	BX343326 BX343326
385	290	13.1	544	17	CG577723	CG577723 OST214224	458	174.5	7.9	749	9	CK808839	CK808839 Raegsc168
C 386	289.5	13.1	570	8	CB480672	CB480672 jns67 G04	459	174	7.9	935	8	CB283214	CB283214 BT1485 B1
387	288	13.0	443	8	CB789377	CB789377 AMGNNUC-N	460	173	7.8	573	3	BJ074280	BJ074280 BJ074280
C 388	288	13.0	657	13	DT890370	DT890370 1471375 M	461	173	7.8	820	9	CK141099	CK141099 AGENCOURT
389	286	12.9	469	14	DB262059	DB262059 DB262059	462	172	7.8	852	5	BX915688	BX915688 BX915688
390	284	12.8	496	14	DA703232	DA703232 DA703232	463	170.5	7.7	664	8	CD675180	CD675180 fsl9h12.Y
391	284	12.8	383	8	CB704160	CB704160 AMGNNUC-M	C 464	170	7.7	1058	5	BX464809	BX464809 BX464809
C 392	280.5	12.7	383	1	AJ735766	AJ735766 AJ735766	465	169.5	7.6	881	6	CR600976	CR600976 full-leng
393	278	12.6	439	12	DY199153	DY199153 001017BEM	466	168.5	7.6	859	12	EB006927	EB006927 GtraSEQ15
394	271	12.3	388	3	BI024344	BI024344 CM3-WT029	C 467	168.5	7.6	995	5	BX360410	BX360410 BX360410
395	270	12.2	480	2	BF889786	BF889786 289362 MA	C 468	167.5	7.6	799	13	DT097656	DT097656 JGI ANNN3
396	269	12.2	439	14	DB444501	DB444501 DB444501	469	167.5	7.6	1032	5	BX375412	BX375412 BX375412
397	265.5	12.0	309	12	DY156872	DY156872 000329BHT	C 470	167	7.6	571	8	CF795191	CF795191 891297 MA
398	260	11.8	693	2	BF698559	BF698559 602130764	471	166	7.5	921	8	CD756203	CD756203 AGENCOURT
399	259.5	11.7	495	9	CJ129964	CJ129964 CJ129964	C 472	165.5	7.5	968	4	BQ957751	BQ957751 AGENCOURT
400	255.5	11.6	493	9	CJ125222	CJ125222 CJ125222	C 473	165	7.5	914	5	BX426287	BX426287 BX426287
401	254.5	11.5	488	9	CJ109938	CJ109938 CJ109938	C 474	165	7.5	1107	5	BX380586	BX380586 BX380586
402	253.5	11.5	564	3	BI342758	BI342758 370696 MA	475	164.5	7.4	533	14	CK403680	CK403680 JGI X2T35
403	252	11.4	697	12	DY548025	DY548025 AGENCOURT	476	164	7.4	839	14	CK146297	CK146297 AGENCOURT
404	252	11.4	777	4	BF682982	BF682982 BP682982	477	163.5	7.4	798	9	CK837216	CK837216 AGENCOURT
C 405	250.5	11.3	233	2	BF365167	BF365167 CM1-WT000	478	162.5	7.3	880	10	CA975376	CA975376 AGENCOURT
406	248	11.2	471	5	BY257469	BY257469 BY257469	479	162.5	7.3	1027	8	CR595092	CR595092 full-leng
407	248	11.2	731	13	DR272792	DR272792 AGENCOURT	480	162.5	7.3	1652	6	CR595092	CR595092 full-leng
408	247.5	11.2	901	4	BQ733749	BQ733749 AGENCOURT	C 481	161	7.3	926	14	CK977372	CK977372 JGI CAAP1
409	246.5	11.1	555	3	BJ040547	BJ040547 BJ040547	482	161	7.3	1036	1	AL571687	AL571687 AGENCOURT
410	246	11.1	580	4	BP291358	BP291358 BP291358	C 483	161	7.3	1348	13	DN687942	DN687942 CGX55-H09
411	245.5	11.1	632	4	BQ384415	BQ384415 NISC-mm06	484	161	7.3	12524	19	DQ036655	DQ036655 Homo sapi
412	245	11.1	796	4	BQ930526	BQ930526 AGENCOURT	485	160.5	7.3	801	9	CK143699	CK143699 AGENCOURT
413	242.5	11.0	439	13	DT659333	DT659333 pgr1n.UA0	486	160	7.2	600	3	BU061738	BU061738 BU061738
414	240.5	10.9	443	8	CB789245	CB789245 AMGNNUC-T	487	160	7.2	601	4	BP239336	BP239336 BP239336
415	238	10.8	641	1	AL584869	AL584869 AL584869	488	160	7.2	5630	6	HSB802522	HSB802522 Homo sapi
416	237.5	10.7	485	9	CJ121986	CJ121986 CJ121986	489	159.5	7.2	720	9	CK808037	CK808037 Raegsc031
417	234	10.6	837	8	CB508437	CB508437 AGENCOURT	490	159.5	7.2	778	4	BU382064	BU382064 603583687
C 418	233	10.5	635	9	CK974320	CK974320 4105089 B	491	159.5	7.2	1071	12	DM613958	DM613958 CLJ2777-H0
C 419	229.5	10.4	669	1	AJ735765	AJ735765 AJ735765	492	158.5	7.2	709	4	BQ608902	BQ608902 BRY 4818
420	228	10.3	707	16	CA482511	CA482511 CH240 310	493	158.5	7.2	1134	19	DQ033549	DQ033549 Homo sapi
421	227.5	10.3	440	7	AV613707	AV613707 AV613707	494	158	7.1	539	2	BE751431	BE751431 203372 MA
C 422	221.5	10.0	1051	1	AL573909	AL573909 AL573909	495	157.5	7.1	531	3	BJ698320	BJ698320 BJ698320
423	221	10.0	510	3	BU094842	BU094842 BU094842	496	157.5	7.1	607	8	CD280904	CD280904 G44218.74
424	216	9.8	303	7	AW346515	AW346515 28312 MAR	497	157.5	7.1	548	9	CK141054	CK141054 AGENCOURT
425	212	9.6	439	14	DB442366	DB442366 DB442366	498	157	7.1	834	17	CE558576	CE558576 tigr-ges-
426	210.5	9.5	872	12	EC350325	EC350325 LIVERF091	499	157	7.1	790	12	EB001717	EB001717 GtraSEQ085
427	206.5	9.3	800	1	AJ735760	AJ735760 AJ735760	500	156.5	7.1	391	1	AJ735761	AJ735761 AJ735761
428	205.5	9.3	1883	6	AK007868	AK007868 Mus muscu	501	156.5	7.1	636	12	DY997129	DY997129 GtraSEQ030
429	204.5	9.3	2196	6	AK154828	AK154828 Mus muscu	C 502	156.5	7.1	1039	5	BX382007	BX382007 BX382007
430	204.5	9.2	1837	6	CR604388	CR604388 full-leng	503	156.5	7.1	2533	6	HSB805820	HSB805820 Homo sapi
431	204.5	9.2	1838	6	CR607549	CR607549 full-leng	504	155.5	7.0	583	8	CB157666	CB157666 K-EST0216
432	204.5	9.2	1871	6	CR597895	CR597895 full-leng	505	155.5	7.0	775	8	CF457419	CF457419 AGENCOURT
433	204.5	9.2	1890	6	CR625680	CR625680 full-leng	506	155	7.0	716	12	EB000536	EB000536 GtraSEQ053
434	204.5	9.2	1894	6	CR623094	CR623094 full-leng	507	155	7.0	845	8	CD648172	CD648172 AUF.102.A
435	204	9.2	465	3	BJ029802	BJ029802 BJ029802	508	154.5	7.0	676	8	CD894182	CD894182 GL18.125J
436	204	9.2	838	8	CA975050	CA975050 AGENCOURT	509	154.5	7.0	779	13	DT357000	DT357000 JGI CABY4
437	202.5	9.2	849	9	CK141394	CK141394 AGENCOURT	510	154.5	7.0	903	10	CV857799	CV857799 gonad_EST

511	154	7.0	655	8	CD899968	CU299968	GL174.114C	584	143	6.5	557	4	BP333860	BP333860
512	153	6.9	662	4	BU294289	BU294289	604164762	585	143	6.5	581	4	BP333703	BP333703
513	152.5	6.9	792	4	BQ806240	BQ806240	WHE3576_D	586	143	6.5	610	8	CF843588	CF843588
514	152	6.9	657	8	CD899404	CD899404	GL174.112E	587	143	6.5	627	8	CF862698	CF862698
515	152	6.9	821	1	AM333355	AM333355	AM333355	588	143	6.5	668	8	CD920707	CD920707
516	151.5	6.9	686	3	BJ236585	BJ236585	BJ236585	589	143	6.5	770	13	DT241942	DT241942
517	151.5	6.9	698	9	CK974635	CK974635	4105575_B	590	143	6.5	770	18	CM860366	CM860366
518	151.5	6.9	703	3	BJ643127	BJ643127	BJ643127	591	143	6.5	874	8	CF821397	CF821397
519	151.5	6.9	4465	6	AK036839	AK036839	Mus muscu	c 592	143	6.5	1300	17	CG749328	CG749328
520	151.5	6.9	4670	6	AK162455	AK162455	Mus muscu	593	142.5	6.4	562	8	CB053073	CB053073
521	151	6.8	767	13	DT190497	DT190497	JGI_CAAAJ1	594	142.5	6.4	573	4	BP334625	BP334625
522	150.5	6.8	549	14	CG807925	CG807925	JGI_CAAAJ1	595	142.5	6.4	581	8	CF569196	CF569196
523	150	6.8	832	2	BG481596	BG481596	602528317	596	142.5	6.4	628	18	DX807117	DX807117
524	149.5	6.8	656	4	BQ805830	BQ805830	WHE3571_E	597	142.5	6.4	670	10	CV527029	CV527029
525	149.5	6.8	664	12	EC093790	EC093790	Sa_mxl_49	598	142.5	6.4	736	4	DT247072	DT247072
526	149.5	6.8	915	4	BQ892334	BQ892334	AGENCOURT	599	142.5	6.4	748	2	BE193839	BE193839
527	149.5	6.8	946	4	BQ933770	BQ933770	AGENCOURT	600	142.5	6.4	1072	12	DT299009	DT299009
528	149	6.7	746	9	CN512903	CN512903	AGENCOURT	601	142.5	6.4	1536	19	DQ035259	DQ035259
529	149	6.7	781	8	CB987182	CB987182	AGENCOURT	602	142	6.4	531	3	BJ233556	BJ233556
530	149	6.7	815	13	DT228334	DT228334	JGI_CAAAT3	603	142	6.4	606	4	BQ806762	BQ806762
531	148.5	6.7	656	10	CN8982514	CN8982514	50976_126	604	142	6.4	625	3	BJ233029	BJ233029
532	148.5	6.7	681	8	CD899045	CD899045	GL174.1100	605	142	6.4	632	4	BQ839049	BQ839049
533	148.5	6.7	766	4	BW211476	BW211476	BW211476	606	142	6.4	633	10	CV070818	CV070818
534	148	6.7	481	4	BQ755857	BQ755857	EBed07_SQ	c 607	142	6.4	678	8	CD453740	CD453740
535	148	6.7	676	1	AJ646204	AJ646204	AJ646204	608	142	6.4	680	10	CV065409	CV065409
536	148	6.7	785	9	CK126791	CK126791	AGENCOURT	609	142	6.4	704	4	BQ806801	BQ806801
537	148	6.7	809	13	DT233015	DT233015	JGI_CAAAT7	610	142	6.4	709	4	BQ807007	BQ807007
538	148	6.7	2338	6	AK138880	AK138880	Mus muscu	611	142	6.4	715	13	DT244392	DT244392
539	148	6.7	2403	6	AK083772	AK083772	Mus muscu	612	142	6.4	728	13	DT221144	DT221144
540	147.5	6.7	567	1	AJ435687	AJ435687	AJ435687	613	142	6.4	785	13	DT237468	DT237468
541	147.5	6.7	1015	5	BY754650	BY754650	BY754650	614	142	6.4	785	13	DT242446	DT242446
542	147.5	6.7	1139	8	CD497067	CD497067	CD425-G09	615	142	6.4	791	4	BQ804207	BQ804207
543	147	6.6	675	9	CK808739	CK808739	Rasgsc152	c 616	142	6.4	827	9	CNS094XO	CNS094XO
544	147	6.6	845	10	CO881331	CO881331	BovGen_09	617	142	6.4	933	6	CNS094XO	CNS094XO
545	146.5	6.6	817	12	DV785250	DV785250	CL_05_R_	618	141.5	6.4	469	5	CA589578	CA589578
546	146.5	6.6	837	12	DV723206	DV723206	RVL14947	619	141.5	6.4	506	5	BWS29321	BWS29321
547	146.5	6.6	965	4	BQ921152	BQ921152	AGENCOURT	620	141.5	6.4	592	13	DV019744	DV019744
548	146	6.6	610	8	CD291670	CD291670	StrPu538_	621	141.5	6.4	645	8	CD902657	CD902657
549	146	6.6	669	14	CK378324	CK378324	JGI_XZT35	622	141.5	6.4	701	13	DT605269	DT605269
550	146	6.6	732	3	BJ702006	BJ702006	BJ702006	623	141.5	6.4	859	10	CV906860	CV906860
551	146	6.6	833	14	CK396051	CK396051	JGI_XZT56	624	141.5	6.4	912	8	CF377246	CF377246
552	146	6.6	936	6	CNS09JUD	CNS09JUD	Single re	625	141.5	6.4	987	6	CNS08Y1A	CNS08Y1A
553	145.5	6.6	712	4	BQ245835	BQ245835	TaE15019P	626	141.5	6.4	1002	6	CNS08YUL	CNS08YUL
554	145.5	6.6	743	5	BX621140	BX621140	BX621140	627	141.5	6.4	1043	3	BI947108	BI947108
555	145.5	6.6	771	13	DT668490	DT668490	He_wd2a1	628	141	6.4	537	4	BQ246345	BQ246345
556	145.5	6.6	1642	3	BI519405	BI519405	603062218_	629	141	6.4	576	8	CD909046	CD909046
557	145	6.6	582	2	BG262246	BG262246	WHE0871_C	630	141	6.4	677	3	BM569289	BM569289
558	145	6.6	966	6	CNS0983C	CNS0983C	Single re	631	141	6.4	686	9	CJ711052	CJ711052
559	145	6.6	1088	2	BE427091	BE427091	PSR6399_I	632	141	6.4	703	13	DR008675	DR008675
560	145	6.6	2155	6	AK017342	AK017342	Mus muscu	c 633	141	6.4	762	13	DT067860	DT067860
561	144.5	6.5	563	11	EC592940	EC592940	FU009b06	634	141	6.4	781	10	CT730352	CT730352
562	144.5	6.5	665	3	BM634316	BM634316	170006875	635	141	6.4	783	10	CR975986	CR975986
563	144.5	6.5	669	6	CNS08YUM	CNS08YUM	Single re	636	141	6.4	787	12	DT516026	DT516026
564	144.5	6.5	683	8	CF847209	CF847209	psHB042xD	637	141	6.4	818	4	BQ806739	BQ806739
565	144.5	6.5	874	6	CNS08EWY	CNS08EWY	Single re	638	141	6.4	834	12	DY562852	DY562852
566	144.5	6.5	1447	10	CR290604	CR290604	CR290604	c 639	141	6.4	1030	19	CNS07BBA	CNS07BBA
567	144.5	6.5	2648	6	HSN805051	HSN805051	Homo sapi	640	141	6.4	2017	6	AK012808	AK012808
568	144	6.5	568	4	BQ245202	BQ245202	TaE15029C	641	141	6.4	2132	6	AK131956	AK131956
569	144	6.5	583	4	BP333251	BP333251	BP333251	642	140.5	6.4	486	8	CD897707	CD897707
570	144	6.5	623	8	CD497066	CD497066	CD425-G09	643	140.5	6.4	613	8	CD891467	CD891467
571	144	6.5	681	13	DT609206	DT609206	ACAG-aab0	644	140.5	6.4	689	1	AJ433321	AJ433321
572	144	6.5	771	3	BJ232827	BJ232827	BJ232827	645	140.5	6.4	748	10	CO048199	CO048199
573	144	6.5	786	4	BQ006117	BQ006117	UI-H-E11-	646	140.5	6.4	853	12	DV763936	DV763936
574	144	6.5	870	12	EB003279	EB003279	GtraSeq11	647	140.5	6.4	987	2	BE454232	BE454232
575	144	6.5	1383	16	CC284063	CC284063	CH261-139	c 648	140.5	6.4	1015	6	CNS090VI	CNS090VI
576	144	6.5	1675	3	BI522940	BI522940	603175412	649	140.5	6.4	1053	6	CNS09PCE	CNS09PCE
577	144	6.5	1933	6	AJ325173	AJ325173	Rattus no	650	140.5	6.4	1117	9	CK206309	CK206309
578	143.5	6.5	618	4	BQ245455	BQ245455	TaE15024D	651	140	6.3	633	4	BQ804424	BQ804424
579	143.5	6.5	804	1	AM208192	AM208192	AM208192	c 652	140	6.3	664	7	AW379283	AW379283
580	143.5	6.5	822	13	DV476700	DV476700	5564_F05	653	140	6.3	696	4	BQ247046	BQ247046
581	143.5	6.5	886	7	AU311102	AU311102	AU311102	654	140	6.3	702	2	BE601867	BE601867
582	143.5	6.5	944	10	CV644541	CV644541	EST923294	655	140	6.3	734	14	CK452514	CK452514
583	143.5	6.5	978	13	DT338303	DT338303	JBW083F07	656	140	6.3	740	7	AV973760	AV973760

BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	BP2333860	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657	140	6.3	743	9	CN051168	v8_pl16_11	730	138	6.2	5	BY917643	BY917643	
658	140	6.3	896	6	BU059716	Single re	731	138	6.2	9	CK499523	CK499523	
659	140	6.3	904	18	DU790810	APRH3814	732	138	6.2	13	DT138380	DT138380	
660	140	6.3	906	5	CA470519	AGENCOURT	733	138	6.2	5	AU002317	AU002317	
661	140	6.3	978	6	CN08W1L	Single re	734	138	6.2	748	BY920972	BY920972	
662	140	6.3	1002	6	CN08ERO	Single re	735	138	6.2	751	BY921027	BY921027	
663	140	6.3	1014	6	CN08WVD	Single re	736	138	6.2	777	BY921068	BY921068	
664	140	6.3	1016	6	CN08WVD	Single re	737	138	6.2	789	BY920900	BY920900	
665	140	6.3	1032	6	CN09PCD	Single re	738	138	6.2	811	BY920900	BY920900	
666	140	6.3	1046	18	CW933263	EDCH90TF	739	138	6.2	835	CZ881734	CZ881734	
667	140	6.3	1159	12	DY277344	IC0AAA43C	740	138	6.2	13	DV364211	DV364211	
668	140	6.3	1968	19	AY406502	Mus muscu	741	138	6.2	905	EB003769	EB003769	
669	139.5	6.3	515	16	CE173795	tigr-gss-	742	138	6.2	932	BE196461	BE196461	
670	139.5	6.3	519	11	EC593728	FU021H03	743	138	6.2	955	DU789737	DU789737	
671	139.5	6.3	529	10	CV918922	PH014G1	744	138	6.2	18	BC044003	BC044003	
672	139.5	6.3	532	4	BU968669	HB08D15r	745	137.5	6.2	500	CD899242	CD899242	
673	139.5	6.3	545	8	CD907099	G468_105P	746	137.5	6.2	8	CD905441	CD905441	
674	139.5	6.3	547	3	BJ288129	BJ288129	747	137.5	6.2	574	BP333422	BP333422	
675	139.5	6.3	707	12	DV816481	LB01719.C	748	137.5	6.2	593	BJ234714	BJ234714	
676	139.5	6.3	722	3	BM645378	170006873	749	137.5	6.2	640	BE427070	BE427070	
677	139.5	6.3	736	3	BM654741	170006873	750	137.5	6.2	642	BJ232970	BJ232970	
678	139.5	6.3	777	9	CK809576	Rasgsc322	751	137.5	6.2	656	5	BM274226	BM274226
679	139.5	6.3	824	17	CL687953	PRI0148a	752	137.5	6.2	685	10	CV515288	CV515288
680	139.5	6.3	936	18	DU783844	HF500_18-	753	137.5	6.2	725	5	BM274223	BM274223
681	139.5	6.3	952	6	CN08RPM	Single re	754	137.5	6.2	742	12	EB448273	EB448273
682	139.5	6.3	1467	2	BE383886	601273223	755	137.5	6.2	744	8	CB681064	CB681064
683	139	6.3	600	1	AJ483284	AJ483284	756	137.5	6.2	750	9	CJ668133	CJ668133
684	139	6.3	633	14	DN135550	tams6h04	757	137.5	6.2	757	12	EB448059	EB448059
685	139	6.3	640	2	BE195136	HVSMRH008	758	137.5	6.2	765	8	CF843146	CF843146
686	139	6.3	643	8	CD908828	G468_111B	759	137.5	6.2	825	12	EB426014	EB426014
687	139	6.3	795	12	EB454809	109934133	760	137.5	6.2	836	12	EB451819	EB451819
688	139	6.3	822	18	CW9633004	AIAA-aaa2	761	137.5	6.2	859	8	CF826554	CF826554
689	139	6.3	841	8	CB642948	OSJNEB03G	762	137.5	6.2	866	12	EB425014	EB425014
690	139	6.3	869	12	BE738594	AGENCOURT	763	137.5	6.2	869	12	EB450932	EB450932
691	139	6.3	881	8	CD381180	PTM06349	764	137.5	6.2	873	8	CD375690	CD375690
692	139	6.3	951	5	CA471119	AGENCOURT	765	137.5	6.2	875	12	EB450493	EB450493
693	139	6.3	951	18	DU792485	APRH4585	766	137.5	6.2	884	8	CF241387	CF241387
694	138.5	6.3	480	1	AJ481119	AJ481119	767	137.5	6.2	887	6	CNS096R2	CNS096R2
695	138.5	6.3	480	1	AJ482119	AJ482119	768	137.5	6.2	884	8	EB018982	EB018982
696	138.5	6.3	540	1	AJ482122	AJ482122	769	137.5	6.2	897	12	EB018982	EB018982
697	138.5	6.3	583	8	CD895691	G174_100J	770	137.5	6.2	936	4	BU524153	BU524153
698	138.5	6.3	618	4	BQ244886	TaE15034A	771	137.5	6.2	1009	6	CNS08RBL	CNS08RBL
699	138.5	6.3	631	3	BJ079911	BJ079911	772	137.5	6.2	1111	6	CNS06QHM	CNS06QHM
700	138.5	6.3	651	4	BU303183	603737737	773	137	6.2	452	4	BQ246719	BQ246719
701	138.5	6.3	657	3	BJ044519	BJ044519	774	137	6.2	539	4	BQ472442	BQ472442
702	138.5	6.3	658	4	BQ246853	TaE15004E	775	137	6.2	578	12	DM201650	DM201650
703	138.5	6.3	658	5	BM265514	BM265514	776	137	6.2	617	13	DT616365	DT616365
704	138.5	6.3	663	5	BM259047	BM259047	777	137	6.2	633	2	BP473033	BP473033
705	138.5	6.3	701	9	CK956208	4096183	778	137	6.2	712	4	BQ805692	BQ805692
706	138.5	6.3	721	13	DY077164	E2Sfmidgu	779	137	6.2	738	6	CNS09D1G	CNS09D1G
707	138.5	6.3	766	13	DR753406	CCRAP3F06	780	137	6.2	742	17	CL682472	CL682472
708	138.5	6.3	795	12	DY674586	STRAV101X	781	137	6.2	775	8	CB677062	CB677062
709	138.5	6.3	832	5	BM273990	BM273990	782	137	6.2	788	9	CB698379	CB698379
710	138.5	6.3	840	8	CD752595	AGENCOURT	783	137	6.2	827	3	BJ235568	BJ235568
711	138.5	6.3	859	18	CZ379368	ZMBF0139	784	137	6.2	935	2	BF580970	BF580970
712	138.5	6.3	863	13	CF824817	EST702199	785	137	6.2	1159	17	CG750976	CG750976
713	138.5	6.3	888	2	BE195446	HVSMRH008	786	137	6.2	1304	13	DN671967	DN671967
714	138.5	6.3	891	12	EB497283	109943521	787	137	6.2	2184	17	CG756648	CG756648
715	138.5	6.3	928	6	CN08QOF	Single re	788	136.5	6.2	501	4	BU986225	BU986225
716	138.5	6.3	962	6	CN09337U	Single re	789	136.5	6.2	501	14	DB330538	DB330538
717	138.5	6.3	978	6	CN08MQM	Single re	790	136.5	6.2	518	8	CD896958	CD896958
718	138.5	6.3	3306	17	CL965284	OsIFCC012	791	136.5	6.2	574	5	BM255622	BM255622
719	138	6.2	480	1	AJ478980	AJ478980	792	136.5	6.2	584	2	BE402376	BE402376
720	138	6.2	534	3	BU763117	BU763117	793	136.5	6.2	584	4	BQ607819	BQ607819
721	138	6.2	550	2	BE402286	CSB006D04	794	136.5	6.2	600	10	CO358455	CO358455
722	138	6.2	550	4	BQ607915	BRB_3814	795	136.5	6.2	624	12	DM208543	DM208543
723	138	6.2	565	4	BP332994	BP332994	796	136.5	6.2	633	8	CB407960	CB407960
724	138	6.2	567	12	EC166805	MNE000018	797	136.5	6.2	643	12	DM202160	DM202160
725	138	6.2	585	4	BQ244835	TaE15034G	798	136.5	6.2	675	3	BJ984581	BJ984581
726	138	6.2	585	12	EC166027	MNE000025	799	136.5	6.2	678	3	BJ984616	BJ984616
727	138	6.2	663	5	BY916489	BY916489	800	136.5	6.2	683	3	BJ985635	BJ985635
728	138	6.2	669	12	DY420539	1538608	801	136.5	6.2	685	10	CO058527	CO058527
729	138	6.2	676	3	BM371823	EBma08_SQ	802	136.5	6.2	694	3	BJ985192	BJ985192

C 803	136.5	6.2	717	7	BB990245	BB990245	876	135.5	6.1	1217	13	DT970234	DT970234
C 804	136.5	6.2	719	3	BJ984644	BJ984644	877	135.5	6.1	1337	13	DT976995	DT976995
C 805	136.5	6.2	719	3	BJ984759	BJ984759	878	135.5	6.1	2139	2	BF128407	BF128407
C 806	136.5	6.2	723	3	BJ985446	BJ985446	879	135	6.1	491	3	BM184713	BM184713
C 807	136.5	6.2	726	7	BB990352	BB990352	880	135	6.1	515	4	BQ245204	BQ245204
C 808	136.5	6.2	727	3	BJ984379	BJ984379	881	135	6.1	521	4	BQ245204	BQ245204
C 809	136.5	6.2	728	8	CD910612	CD910612	882	135	6.1	525	4	BU975275	BU975275
C 810	136.5	6.2	744	3	BJ983223	BJ983223	883	135	6.1	525	4	BU975437	BU975437
C 811	136.5	6.2	756	8	CB565469	CB565469	884	135	6.1	530	4	BQ464672	BQ464672
C 812	136.5	6.2	835	2	BE194402	BE194402	885	135	6.1	532	5	CA557042	CA557042
C 813	136.5	6.2	855	13	DR879237	DR879237	886	135	6.1	535	4	BU966695	BU966695
C 814	136.5	6.2	873	13	DT435822	DT435822	887	135	6.1	537	4	BU968991	BU968991
C 815	136.5	6.2	923	2	BE196299	BE196299	888	135	6.1	549	4	BU968705	BU968705
C 816	136.5	6.2	975	6	CNS08BRP	CNS08BRP	889	135	6.1	551	4	BU968512	BU968512
C 817	136.5	6.2	993	17	CL960565	CL960565	890	135	6.1	556	5	CA558769	CA558769
C 818	136.5	6.2	1007	12	DY303037	DY303037	891	135	6.1	561	4	BU967514	BU967514
C 819	136.5	6.2	1116	16	CC296896	CC296896	892	135	6.1	569	8	CD897643	CD897643
C 820	136	6.2	518	4	BQ607049	BQ607049	893	135	6.1	574	12	EB099446	EB099446
C 821	136	6.2	528	4	BU988890	BU988890	894	135	6.1	588	4	BU969031	BU969031
C 822	136	6.2	628	8	CF915716	CF915716	895	135	6.1	595	5	CA560020	CA560020
C 823	136	6.2	635	4	BU989593	BU989593	896	135	6.1	597	10	CV065784	CV065784
C 824	136	6.2	647	4	BQ805480	BQ805480	897	135	6.1	598	4	BU969253	BU969253
C 825	136	6.2	673	4	BQ806706	BQ806706	898	135	6.1	607	4	BU990058	BU990058
C 826	136	6.2	674	8	CF428050	CF428050	899	135	6.1	619	3	BU236211	BU236211
C 827	136	6.2	675	14	CK611100	CK611100	900	135	6.1	630	3	BU235111	BU235111
C 828	136	6.2	678	4	BQ807117	BQ807117	901	135	6.1	636	3	BU244387	BU244387
C 829	136	6.2	703	3	BJ290249	BJ290249	902	135	6.1	643	8	CF914438	CF914438
C 830	136	6.2	704	5	BA478868	BA478868	903	135	6.1	648	8	CF915734	CF915734
C 831	136	6.2	734	8	CF870512	CF870512	904	135	6.1	649	4	BQ789334	BQ789334
C 832	136	6.2	738	13	DR722706	DR722706	905	135	6.1	659	12	DM191574	DM191574
C 833	136	6.2	740	14	CK618749	CK618749	906	135	6.1	665	12	CB366812	CB366812
C 834	136	6.2	746	4	BQ807120	BQ807120	907	135	6.1	665	12	EB008943	EB008943
C 835	136	6.2	802	8	CB900701	CB900701	913	135	6.1	736	9	CJ664671	CJ664671
C 836	136	6.2	837	12	BE025460	BE025460	914	135	6.1	738	9	CJ668022	CJ668022
C 837	136	6.2	856	6	CNS0900V	CNS0900V	915	135	6.1	743	9	CJ716530	CJ716530
C 838	136	6.2	865	8	CB566685	CB566685	916	135	6.1	745	9	CJ724800	CJ724800
C 839	136	6.2	1095	9	CK214375	CK214375	917	135	6.1	751	9	CJ722701	CJ722701
C 840	136	6.2	1725	17	CL975488	CL975488	918	135	6.1	756	9	CJ667501	CJ667501
C 841	136	6.2	2149	19	DQ029920	DQ029920	919	135	6.1	758	9	CJ722080	CJ722080
C 842	136	6.2	2536	6	BE402057	BE402057	920	135	6.1	761	9	CJ666815	CJ666815
C 843	135.5	6.1	541	4	BQ607515	BQ607515	921	135	6.1	770	9	CJ661871	CJ661871
C 844	135.5	6.1	541	4	BQ607515	BQ607515	922	135	6.1	776	9	CJ668073	CJ668073
C 845	135.5	6.1	569	1	AJ432963	AJ432963	923	135	6.1	783	5	BW715554	BW715554
C 846	135.5	6.1	573	2	BE500125	BE500125	924	135	6.1	790	18	CZ874023	CZ874023
C 847	135.5	6.1	597	2	BE501524	BE501524	925	135	6.1	791	4	BU444648	BU444648
C 848	135.5	6.1	617	8	CF175082	CF175082	926	135	6.1	800	17	CL656337	CL656337
C 849	135.5	6.1	622	3	BU798476	BU798476	927	135	6.1	833	9	CK193488	CK193488
C 850	135.5	6.1	627	3	BU054923	BU054923	928	135	6.1	878	4	BQ943319	BQ943319
C 851	135.5	6.1	645	3	BU055129	BU055129	929	135	6.1	929	4	BU841382	BU841382
C 852	135.5	6.1	650	8	CF174393	CF174393	930	135	6.1	2263	6	CR606886	CR606886
C 853	135.5	6.1	661	8	CD921444	CD921444	931	135	6.1	2520	17	CL979986	CL979986
C 854	135.5	6.1	675	8	CF172040	CF172040	932	134.5	6.1	495	4	BU975783	BU975783
C 855	135.5	6.1	677	4	BQ608489	BQ608489	933	134.5	6.1	524	4	BU985039	BU985039
C 856	135.5	6.1	707	12	DY783730	DY783730	934	134.5	6.1	524	4	BU988031	BU988031
C 857	135.5	6.1	724	8	CF523607	CF523607	935	134.5	6.1	525	4	BU989876	BU989876
C 858	135.5	6.1	727	3	BI281272	BI281272	936	134.5	6.1	559	9	CJ329206	CJ329206
C 859	135.5	6.1	730	13	DR041524	DR041524	937	134.5	6.1	595	4	BU986566	BU986566
C 860	135.5	6.1	757	12	DY238186	DY238186	938	134.5	6.1	614	8	CF173687	CF173687
C 861	135.5	6.1	759	8	CB671800	CB671800	939	134.5	6.1	629	8	CD281214	CD281214
C 862	135.5	6.1	772	2	BE193188	BE193188	940	134.5	6.1	639	2	BE414402	BE414402
C 863	135.5	6.1	779	10	CV643503	CV643503	941	134.5	6.1	641	3	BM625487	BM625487
C 864	135.5	6.1	843	3	BI946806	BI946806	942	134.5	6.1	645	5	CA559798	CA559798
C 865	135.5	6.1	858	11	BE184283	BE184283	943	134.5	6.1	675	3	BJ098483	BJ098483
C 866	135.5	6.1	892	18	CZ216254	CZ216254	944	134.5	6.1	677	3	BJ237074	BJ237074
C 867	135.5	6.1	901	4	BQ922333	BQ922333	945	134.5	6.1	681	7	BB990655	BB990655
C 868	135.5	6.1	1003	2	BE196487	BE196487	946	134.5	6.1	682	3	BU983340	BU983340
C 869	135.5	6.1	1014	6	CNS08HPL	CNS08HPL	947	134.5	6.1	686	4	BQ245977	BQ245977
C 870	135.5	6.1	1170	18	CW934254	CW934254	948	134.5	6.1	701	3	BU983659	BU983659

C 949	134.5	6.1	717	3	BJ983611	BJ983611	1022	133.5	6.0	632	8	CD898029
C 950	134.5	6.1	717	7	BB990525	BB990525	1023	133.5	6.0	649	8	CD312012
C 951	134.5	6.1	718	3	BJ983290	BJ983290	1024	133.5	6.0	652	5	BM239427
C 952	134.5	6.1	718	3	BJ983320	BJ983320	1025	133.5	6.0	675	3	BJ983463
C 953	134.5	6.1	718	3	BJ983357	BJ983357	1026	133.5	6.0	677	8	CF916423
C 954	134.5	6.1	718	3	BJ984171	BJ984171	1027	133.5	6.0	678	4	BM245396
C 955	134.5	6.1	743	3	BJ983322	BJ983322	1028	133.5	6.0	679	2	BF473065
C 956	134.5	6.1	747	7	BB990271	BB990271	1029	133.5	6.0	681	5	BM308031
C 957	134.5	6.1	828	9	CK811348	Rasgsc692	1030	133.5	6.0	690	8	CD294616
C 958	134.5	6.1	829	9	CK239262	AGENCOURT	1031	133.5	6.0	706	4	BM213510
C 959	134.5	6.1	888	12	EB024301	Lscose040	1032	133.5	6.0	710	4	BQ247102
C 960	134.5	6.1	936	2	BE196491	BE196491	1033	133.5	6.0	714	12	EC392273
C 961	134.5	6.1	936	12	EB003879	EB003879	1034	133.5	6.0	715	12	BE455174
C 962	134.5	6.1	939	2	BE196573	BE196573	1035	133.5	6.0	726	12	DY997425
C 963	134.5	6.1	1112	13	BE122909	49329377	1036	133.5	6.0	734	4	BQ245390
C 964	134.5	6.1	1531	2	BE306182	601101310	1037	133.5	6.0	751	13	DN744030
C 965	134	6.1	393	10	CV354692	MR4-CN014	1038	133.5	6.0	754	2	BE193536
C 966	134	6.1	480	1	AJ483282	AJ483282	1039	133.5	6.0	778	8	CB654692
C 967	134	6.1	500	4	BU967231	BU967231	1040	133.5	6.0	780	4	BQ804567
C 968	134	6.1	509	4	BU969161	BU969161	1041	133.5	6.0	799	2	BG367090
C 969	134	6.1	551	8	CB879363	HP11016T	1042	133.5	6.0	804	8	CF436558
C 970	134	6.1	552	2	BE606272	WHE0905.H	1043	133.5	6.0	812	14	CK995840
C 971	134	6.1	555	4	BU969192	HB10N04T	1044	133.5	6.0	822	2	BG366988
C 972	134	6.1	558	2	BF432736	rad12e05.	1045	133.5	6.0	823	8	CD818579
C 973	134	6.1	559	4	BU975214	HB30G24r	1046	133.5	6.0	834	3	BI951055
C 974	134	6.1	565	1	AJ435660	AJ435660	1047	133.5	6.0	884	10	CO545357
C 975	134	6.1	566	4	BU984508	HF04C04r	1048	133.5	6.0	899	4	BQ277541
C 976	134	6.1	573	2	BE194117	HVSMeh008	1049	133.5	6.0	978	6	CNS092XP
C 977	134	6.1	584	19	DE225508	TriFolium	1050	133.5	6.0	1067	6	CNS08MOV
C 978	134	6.1	610	13	DN245792	DN245792	1051	133.5	6.0	2105	6	EC075667
C 979	134	6.1	618	4	BU987557	BU987557	1052	133	6.0	360	1	AJ484922
C 980	134	6.1	630	4	BQ239992	TAE05023H	1053	133	6.0	458	4	BU984125
C 981	134	6.1	639	8	CD902543	G356.107F	1054	133	6.0	480	1	AJ483285
C 982	134	6.1	651	8	CF913839	CF913839	1055	133	6.0	503	14	CK807924
C 983	134	6.1	660	17	CL696555	PR1019b.E	1056	133	6.0	538	5	CA559656
C 984	134	6.1	661	8	CD901091	GJ56.102L	1057	133	6.0	539	5	CA556312
C 985	134	6.1	661	14	DN136070	tam64e11.	1058	133	6.0	539	5	CA558048
C 986	134	6.1	668	1	AL642887	AL642887	1059	133	6.0	545	1	AJ904299
C 987	134	6.1	671	8	CF862249	PRZS003xA	1060	133	6.0	554	4	BU985818
C 988	134	6.1	690	4	BQ246985	TAE15002G	1061	133	6.0	567	5	CA559283
C 989	134	6.1	707	4	BQ247122	TAE15001B	1062	133	6.0	574	4	BQ805851
C 990	134	6.1	710	1	AU002237	AU002237	1063	133	6.0	574	4	BQ805851
C 991	134	6.1	720	3	BM576218	BM576218	1064	133	6.0	578	8	CF696569
C 992	134	6.1	724	12	DV819897	DV819897	1065	133	6.0	584	4	BQ244692
C 993	134	6.1	739	3	BJ983897	BJ983897	1066	133	6.0	591	5	CA561439
C 994	134	6.1	740	2	BE603128	BE603128	1067	133	6.0	594	5	CA561924
C 995	134	6.1	754	7	BB990227	BB990227	1068	133	6.0	597	5	CA559493
C 996	134	6.1	755	4	BQ245996	BQ245996	1069	133	6.0	600	1	AJ483321
C 997	134	6.1	756	2	BE193514	BE193514	1070	133	6.0	600	5	CA560259
C 998	134	6.1	757	13	DT063631	DT063631	1071	133	6.0	601	5	CA557320
C 999	134	6.1	764	3	BJ983747	BJ983747	1072	133	6.0	602	5	CA561917
C 1000	134	6.1	776	17	CL674503	CL674503	1073	133	6.0	615	5	CA559956
C 1001	134	6.1	805	2	BE195121	BE195121	1074	133	6.0	621	1	AJ436631
C 1002	134	6.1	813	6	CNS08SXX	Single re	1075	133	6.0	623	5	CA558825
C 1003	134	6.1	822	19	DE266607	Oryzias 1	1076	133	6.0	624	5	CA560196
C 1004	134	6.1	889	12	EB450211	EB450211	1077	133	6.0	630	12	DV646385
C 1005	134	6.1	891	9	CK154529	CK154529	1078	133	6.0	635	8	CF174340
C 1006	134	6.1	908	11	EB048236	ZM_BPC012	1079	133	6.0	636	4	BQ244610
C 1007	134	6.1	1183	13	DN733739	DN733739	1080	133	6.0	640	2	BE427016
C 1008	134	6.1	1327	12	DY291280	DY291280	1081	133	6.0	640	3	BU233156
C 1009	133.5	6.0	474	7	AU242628	AU242628	1082	133	6.0	641	2	BG262155
C 1010	133.5	6.0	480	1	AJ482311	AJ482311	1083	133	6.0	643	1	AJ433357
C 1011	133.5	6.0	480	1	AJ482312	AJ482312	1084	133	6.0	648	4	BQ246938
C 1012	133.5	6.0	500	4	BU984352	BU984352	1085	133	6.0	649	8	CF914947
C 1013	133.5	6.0	506	4	BU972187	BU972187	1086	133	6.0	652	8	CF914947
C 1014	133.5	6.0	513	4	BU989293	BU989293	1087	133	6.0	653	5	BY725915
C 1015	133.5	6.0	535	1	AA495649	c079_Zhou	1088	133	6.0	656	9	CK808723
C 1016	133.5	6.0	535	7	AV962757	AV962757	1089	133	6.0	677	9	CJ713065
C 1017	133.5	6.0	558	4	BU986245	BU986245	1090	133	6.0	695	9	CJ713065
C 1018	133.5	6.0	571	10	CV894467	CV894467	1091	133	6.0	704	1	AJ904240
C 1019	133.5	6.0	610	13	DR438063	DR438063	1092	133	6.0	725	12	BQ246336
C 1020	133.5	6.0	614	4	BQ246658	TAE15007C	1093	133	6.0	725	12	EB013422
C 1021	133.5	6.0	616	4	BQ240366	TAE05018E	1094	133	6.0	726	8	CD910419

1095	133	6.0	738	12	EB013413	RB6013413 LedosEQ34	cl168	132.5	6.0	835	17	CL669986	CL669986 PRI0160d_
1096	133	6.0	739	2	BE603255	BE603255 HVSMER010	cl169	132.5	6.0	869	9	CK159167	CK159167 FGAS04056_
1097	133	6.0	742	2	BG262242	BG262242 WHE0871_C	1170	132.5	6.0	870	12	DW242488	DW242488 GH_TSMB_1
1098	133	6.0	749	1	AJ894074	AJ894074 AJ894074	1171	132.5	6.0	884	4	BQ389992	BQ389992 HVSMER009
1099	133	6.0	761	8	CF438936	CF438936 EST675281	1172	132.5	6.0	895	2	BE454277	BE454277 HVSMER009
1100	133	6.0	771	5	BW728626	BW728626 BW728626	1173	132.5	6.0	920	17	CL461353	CL461353 SAIL_1145
1101	133	6.0	772	8	CF435316	CF435316 ESU671661	1174	132.5	6.0	964	6	CNS08EMV	BX008387 Single re
1102	133	6.0	774	17	CL979366	CL979366 OSIFCC033	cl175	132.5	6.0	971	6	CNS0937V	BX040247 Single re
1103	133	6.0	775	5	BW730182	BW730182 BW730182	1176	132.5	6.0	977	6	CNS08E4C	BX007720 Single re
1104	133	6.0	813	12	EB014561	EB014561 LedosEQ50	1177	132.5	6.0	1066	18	CW924086	CW924086 EDCB241TR
1105	133	6.0	818	12	ED016279	ED016279 LedosEQ73	1178	132.5	6.0	1086	12	DY273578	DY273578 IC0AAA34B
1106	133	6.0	822	12	EB426847	EB426847 KPBC_108E	1179	132.5	6.0	1163	12	DY288996	DY288996 IC0AAA71A
1107	133	6.0	829	12	EB015180	EB015180 LedosEQ59	1180	132.5	6.0	1188	6	CNS0FHAL	CR671751 Tetradon
1108	133	6.0	830	12	EB015499	EB015499 LedosEQ63	1181	132.5	6.0	1649	6	CR615151	CR615151 full-leng
1109	133	6.0	831	12	EB018045	EB018045 LedosEQ96	1182	132.5	6.0	2585	6	AK164929	AK164929 Mus muscu
1110	133	6.0	849	12	EB013133	EB013133 LedosEQ30	1183	132.5	6.0	2602	6	AK131887	AK131887 Mus muscu
1111	133	6.0	857	12	EC319940	EC319940 EMBRYOF08	1184	132.5	6.0	3075	19	DQ052043	DQ052043 Homo sapi
1112	133	6.0	900	12	EB450888	EB450888 K77C_109A	1185	132.5	6.0	4082	6	HSM801801	AL136833 Homo sapi
1113	133	6.0	991	2	BE196284	BE196284 HVSMER009	1186	132	6.0	485	4	BU990034	BU990034 Hf23M19r
1114	133	6.0	1105	8	CD054339	CD054339 CDAY73-F11	1187	132	6.0	492	4	BU972719	BU972719 HB22108r
1115	133	6.0	1216	13	DN696618	DN696618 CLJ08-A07	1188	132	6.0	493	2	BE591055	BE591055 WHE0861_G
1116	133	6.0	1455	6	AK089214	AK089214 Mus muscu	1189	132	6.0	494	4	BU969388	BU969388 HB11G05r
1117	133	6.0	1601	6	AK172077	AK172077 Mus muscu	1190	132	6.0	495	4	BU972055	BU972055 HB20H12r
1118	133	6.0	1634	2	BG028384	BG028384 G02295453	1191	132	6.0	495	4	BU989074	BU989074 HF19L01r
1119	133	6.0	2219	6	AK139822	AK139822 Mus muscu	1192	132	6.0	511	3	BM004465	BM004465 T9EST2ya8
1120	133	6.0	3240	19	AJ405254	AJ405254 Mus muscu	1193	132	6.0	514	5	CA555934	CA555934 K0204H08-
1121	132.5	6.0	420	1	AJ481830	AJ481830 AJ481830	1194	132	6.0	516	4	BU975347	BU975347 HB30004r
1122	132.5	6.0	420	1	AJ481831	AJ481831 AJ481831	1195	132	6.0	522	4	BU969002	BU969002 HB10D18r
1123	132.5	6.0	420	1	AJ485287	AJ485287 AJ485287	1196	132	6.0	523	4	BU968362	BU968362 HB07E15r
1124	132.5	6.0	470	4	BU975350	BU975350 HB30008r	1197	132	6.0	526	4	BU972981	BU972981 HB23F23r
1125	132.5	6.0	507	4	BU975519	BU975519 HB31G16r	1198	132	6.0	532	5	CA718482	CA718482 wdk5c.pk0
1126	132.5	6.0	518	3	BJ088321	BJ088321 BJ088321	1199	132	6.0	538	4	BU969115	BU969115 HB10116r
1127	132.5	6.0	534	3	BY948392	BY948392 HVSMER1000	1200	132	6.0	538	4	BU973334	BU973334 HB24J05r
1128	132.5	6.0	535	5	CA717672	CA717672 wdk4c.pk0	1201	132	6.0	539	4	BU968870	BU968870 HB08N10r
1129	132.5	6.0	540	1	AJ481829	AJ481829 AJ481829	1202	132	6.0	539	5	CA561723	CA561723 K0291C02-
1130	132.5	6.0	570	4	BU968447	BU968447 HB07121r	1203	132	6.0	540	4	BU975714	BU975714 HB32B09r
1131	132.5	6.0	582	4	BU968521	BU968521 HB07M16r	1204	132	6.0	544	2	BE402545	BE402545 CSB009A11
1132	132.5	6.0	589	7	BB936609	BB936609 BB936609	1205	132	6.0	544	4	BQ608208	BQ608208 BRY_4112
1133	132.5	6.0	595	4	BQ472381	BQ472381 HB09M16T	1206	132	6.0	544	5	CA734311	CA734311 wde6f.pk0
1134	132.5	6.0	599	5	BY929517	BY929517 BY929517	1207	132	6.0	550	5	CA561080	CA561080 K0282B06-
1135	132.5	6.0	605	8	CD311352	CD311352 StrPu691.	1208	132	6.0	557	10	CV930252	CV930252 PM039C12
1136	132.5	6.0	606	4	BQ245034	BQ245034 TaE15032A	1209	132	6.0	561	5	CA556446	CA556446 K0212B05-
1137	132.5	6.0	607	3	BN307956	BN307956 sak40a11.	1210	132	6.0	562	4	BU973468	BU973468 HB25A20r
1138	132.5	6.0	611	5	BY916359	BY916359 BY916359	1211	132	6.0	563	5	CA560353	CA560353 K0271C04-
1139	132.5	6.0	617	3	BJ233981	BJ233981 BJ233981	1212	132	6.0	565	4	BU971853	BU971853 HB19N21r
1140	132.5	6.0	623	3	BJ818316	BJ818316 BJ818316	1213	132	6.0	569	4	BU974183	BU974183 HB27C09r
1141	132.5	6.0	632	3	BU080503	BU080503 BJ080503	1214	132	6.0	569	5	CA734306	CA734306 wde2f.pk0
1142	132.5	6.0	637	12	DY215293	DY215293 000513BSI	1215	132	6.0	571	5	CA734330	CA734330 wde2f.pk0
1143	132.5	6.0	644	3	BJ233232	BJ233232 BJ233232	1216	132	6.0	572	4	BU990606	BU990606 HF25116r
1144	132.5	6.0	653	3	BJ984281	BJ984281 BJ984281	1217	132	6.0	573	4	BU990629	BU990629 HF25J17r
1145	132.5	6.0	657	9	CK494148	CK494148 rseba0.00	1218	132	6.0	575	4	BU970547	BU970547 HB14P15r
1146	132.5	6.0	669	8	CB307515	CB307515 HF1G500_H	1219	132	6.0	575	5	CA555615	CA555615 K0200D01-
1147	132.5	6.0	686	3	BU985245	BU985245 BJ985245	1220	132	6.0	578	4	BQ607175	BQ607175 BRY_3063
1148	132.5	6.0	690	13	DT467748	DT467748 GH_CHX200	1221	132	6.0	584	4	BU970446	BU970446 HB14K17r
1149	132.5	6.0	698	13	BJ984116	BJ984116 BJ984116	1222	132	6.0	585	3	BJ235257	BJ235257 BRY235257
1150	132.5	6.0	699	13	DR118856	DR118856 RTWG1_19	1223	132	6.0	586	4	BQ246110	BQ246110 TaE15016A
1151	132.5	6.0	702	1	AJ433139	AJ433139 AJ433139	1224	132	6.0	592	8	CF172080	CF172080 B0902B08-
1152	132.5	6.0	703	3	BJ794932	BJ794932 BJ794932	1225	132	6.0	605	5	CA734391	CA734391 wde2f.pk0
1153	132.5	6.0	706	7	AW448684	AW448684 BRY_1107	1226	132	6.0	606	4	BQ244875	BQ244875 TaE15034B
1154	132.5	6.0	719	3	BJ985374	BJ985374 BJ985374	1227	132	6.0	607	4	BU971786	BU971786 HB19K17r
1155	132.5	6.0	732	3	BJ984396	BJ984396 BJ984396	1228	132	6.0	611	5	CA559368	CA559368 K0257G09-
1156	132.5	6.0	733	2	BE602094	BE602094 HVSMER010	1229	132	6.0	611	5	CA727303	CA727303 wde1f.pk0
1157	132.5	6.0	735	10	CO157883	CO157883 FLD1_2_G0	1230	132	6.0	613	2	BE590559	BE590559 WHE0858_H
1158	132.5	6.0	738	17	CL671012	CL671012 PRI0163C	1231	132	6.0	615	2	BF484916	BF484916 WHE23333_B
1159	132.5	6.0	749	9	CK123232	CK123232 BES182410	1232	132	6.0	615	4	BU975104	BU975104 HB30B18r
1160	132.5	6.0	752	12	EB017088	EB017088 LedosEQ83	1233	132	6.0	615	5	CA727069	CA727069 wde1f.pk0
1161	132.5	6.0	752	17	CL653959	CL653959 PRI0119d	1234	132	6.0	618	2	BE401906	BE401906 CSB002D08
1162	132.5	6.0	754	2	BE193541	BE193541 HVSMER008	1235	132	6.0	618	4	BQ607600	BQ607600 BRY_3494
1163	132.5	6.0	758	3	BM169717	BM169717 EST572240	1236	132	6.0	618	5	CA727346	CA727346 wde1f.pk0
1164	132.5	6.0	760	13	DR163927	DR163927 RTPE1_45	1237	132	6.0	620	3	CF914440	CF914440 B0564A11-
1165	132.5	6.0	806	6	CNS08LQJ	BX017591 Single re	1238	132	6.0	621	8	BU971376	BU971376 HB17G24r
1166	132.5	6.0	810	13	DR744562	DR744562 RTCU1_23	1239	132	6.0	621	4	CF276479	CF276479 14ETL--01
1167	132.5	6.0	818	10	CO163724	CO163724 FLD1_43_H	1240	132	6.0	624	8	CF276479	CF276479 14ETL--01

1241	132	6.0	627	5	CA734355	wde2f.pk0	CA734355	1314	131.5	5.9	593	4	BU986813	HF12P18r
1242	132	6.0	628	8	CF913543	BU950C07 -	CF913543	1315	131.5	5.9	594	4	BU988787	HF18111r
1243	132	6.0	631	3	BJ234843	BJ234843	BJ234843	1316	131.5	5.9	594	4	BU990742	HF25021r
1244	132	6.0	631	4	BU970367	HB14G09r	BU970367	1317	131.5	5.9	596	4	BU972894	HB23806r
1245	132	6.0	631	8	CD919465	G608.113H	CD919465	1318	131.5	5.9	596	4	BU990659	HF25L03r
1246	132	6.0	633	5	CA734173	wde2f.pk0	CA734173	1319	131.5	5.9	599	4	BU969241	HB10P10r
1247	132	6.0	634	2	BG262160	WHE0871_F	BG262160	1320	131.5	5.9	601	4	BU987556	HF15805r
1248	132	6.0	635	2	BE590791	WHE0857_B	BE590791	1321	131.5	5.9	602	4	BU970331	HB14F06r
1249	132	6.0	637	4	BQ245757	TaE15020E	BQ245757	1322	131.5	5.9	603	4	BU971328	HB17E18r
1250	132	6.0	640	2	BE427078	PSR6382_I	BE427078	1323	131.5	5.9	606	4	BU973159	HB23P04r
1251	132	6.0	642	5	CA726954	wde1f.pk0	CA726954	1324	131.5	5.9	609	4	BU968507	HB29L22r
1252	132	6.0	646	9	CN141007	OX1_48_F0	CN141007	1325	131.5	5.9	609	4	BU974986	HB29L23r
1253	132	6.0	648	8	CF915856	BU986B12 -	CF915856	1326	131.5	5.9	614	5	CA012993	HT07B05r
1254	132	6.0	649	4	BU987815	HF15N11r	BU987815	1327	131.5	5.9	620	4	BU968452	HB07J04r
1255	132	6.0	655	8	CF914014	BU957G05 -	CF914014	1328	131.5	5.9	622	4	BU968817	HB08K23r
1256	132	6.0	668	4	BQ789089	WHE4157_D	BQ789089	1329	131.5	5.9	622	4	BU986885	HF13D01r
1257	132	6.0	670	4	BQ245752	TaE15020F	BQ245752	1330	131.5	5.9	623	4	BQ606982	BRY_2860
1258	132	6.0	670	4	BQ245935	TaE15018C	BQ245935	1331	131.5	5.9	623	4	BU987810	HF15N06r
1259	132	6.0	679	4	BQ246243	TaE15014D	BQ246243	1332	131.5	5.9	626	13	DR631147	EST102127
1260	132	6.0	682	4	BQ245343	TaE15025H	BQ245343	1333	131.5	5.9	634	18	CZ338619	ZWMBF0106
1261	132	6.0	695	3	BJ984589	BU984589	BJ984589	1334	131.5	5.9	639	12	BU987615	HF15E06r
1262	132	6.0	703	3	BJ984619	BU984619	BJ984619	1335	131.5	5.9	639	12	DX251055	PMAH-aa40
1263	132	6.0	722	4	BQ246023	TaE15017B	BQ246023	1336	131.5	5.9	642	4	BU968699	HB08E24r
1264	132	6.0	726	5	BW712644	BW712644	BW712644	1337	131.5	5.9	645	4	BQ606993	BRY_2871
1265	132	6.0	728	4	BQ245556	TaE15023B	BQ245556	1338	131.5	5.9	645	4	BU970238	HB14A24r
1266	132	6.0	728	12	DY999472	GtRaSEQ38	DY999472	1339	131.5	5.9	645	4	BU971636	HB19D12r
1267	132	6.0	728	12	EB489391	EB489391	EB489391	1340	131.5	5.9	649	3	BI641907	SD25571.5
1268	132	6.0	747	5	BW717680	BW717680	BW717680	1341	131.5	5.9	652	4	BU967464	HB04G09r
1269	132	6.0	754	18	DX954702	CHOR1105 -	DX954702	1342	131.5	5.9	659	4	BQ464258	HF01M10T
1270	132	6.0	762	9	CN322012	AGENCOURT	CN322012	1343	131.5	5.9	659	5	CA734124	wde2f.pk0
1271	132	6.0	772	10	CV639858	EST918611	CV639858	1344	131.5	5.9	662	4	BQ472453	HB09J004T
1272	132	6.0	776	5	BW724093	BW724093	BW724093	1345	131.5	5.9	664	2	BE194933	BE194933
1273	132	6.0	781	5	BW724392	BW724392	BW724392	1346	131.5	5.9	670	3	BJ232465	BJ232465
1274	132	6.0	782	8	CB665147	OSJNE411F	CB665147	1347	131.5	5.9	675	4	BU988134	HF16M05r
1275	132	6.0	796	12	EB602461	AGENCOURT	EB602461	1348	131.5	5.9	683	13	DN956804	Ph_mx0.23
1276	132	6.0	814	4	BQ605974	BRY_1570	BQ605974	1349	131.5	5.9	688	4	BQ608967	BRY_4884
1277	132	6.0	814	7	AW448827	BRY_1570	AW448827	1350	131.5	5.9	700	4	BQ464239	HF01L15T
1278	132	6.0	823	17	CL653867	PR10119C	CL653867	1351	131.5	5.9	708	5	BW435192	BW435192
1279	132	6.0	842	8	CB668023	OSJNE415K	CB668023	1352	131.5	5.9	725	8	CF841495	pGHBO14xL
1280	132	6.0	855	17	CL129509	ISB1-96M1	CL129509	1353	131.5	5.9	729	9	CK808946	Raegsc192
1281	132	6.0	857	11	EC884606	ZM_BFC002	EC884606	1354	131.5	5.9	731	5	BW435376	BW435376
1282	132	6.0	870	12	EB463520	AGENCOURT	EB463520	1355	131.5	5.9	733	4	BQ472079	TaE15001F
1283	132	6.0	891	11	EE182981	ZM_BFC016	EE182981	1356	131.5	5.9	748	4	BQ807161	WHE3587_E
1284	132	6.0	893	11	EC899901	ZM_BFC004	EC899901	1357	131.5	5.9	751	5	BW712172	BW712172
1285	132	6.0	895	12	EB004877	GtRaSEQ69	EB004877	1358	131.5	5.9	755	14	DN124497	DN124497
1286	132	6.0	899	5	BX373599	BX373599	BX373599	1359	131.5	5.9	767	12	EB628381	AGENCOURT
1287	132	6.0	955	2	BE195650	HVSMER009	BE195650	1360	131.5	5.9	768	8	CF450211	EST686556
1288	132	6.0	987	18	DY777961	ASXB1940.	DY777961	1361	131.5	5.9	774	14	CA9395841	JGI_CAA1
1289	132	6.0	1336	19	AA7416946	Homo sapi	AA7416946	1362	131.5	5.9	775	18	DX947674	CHOR1105 -
1290	132	6.0	4599	19	DQ053423	Homo sapi	DQ053423	1363	131.5	5.9	784	12	EB622068	AGENCOURT
1291	131.5	5.9	388	5	BY133746	BY133746	BY133746	1364	131.5	5.9	802	12	EB021319	LscoseQ13
1292	131.5	5.9	469	4	BU985259	HF06J15r	BU985259	1365	131.5	5.9	843	16	BZ643413	OGAOW57TM
1293	131.5	5.9	484	4	BU974972	HB29L07r	BU974972	1366	131.5	5.9	855	4	BU912494	AGENCOURT
1294	131.5	5.9	500	4	BU975415	HB31B02r	BU975415	1367	131.5	5.9	865	12	EB483329	AGENCOURT
1295	131.5	5.9	500	4	BU987295	HF14F20r	BU987295	1368	131.5	5.9	871	8	CB199736	CB199736
1296	131.5	5.9	507	4	BU988714	HF18H16r	BU988714	1369	131.5	5.9	875	8	CD378055	PTMM03224
1297	131.5	5.9	519	4	BU975838	HB32H09r	BU975838	1370	131.5	5.9	892	2	BE454215	HVSMER009
1298	131.5	5.9	522	4	BU985356	HF06O04r	BU985356	1371	131.5	5.9	900	9	CN330418	AGENCOURT
1299	131.5	5.9	536	4	BU972829	HB22N12r	BU972829	1372	131.5	5.9	908	4	BQ952669	AGENCOURT
1300	131.5	5.9	540	13	DT615857	ACAHA-aab1	DT615857	1373	131.5	5.9	911	8	CD381062	PTMM02631
1301	131.5	5.9	550	4	BU973533	HB25D23r	BU973533	1374	131.5	5.9	916	13	DR846419	JGI_CABET
1302	131.5	5.9	551	9	CJ635447	CJ635447	CJ635447	1375	131.5	5.9	920	13	DT773879	EST660375
1303	131.5	5.9	556	4	BU986590	HF12F05r	BU986590	1376	131.5	5.9	941	8	CD789014	EST660375
1304	131.5	5.9	567	4	BU970400	HB14I11r	BU970400	1377	131.5	5.9	954	6	CNS08NTW	AG139608
1305	131.5	5.9	567	4	BU971896	HB19P23r	BU971896	1378	131.5	5.9	966	6	CNS08NTW	AG139608
1306	131.5	5.9	576	17	CL651500	PR10112b -	CL651500	1379	131.5	5.9	986	6	CNS08GHO	AG139608
1307	131.5	5.9	577	4	BU988097	HF16K13r	BU988097	1380	131.5	5.9	1128	19	DY263081	IC0AAA10D
1308	131.5	5.9	581	4	BU971635	HB19D11r	BU971635	1381	131.5	5.9	1279	12	AG139608	DY263081
1309	131.5	5.9	582	4	BU988569	HF18A11r	BU988569	1382	131.5	5.9	477	5	CA743784	wr1ls.pk0
1310	131.5	5.9	584	4	BU988716	HF18H16r	BU988716	1383	131.5	5.9	486	4	BU971530	HB17O13r
1311	131.5	5.9	588	9	CJ632047	CJ632047	CJ632047	1384	131.5	5.9	509	8	CD899086	G174.111A
1312	131.5	5.9	590	4	BU966995	HB02P24r	BU966995	1385	131.5	5.9	526	8	CB931796	r163c08.Y
1313	131.5	5.9	590	4	BU990186	HF24F09r	BU990186	1386	131.5	5.9	532	8	CD098608	G468.110G

1387	131	5.9	570	4	BU970459	BU970459 HB14108r	1460	130.5	5.9	826	12	DW228724	DW228724 GH ONEFM
1388	131	5.9	583	4	BU968659	BU968659 HB08D04r	1461	130.5	5.9	834	2	BE194417	BE194417 HVSMH008
1389	131	5.9	605	4	BQ244707	BQ244707 TaE15038P	1462	130.5	5.9	864	12	EB029126	EB029126 LSCOSEQ98
1390	131	5.9	611	4	BQ472392	BQ472392 HB09M02t	1463	130.5	5.9	895	12	DW243137	DW243137 GH_TSnorm
1391	131	5.9	617	5	CA558994	CA558994 K025G03-	1464	130.5	5.9	901	12	EB022095	EB022095 LSCOSEQ14
1392	131	5.9	640	2	BE427257	BE427257 PSR6175 I	1465	130.5	5.9	911	12	DW875472	DW875472 LB02527.C
1393	131	5.9	642	2	BE194902	BE194902 HVSMH008	1466	130.5	5.9	917	2	BE196084	BE196084 HVSMH009
1394	131	5.9	652	8	CB619065	CB619065 OS1FA03G	1467	130.5	5.9	919	6	QNS08VMK	QNS08VMK Single re
1395	131	5.9	654	2	BQ467984	BQ467984 Na_L4_02C	1468	130.5	5.9	924	4	BQ956745	BQ956745 AGENCOURT
1396	131	5.9	663	4	BQ605715	BQ605715 BRY_1243	1469	130.5	5.9	988	2	BF585034	BF585034 602098925
1397	131	5.9	687	5	BW427336	BW427336 BW427336	1470	130.5	5.9	1029	2	BF584192	BF584192 602096332
1398	131	5.9	688	5	BW427326	BW427326	1471	130.5	5.9	1092	18	DX906125	DX906125 KBTH040N0
1399	131	5.9	703	16	CC647789	CC647789 OGWEZ90TH	1472	130.5	5.9	1169	13	DN660549	DN660549 CSC47-D11
1400	131	5.9	707	9	CJ633221	CJ633221 CJ633221	1473	130.5	5.9	1416	13	DN662502	DN662502 CFW09-D04
1401	131	5.9	709	12	DM204365	DM204365 EST20629	1474	130.5	5.9	1536	19	DQ035260	DQ035260 Pan trogl
1402	131	5.9	718	8	CF387722	CF387722 RTDR1_19	1475	130	5.9	420	1	AJ485890	AJ485890 AJ485890
1403	131	5.9	726	13	DR434535	DR434535 ACAB-aaa4	1476	130	5.9	420	4	BU038466	BU038466 DH11901 H
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ALIGNMENTS

RESULT 1	AY401136	1296 bp	DNA	linear	GSS 12-DEC-2003
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DEFINITION	AY401136	GSS.			
ACCESSION	AY401136.1	GI:39757125			
VERSION	AY401136.1	GI:39757125			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
PUBMED					
AUTHORS					
TITLE					

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 19 Gaps: 0
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 LOCUS Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY401137
 VERSION AY401137.1 GI:39757126
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 1296)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1296)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES Location/Qualifiers
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ORGANISM         Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catharrhini; Hominoidea; Pongo.
1 (bases 1 to 4613)
Osanger,A., Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp469A172) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469A172
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

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gene

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Query Match: 95.5% Indels: 0		Db	1360	GAGGCCAGTCCAGGAGTCTCTCCAGGCGAGGTTCCAGAAATCAGTATGGCTTCCA	1419
DB: 6 Gaps: 0		QY	381	PheGluLysTrpLeuLeuIleGlySerLeuPheGlyValLeuPheLeuValIleGly	400
US-09-944-929-83 (1-431) x CR858919 (1-4613)		Db	1420	TTTGAAGAGTGGCTTCTTATCGGGTCCCTCTCTTTGGTGTCTGTTCTCTGGTATAGGC	1479
QY 1 MetPhePheGlyGlyGlySerLeuThrThrThrLeuValIleIleCysPheLeuThr 20		QY	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu	420
Db 280 ATGTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTCGACA 339		Db	1480	CTCATCTCTCTGGGTAGAACTCTCTCGAAATCACTCCGCGAGGAAACGTTACTCAAGACTG	1539
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40		QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle 431	
Db 340 CTAAGGCTGTCTGCTAGTCAGGATTCCTCAACAGAGCTAGAGATGTTGTCTATTGAC 399		Db	1540	GATTATTTGATCAATGGGATCTATGTGGACATC 1572	
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60		RESULT 4			
Db 400 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGCAATGAGGCCATATATATCTTCAACTCAA 459		CR621081		1965 bp mRNA linear HTC 21-JUL-2004	
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80		LOCUS		full-length cDNA clone CS0D1054VH07 of Placentia Cot 25-normalized	
Db 460 GAAGACTGCATTAATCTTGTCTGTCTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 519		DEFINITION		of Homo sapiens (human).	
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100		ACCESSION		CR621081	
Db 520 TTGATGATCTTCGACACTCGAAAAACAGTAGACCAACCCACTGCTACCTATTTTCTGT 579		VERSION		CR621081.1 GI:50501888	
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120		KEYWORDS		HTC; CNSLT cDNA.	
Db 580 CCGGATGAGGAAGCCTGCTCCATGAGCCAGCAAAAGGACTTATGAGTTACAGGATAAT 639		SOURCE		Homo sapiens (human)	
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140		ORGANISM		Homo sapiens	
Db 640 AGAGATTTTCCATCTTTGACCAAGAAATTTGTCAAGCCCAAGAGTTACCCAGGGAAGATTCT 699				Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo.	
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160				1 (bases 1 to 1965)	
Db 700 CTCCTTACATGGCAATTTTACAGAGTCATCTCCCTAGCCCATCATCACAGATTAT 759		REFERENCE		Li, W.B., Gruber, C., Jessee, J., and Polayes, D.	
QY 161 SerLysProThrAspLysSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180		AUTHORS		Full-length cDNA libraries and normalization	
Db 760 TCAAGCCCAACCGATATCTCATGGAGACACACTTTTCTCAGAAGTTTGGATCCTCAGAT 819		JOURNAL		Unpublished	
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200		REMARK		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue	
Db 820 CACTTGGAGAAATATTTAAGATGGACGAAGCAAGTGCAGCTCCTTGTCTTAAGGAA 879				2 (bases 1 to 1965)	
QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220		REFERENCE		Genoscope.	
Db 880 AAAGGCCATTTCTCAGAGTTTCTCTGTATCAAGAAACGGCTCATCTGCTGCTCCT 939		AUTHORS		Direct Submission	
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla 240		TITLE		Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :	
		JOURNAL		BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr	
		COMMENT		- Web : www.genoscope.cns.fr)	
				1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	
				into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	
				was normalized. Library was constructed by Life Technologies, a	
				division of Invitrogen.	

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FEATURES
  source      Location/Qualifiers
1..1965      /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0D1054YH07"
              /tissue_type="Placenta Cot 25-normalized"
              /plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.:      5,87e-151      Length:      1965
Score:          1831.00      Matches:      357
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      82.8%      Indels:      0
DB:              6      Gaps:      0

US-09-944-929-83 (1-431) x CR621081 (1-1965)

QY 75 GlyAspLysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsn 94
DB 147 GGGCAACAGCATGTAACCTTGATGATCTTCGACACTCGAATAACAGCTAGACACCCCAAC 206
QY 95 CysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu 114
DB 207 TGTACCTATTCTTCTGCCAACGAGGAGCCTGTCATTGAAACCCAGCAAAAGGACATT 266
QY 115 MetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGlu 134
DB 267 ATGAGTTACAGATAATATACAGATTTCATCTTTGACACAGAAATTTGCCAAGCCAAAGAG 326
QY 135 LeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAla 154
DB 327 TTACCCCGAGAGATCTCTCTTACATGCCCAATTTTACAGCAGTACTCCCTAGGCC 386
QY 155 HisHisThrAspTyrSerLysProThrAspIleSerTyrArgAspThrLeuSerGln 174
DB 387 CATCATCACACAGATTATTCAAAGCCACCGATATCTCATGAGAGACACACTTTCTCTAG 446
QY 175 LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194
DB 447 AAGTTTGGATCCTCAGATCAGCTTGGAGAACTATTAAAGATGGATGAAGCAAGTGCCTAG 506
QY 195 LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214
DB 507 CTCCTTGCTTAAAGAAAGAGCCATCTCAGAGTTCAAAATTTCTCTCATCAAGAA 566
QY 215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
DB 567 ATAGCTCATCTGCTGCCTGAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCT 626
QY 235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254
DB 627 CCACATACCACCTCGCTACTCCAAAGCCGCCACCTCTCTACCCACCAATGCTTCAGTG 686
QY 255 ThrProSerGlyThrSerGlnProGlnLeuAlaThrAlaProProValThrThrVal 274
DB 687 ACACCTTCTGGACTTCCAGCCACAGCTGGCCACACAGCTCCACCTGTAACTACCTGTC 746
QY 275 ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294
DB 747 ACTTCTCAGCTTCCACAGACCTCATTTCTACAGTTTTTTTACACGGGCTCGGCTACACTC 806
QY 295 GlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLys 314
DB 807 CAAAGCAATGGCTACAAACAGCAGTCTCTGACTACCACCTTTTCAGGCACCTACGAGCTCGAAA 866
QY 315 GlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsn 334
DB 867 GGCAGCTTAGAAACCATACCTCGTTTACAGAAATCTCCAACTAACTTTGAACACAGGGAAT 926
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FEATURES
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0D1054YH07"
              /tissue_type="PLACENTA Cot 25-NORMALIZED"
              /clone_lib="Homo sapiens PLACENTA Cot 25-NORMALIZED"
              /note="1st strand cDNA was primed with a NotI-oligo(dT)
              primer. Five prime end enriched, double-strand cDNA was
              digested with Not I and cloned into the Not I and EcoR V
              sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      8.5e-112      Length:      884
Score:          1383.00      Matches:      283
Percent Similarity: 97.3%      Conservative: 1
Best Local Similarity: 96.9%      Mismatches: 8
Query Match:      62.6%      Indels:      3
DB:              5      Gaps:      0

US-09-944-929-83 (1-431) x BX350141 (1-884)

RESULT 5
BX350141/c
LOCUS
DEFINITION
BX350141 Homo sapiens PLACENTA Cot 25-NORMALIZED Homo sapiens cDNA
clone CS0D1054YH07 3-PRIME, mRNA sequence.
ACCESSION
BX350141
VERSION
BX350141.1 GI:30365418
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 884)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6656.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA1023ZA03_CS02129_1&c=6656.r

FEATURES
  source      Location/Qualifiers
1..884        /organism="Homo sapiens"
              /mol_type="mRNA"
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              /clone="CS0D1054YH07"
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              /clone_lib="Homo sapiens PLACENTA Cot 25-NORMALIZED"
              /note="1st strand cDNA was primed with a NotI-oligo(dT)
              primer. Five prime end enriched, double-strand cDNA was
              digested with Not I and cloned into the Not I and EcoR V
              sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      8.5e-112      Length:      884
Score:          1383.00      Matches:      283
Percent Similarity: 97.3%      Conservative: 1
Best Local Similarity: 96.9%      Mismatches: 8
Query Match:      62.6%      Indels:      3
DB:              5      Gaps:      0

US-09-944-929-83 (1-431) x BX350141 (1-884)

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QY 125 SerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeuLeuHisGly 144
Db TCTTGGACCAAGAAATTTGGCAAGCCAGAGTTACCCAG-GAAGATTCTCTTACATGCC 824
QY 145 GlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyrSerLysProThr 164
Db TTTTTCACAGCAGTCACTCCCTCCAGCATCATCACAGATATTTCANAGCCACC 765
QY 165 AspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLys 184
Db AATATCTCATGAGAGACACACT-TCTCAGAAGTTTGATCCCTCAGATCACCTGGAGAA 706
QY 185 LeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSer 204
Db CTAATTAAGATGGATGAAGCAAGTCCCGAGCTCTTGTCTTATAAGGAAAGGCCATCT 646
QY 205 GlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnValSer 224
Db CAGAGTTCCACAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCCTGAAATGTGAGT 586
QY 225 AlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThrProLysPro 244
Db GCGCTCCAGCTACGCTGGCAGTGTCTTCACATACACCTCGCTACTCCAAAGCC 526
QY 245 AlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnProGlnLeu 264
Db GCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGACTTCCAGCCACAGCTG 466
QY 265 AlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIleSer 284
Db GCCACACAGCTCCACCTGTACCACTGTCTTCTCAGCCCTCCACGACCTCATTTCT 406
QY 285 ThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeuThr 304
Db ACAGTTTTTACACGGCTGCGGCTACACTCCCAAGCAATGGCTACACAGCATTTCTGAT 346
QY 305 ThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIleProPheThrGlu 324
Db ACCACCTTTCAGGCACCTACGGACTCAAAAGGCAGCTTAGAAACCATACCGTTTACAGAA 286
QY 325 IleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeuSerMetSer 344
Db ATCTCAAACTTAACTTTGAACACAGGGAATGTGTATTAACCTTCTGATGTCA 226
QY 345 AsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerPro 364
Db AATGTGGAGTCTTCACATATGAATAAACTGCTTCTGGGAAGGTAGGAGGCCAGTCCA 166
QY 365 GlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuProPheGluLysTrp 384
Db GGCAGTTCTCCACGGGCAGTGTTCAGAAATCAGTACGGCTTCCATTTGAAAATGG 106
QY 385 LeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
Db CTTCTTATCGGTCCTGCTCTTGTGTCTGTCTTCTGTCATAGGCTCGTCTCTCTCTG 46
QY 405 GlyArgIleLeuSerLeuSerLeuArgArgLysArg 416
Db GGTAGAATCTCTCGGAATCACTCCGCGAGGAACGT 10

RESULT 6
BO424639
LOCUS BO424639
DEFINITION AGENCOURT_7896936 NTH_MGC_72 Homo sapiens cDNA clone IMAGE:6159709
5', mRNA sequence.
ACCESSION BO424639
VERSION BO424639.1 GI:21119954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Hominidae; Homo.
```

REFERENCE

1 (bases 1 to 853)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13509 row: d column: 14
High quality sequence stop: 735.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 3,35e-111 Length: 853
Score: 1376.00 Matches: 272
Percent Similarity: 99.3% Conservative: 2
Best Local Similarity: 98.6% Mismatches: 0
Query Match: 62.2% Indels: 2
DB: 4 Gaps: 0

US-09-944-929-83 (1-431) x BQ424639 (1-853)

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Db TTTTTCACAGCAGTCACTCCCTCCAGCATCATCACAGATATTTCANAGCCACCAGTCA 76
QY 93 ProAsnCysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLys 112
Db CCCAATCTGCTACCTATTTTCTGTCCCAACGAGGAAGCTGTCCATTGAACACCAGCAA 136
QY 113 GlyLeuMetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSer 132
Db GGACTTATGAGTTACAGGATAATTACAGATTTTTCATCTTTGACAGAAATTTGCCAAGC 196
QY 133 GlnGluLeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrPro 152
Db CAAAGAGTTACCCAGGGAAGATTCTCTTTCATGCGCAATTTTCACAGCAGTCACTCCC 256
QY 153 LeuAlaHisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeu 172
Db CTAGCCCATCATCACAGATATTTCAGAGCCCACTATCTCATGGAGAGACACACTT 316
QY 173 SerGlnLysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSer 192
Db TCTCAGAAGTTTGGATCTCTCAGATCACCTGAGAAACTATTTAAGATGGATGAAGCAAGT 376
QY 193 AlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAsp 212
Db GCCCAGCTCTTGTCTTATAAGGAAAGGCCATCTCTCAGAGTTTCACATTTTCTCTCAT 436
QY 213 GlnGluIleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaVal 232
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QY 233 AlaSerProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAla 252
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Db 497 GCTTCTCCATACACCTCGGCTACTCAAAGCCGCGCACCTTCTACCCACCAATGCT 556
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 Qy 273 ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAla 292
 Db 617 ACTGTCACTTCTCAACCTCCACAGCCCTCATTTCTACAGTTTTCACAGGGCTGGGCT 676
 Qy 293 ThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrPheGlnAlaProThrAsp 312
 Db 677 ACACCTCAAGCAATGGCTACACAGAGTTCTGACTTACCCTTTTCAGGACCTACGGAC 736
 Qy 313 SerLysGlySerLeuGluThrThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThr 332
 Db 737 TCGAAGGCGAGCTTAGAACCACATACCGTTTACAGAAATCTCCCACTTAACCTTTGAACACA 796
 Qy 333 GlyAsnValThrAsn-ProThrAlaLeuSerMetSerAsnVal 346
 Db 797 GGGGAATGTATACCCCTACTGCACTTCTTATGTCAAATGTG 840

RESULT 7
 AL525434 1050 bp mRNA linear EST 24-MAR-2004
 LOCUS AL525434 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CSODC011YG07 5-PRIME, mRNA sequence.

ACCESSION AL525434
 VERSION AL525434.3 GI:45700628
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
 Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1050)
 Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:31063298.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: secre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6656.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSODC011AD04QP1&c=6656.r>.

FEATURES

source

Location/Qualifiers
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 /clone="CSODC011YG07"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
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ORIGIN

Alignment Scores:
 Pred. No.: 6, 92e-98 Length: 1050
 Score: 1227.50 Matches: 244
 Percent Similarity: 93.1% Conservative: 0
 Best Local Similarity: 93.1% Mismatches: 16
 Query Match: 55.5% Indels: 3

DB: 1 Gaps: 1
 US-09-944-929-83 (1-431) x AL525434 (1-1050)
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 Db 248 ATGTTCTTCGGGGGAGAGGGAGCTTGACCTTACACTTTTGGTAATAATTTGCTTCTCTGACA 307
 Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuIleSerLeuGluAspValIleAsp 40
 Db 308 CTAAGGCTGTCTAGTACAGAAATTCCTCAAAAGAGTCTAGAAGATGTTGTTCATTGAC 367
 Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
 Db 368 ATCCAGTCTACTCTCTTTCTAAGGGAATCAGAGGCAATGAGCCGATATATACATTCAACTCAA 427
 Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
 Db 428 GAAGACTGCATTAATTTCTGCTTCAACAAAACATATACAGGGGACAAAGCATGTTAC 487
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
 Db 488 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCCACTGCTACCTATTTCTGT 547
 Qy 101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
 Db 548 CCCAAGCAGGAGAGCCTGTTCATTTCAAAACAGCAAAAGGACTTATGAGTTACAGGATAATT 607
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
 Db 608 ACAGATTTTCCATCTTTTGACCAAAATTTGCCAAGCCAAGAGTTACCCCAAGAAATTTCT 667
 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
 Db 668 CTCTTACATGGCCAAATTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 727
 Qy 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
 Db 728 TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCTCAGAAAGTTGGATCTCTCAGAT 787
 Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200
 Db 788 CACCTCGAGAAACTATTTAAGATGGATGAACAAAGTCCCACTCTTTCCTTATAAGGAA 847
 Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeu-LeuPr 220
 Db 848 AAGGCCATTTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCC 907
 Qy 220 oGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAl 240
 Db 908 TGAATAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACMACTC--GG 965
 Qy 240 aThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSe 260
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 LOCUS AY401138
 DEFINITION Mus musculus HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY401138
 VERSION AY401138.1 GI:39757127
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
Location/Qualifiers

FEATURES

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Alignment Scores:

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US-09-944-929-83 (1-431) x AK171842 (1-2284)

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QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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RESULT 10

LOCUS

AK033526

DEFINITION

Mus musculus adult male colon cDNA, RIKEN full-length enriched

library, clone:903060P12 product:weakly similar to NT2RM100115

PROTEIN (Homo sapiens), full insert sequence.

ACCESSION

AK033526

VERSION

AK033526.1 GI:26329204

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

AK033526 2235 bp mRNA linear HTC 02-SEP-2005
Mus musculus adult male colon cDNA, RIKEN full-length enriched
library, clone:903060P12 product:weakly similar to NT2RM100115
PROTEIN (Homo sapiens), full insert sequence.

ACCESSION AK033526
VERSION AK033526.1 GI:26329204
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipipette sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
REFERENCE AUTHORS TITLE JOURNAL PUBMED	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, E.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Brownstein, M.J., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Maszarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 11217851
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CONSRMT TITLE JOURNAL PUBMED REFERENCE AUTHORS	Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851
	6 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, K., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liu, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiuira, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, E.T., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Bruscia, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y. FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group) The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005) 16141072
	7 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yaguchi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C. RIKEN Genome Exploration Research Group; Genome Science Group (Genome Network Project Core Group); FANTOM Consortium Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073
	8 (bases 1 to 2235) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tgawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES

source

Location/Qualifiers

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US-09-944-929-83 (1-431) x AK033526 (1-2235)

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Db 1210 CCCTTTCAAGGAGGCTCTACGCTGACT-----TCAGACCCGAGGCAC 1251

Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360

Db 1252 GGGAAAGCTCAACCTCAGAGTCTTCCATTACAACCAAGACTGCTTCTCGGAGGACAGG 1311

Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380

Db 1312 AGGTCAGTGTAGGCGCGCATCGCTGAACAAGGGTCCAAAAGCCAGCATGGCCTTTCA 1371

Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuLeuPheLeuValIleGly 400

Db 1372 TTTGAGAAGTGGCTTCTCATTTGGGACCTCCTCTTGTGTGTTTGTCTGTATAGGT 1431

Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuLeuArgLysArgTyrSerArgLeu 420

Db 1432 CTGCTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCGTAGGAAACGGTATTCAAGACTT 1491

Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1492 GACTACTTGATCAACGGGATCTATGTTGACATC 1524

RESULT 11
AK018635

LOCUS AK018635 2265 bp mRNA linear HTC 02-SEP-2005
 DEFINITION Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130017n16 product:weakly similar to NTR1W100115
 PROTEIN [Homo sapiens], full insert sequence.
 ACCESSION AK018635
 VERSION 1 GI:12859442
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCE Carninci, P. and Hayashizaki, Y.
 AUTHORS High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 10349636
 2
 REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 11042159
 3
 REFERENCE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Nakamura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 AUTHORS RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 11076861
 4
 REFERENCE Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
 AUTHORS RIKEN Genome Exploration Research Group Phase II team and the PANTOM Consortium
 JOURNAL Functional annotation of a full-length mouse cDNA collection
 NATURE 409 (6821), 685-690 (2001)
 PUBMED 11217851
 5
 REFERENCE Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oshino, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chochois, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Malais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempole, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kitahara, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 AUTHORS PANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team
 JOURNAL Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 NATURE 420 (6915), 563-573 (2002)
 PUBMED 12466851
 6
 REFERENCE Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Gatta, G., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashizaki, Y., Hensch, T. K., Hirokawa, N., Hill, D., Huminecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, D., Kanapin, A., Katoh, M., Kawasawa, Y., Keiso, J., Kitamura, H., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Fabriz, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempole, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiuira, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
 AUTHORS PANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)
 JOURNAL The transcriptional landscape of the mammalian genome
 SCIENCE 309 (5740), 1559-1563 (2005)
 PUBMED 16141072
 7
 REFERENCE Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Fang, K. C., Hallinan, J., Mattick, J., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Faghihi, M. A., Sandelin, A., Chalk, A. M., Mottagui-Fabriz, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

CONSTRM	RIKEN Genome Exploration Research Group; Genome Science Group (Genome Network Project Core Group); FANTOM Consortium
TITLE	Antisense transcription in the mammalian transcriptome
JOURNAL	Science 309 (5740), 1564-1566 (2005)
PUBMED	16141073
REFERENCE	8 (bases 1 to 2265)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers
FEATURES	<p>source</p> <p>1..2265</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="FANTOM DB:9130017N16"</p> <p>/db_xref="MGI:1897756"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="9130017N16"</p> <p>/sex="male"</p> <p>/tissue_type="cecum"</p> <p>/clone_lib="RIKEN full-length enriched mouse cDNA library"</p> <p>/dev_stage="adult"</p> <p>262..1506</p> <p>/note="unlabeled protein product; putative weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR Q9NW60, evidence: FASTV, 58.3%ID, 96.7%length, match=1104)"</p> <p>/codon_start=1</p> <p>/protein_id="BAB31319.1"</p>
CDS	
Alignment Scores:	
Pred. No.:	9,34e-92 Length: 2265
Score:	1164.50 Matches: 258
Percent Similarity:	68.4% Conservative: 37
Best Local Similarity:	59.9% Mismatches: 119
Query Match:	52.7% Indels: 17
DB:	6 Gaps: 6
US-09-944-929-83 (1-431) x AK018635 (1-2265)	
QY	1 MetPheGlyGlyGluGlySerLeuThrThrThrLeuValIleCysPheLeuThr 20
Db	262 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTCGTGCTCACTTCCTCTGACA 318
QY	21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLeuLysSerLeuGluAspValValIleAsp 40
Db	319 CCAAGGTCGCTGCTGCTCAGAACTGCCTCACCAGAGTCTAGAGACGTTGTTCATTGAC 378
QY	401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgLysArgLysArgLys 420
QY	41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
Db	379 ATCCAATCGTCGCTTTTCAAAGGCAATTCGAGGCAATGAGCCCATCTTGGCAACTCAG 438
QY	61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db	439 GAAGACTGTATCGGTGCTGCTGTTCAACAAGACATACAGGGGACAGGCATGTAAT 498
QY	81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
Db	499 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTCTGT 558
QY	101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
Db	559 CCCAGGAGGATGCTGTCGCTGAAGCCAGCCAGGGCCCTTGTGACCTACAGGCTCATC 618
QY	121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
Db	619 AGAGATTTTCCGCTGACCGGCTAATTCATCACTCCACAGTTTAACAACAGGAGAGTTT 678
QY	141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
Db	679 CTCTTACTTGACCATTCGTCACAGGAGCCACCCCTGGTTCGTACCCAGCAGGTTAC 738
QY	161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db	739 CCAAGCCACCCCGGCTGCTTGGAGTGACAGATCTTCTGAAGTCACACGCCCCCTG 798
QY	181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db	799 CACTTGGCAACACATCAAGGCTGATGAACAAGCATGTCAGCTC-----CCTGAAGAA 852
QY	201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
Db	853 AAAAGCCATCTCAGAGTTTACAGCTTCCCTCAGAACTAAAATGGCTCATCTGCTCCT 912
QY	221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisHisThrSerAla 240
Db	913 AAAACTGTGCGGACTCCACCTACCTAGCTAGCTGCTGCTCCCTCCGCTAAGCTCTCGCC 972
QY	241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db	973 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTTCAGTGACAGCTTAAGCTTTGAAG 1029
QY	261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
Db	1030 CAGAAGGAG---GCCACCACAGCATCACCTGTCCACACCGTACCTCGAAGCTCCAGGA 1086
QY	281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Db	1087 GTCCAGGGTCTACAAGTTTTTACA-----CCCGTGGTTACACATCAG 1128
QY	301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db	1129 GCAGCTTTGACTAACACCTTTTCAGGCAATACAGACTCCAAAAGGCATCTTAGAACCAATG 1188
QY	321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
Db	1189 CCCTTTTCAAGAGGCTCTACGCTGACT-----TCAGACCCGAGGCAC 1230
QY	341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db	1231 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCTCTGGGAGACAGG 1290
QY	361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db	1291 AGGGTCAGTGTAGGACGCGCATCGCTGAACAAGGGTCCAAAAGCCAGCATGGCGCTTCA 1350
QY	381 PheGluLysTrpLeuLeuIleGlySerLeuPheGlyValLeuPheLeuValIleGly 400
Db	1351 TTTGAGAAGTGGCTTCTCATTTGGGACCCCTCCTTTGTTGGTGTGTTTCTCGTAAATAGT 1410

Db	1411	CTCGTCTCTGGGTAGGATCGTGTGAGCCCTCCGTAGGAACGGTATTCAGACTT	1470
QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1471	GACTACTTGATCAACGGGATCTATGTGCATC	1503
RESULT 12			
AK046837			
LOCUS			
DEFINITION			
ACCESSION	AK046837	2265 bp mRNA linear	HTC 02-SEP-2005
VERSION	AK046837.1	GI:26338441	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohtsuki, S. and Hayashizaki, Y.		
CONSRMT			
TITLE	RIKEN Genome Exploration Research Group Phase II team and the FANTOM Consortium		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409 (6821), 685-690 (2001)		
PUBMED	11217851		
REFERENCE			
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,		

CONSRMT			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420 (6915), 563-573 (2002)		
PUBMED	12466851		
REFERENCE			
AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Banerji, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Humenick, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. P., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincilar, B., Sperling, S., Stupka, E., Sugliura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brucic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.		
CONSRMT			
TITLE	The transcriptional landscape of the mammalian genome		

Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
 Db 1289 AGGTCAGTGTAGGAGGCGCATCGTGCACAGGTCCTCAAAAGCCAGCATGCGCTTTCA 1348
 Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
 Db 1349 TTTGAGAAGTGGCTTCTCATTTGGGACCCCTCTTTGTGGTGTGTTTGTTCGTGTAATAGGT 1408
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuLeuArgArgIleGlyTyrSerArgLeu 420
 Db 1409 CTCGTCCTCTTTGGGTAGGATGCTGTGTGAAGCCCTCGTAGGAACCGGTATTTCAAGACTT 1468
 Qy 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431
 Db 1469 GACTACTTGATCAACGGGATCTATGTGTGACATC 1501

RESULT 13
 AK018660
 LOCUS
 DEFINITION Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403P13 product:weakly similar to NT2RM100115
 PROTEIN [Homo sapiens], full insert sequence.
 AK018660
 ACCESSION AK018660-1 GI:12858477
 VERSION
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 AUTHORS
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 10349636
 REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL 11042159
 PUBMED
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 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Toga, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL 11076861
 PUBMED
 REFERENCE 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saio, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saio, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavani, R., Fleschmann, W., Gaasterland, T., Gissi, C., King, B., Kouchi, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiyama, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.

and Hayashizaki, Y.
 RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
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 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kiyosawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 PANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420 (6915), 563-573 (2002)
 12466851
 6
 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Imbimbato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kohli, G., Krishnan, S. P., Kruger, A., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, P., Miyake, S., Moris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakamura, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, R., Sinclaire, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. K. F., Teasdale, R. D., Liu, B. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, N.

Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyAsnProThrAla 340
 ||||| ||||| :|||
 Db 1211 CCCTTTCAAGGAGCTCTACCTGACT-----TCAGACCCGAGGCAC 1252
 ||||| ||||| :|||
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360
 ||||| ||||| :|||
 Db 1253 GGGAAAGCTCACTCAGATCTTCATTCATCAACAAGACTGCTTCTCTGGAGACAGG 1312
 ||||| ||||| :|||
 Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
 ||||| ||||| :|||
 Db 1313 AGGTCTAGTGTAGGACGCGCATCGTGAACAAGGTCCTCAAAAGCCAGCATGGCTTTCA 1372
 ||||| ||||| :|||
 Qy 381 PheGluLysTyrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
 ||||| ||||| :|||
 Db 1373 TTTGAGAAGTGGCTCTCATTTGGGACCCCTCTTTGCTGGTGTGTTCTTCTGTAATAGGT 1432
 ||||| ||||| :|||
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgGlyLeuArgTyrSerArgLeu 420
 ||||| ||||| :|||
 Db 1433 CTCGGCTCTTTGGGTAGGATCTGTTGAAGCCCTCCGTAGGAACGGTATTCAAGACTT 1492
 ||||| ||||| :|||
 Qy 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431
 ||||| ||||| :|||
 Db 1493 GACTACTTGATCAACGGGATCTATGTTGCATC 1525
 ||||| ||||| :|||

RESULT 14
 AK033557
 LOCUS AK033557 2375 bp mRNA linear HTC 02-SEP-2005
 DEFINITION Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030619P12 product:weakly similar to NT2RM100115
 PROTEIN [Homo sapiens], full insert sequence.
 AK033557
 VERSION AK033557.1 GI:26329236
 KEYWORDS HTC; CAP trapper
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 10349636

2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 11042159

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 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 11076861

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 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaj, H., Kotsuki, S. and Hayashizaki, Y.
 RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 PUBMED 11217851

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 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oatso, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Ratetsky, N., Pillai, R., Pontius, J. D., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 TITLE PANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team
 ANALYSIS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420 (6915), 563-573 (2002)
 PUBMED 12465851

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 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Belsel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashizaki, Y., Hensch, T. K., Hirokawa, N., Hill, D., Humenicki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Moris, K., Mottagui-Fabriz, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A.,

Db 1140 CAGAGGAG---GCCACCACAGCATCACCTGTGTACCCACCGTGACCTCGAAGCTCCACGGA 1196

Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300

Db 1197 GTCCAGGGTCTACAAAGTTTATCA-----CCCGTGGTTACACATCAG 1238

Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320

Db 1239 GCAGCTTGACTAACACCTTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACATG 1298

Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340

Db 1299 CCTTTCAGGAGGCTCTACGCTGACT-----TCAGACCGAGGCAC 1340

Qy 341 LeuSerMetSerAsnValGluSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360

Db 1341 GGGAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1400

Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380

Db 1401 AGGTCAGTGTAGGAGCGCATCGCTGAAACAAGGGTCCAAAAAGCCAGCATGCGCTTCA 1460

Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuPheGlyValLeuPheLeuValIleGly 400

Db 1461 TTTGAGAGTGCTCTCTCATGGGACCTTCCTTTGGTGGTGTGTTCTGTAATAGGT 1520

Qy 401 LeuValLeuGluGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420

Db 1521 CTCGTCCTCTGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1580

Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1581 GACTACTTGATCAACGGGATCTATGTGATC 1613

RESULT 15

CV024215

LOCUS

DEFINITION

1439 Full length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC032998, mRNA sequence.

ACCESSION

CV024215

VERSION

CV024215.1 GI:51482047

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 623)

Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M. Human ORFome version 1.1: a platform for reverse proteomics Genome Res. 14 (10B), 2128-2135 (2004)

TITLE

JOURNAL

PUBLISHED

15489335

COMMENT

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ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers

FORWARD: ATGTTCCTTCGGGGAGAGGGAG

BACKWARD: TAGATGCCACATAGATCCCAT

Insert length: 623 Std Error: 122.00

Plate: 11036 row: 12 column: E

Seq primer: ACTGGCGCTGTTTACACAGCTGCTGACTGGGAAAC

High quality sequence start: 94

High quality sequence stop: 622

POLYA-No.

FEATURES

source

1..623

/Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="mixed"

/clone_lib="Full Length cDNA from the Mammalian Gene Collection"

/notes="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.: 4.35e-85 Length: 623

Score: 1079.00 Matches: 204

Percent Similarity: 99.0% Conservative: 1

Best Local Similarity: 98.6% Mismatches: 2

Query Match: 48.8% Indels: 0

DB: 10 Gaps: 0

US-09-944-929-83 (1-431) x CV024215 (1-623)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20

Db 1 ATGCTTCTCGGGGAGAGGGAGCTTGACTTTGGTAATTAATTTGCTTCCTGACA 60

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40

Db 61 CTAAAGCTGTCTGTAGTCAGAAATTGCTCTCAAAAGAGCTCTAGAGAGATGTTGTCTATGAC 120

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db 121 ATCCAGTCACTCTCTTCTAAGGGAATCAGAGGCAATCAGGCCATATATACCTCACTCAA 180

Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80

Db 181 GAAGACTGCACTTAATTTCTGCTGTTCACAAAAACATATCAGGGGACAAAGCATGTAAAC 240

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

Db 241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCAACTGCTACTATTTTCTGT 300

Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120

Db 301 CCCAACGAGGAGCGCTGCTCCATTGAAACACGACAAAGAGCTATGAGTTACAGGATAAT 360

Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

Db 361 ACAGATTTTCCATCTTTGACCATAAATTTGCCAAGCCAAAGATTTACCCAGGAAGATTCT 420

Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160

Db 421 CTCTTACATGGCCAATTTTCACAGCAGTCACTCCCTTAGCCCATCATCACACAGATTAT 480

Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180

Db 481 TCNAAGCCCAACCATATCTCTATGAGAGACACACTTTCTCAGAAAGTTGGATTCCTCAGAT 540

Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200

Db 541 CACTTGGAGAAACTATTTAAGATGATGAAGCATGTGCCAGCTCTCTTCTTATAAGGA 600

Qy 201 LysGlyHisSerGlnSerSer 207

Db 601 AAAGGGCATTTCTCAGAGTTCA 621

Search completed: September 20, 2007, 02:28:00
Job time : 6923 secs
